```
Contig ID
                   91963 1.R1010
5'-most EST
                   jC-at\overline{X}LIB327431P4g03b1
Method
                  BLASTN
NCBI GI
                  q4519194
BLAST score
                   244
E value
                   1.0e-134
                   389
Match length
                   91
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHM17, complete sequence
                   133797
Seq. No.
Contig ID
                   91975 1.R1010
5'-most EST
                  jC-at\overline{X}24047Q1E1A04a1
Seq. No.
                   133798
Contig ID
                   92000 1.R1010
5'-most EST
                   jC-atXLIB327432P1b01a1
                   BLASTX
Method
NCBI GI
                   q1171999
BLAST score
                   219
E value
                   1.0e-17
                   76
Match length
% identity
                   59
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 563243 (U16130)
                  phenylalanine ammonia lyase [Persea americana]
                   133799
Seq. No.
Contig ID
                   92015 1.R1010
5'-most EST
                   jC-atXLIB327432P1b12a1
Method
                   BLASTN
NCBI GI
                   g3282170
BLAST score
                   425
                   0.0e + 00
E value
                   437
Match length
% identity
                   83
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F8K4 sequence,
                   complete sequence [Arabidopsis thaliana]
                   133800
Seq. No.
                   92030 1.R1010
Contig ID
5'-most EST
                   jC-atXP2C77G9T7064a1
Method
                   BLASTX
                   q4512625
NCBI GI
BLAST score
                   517
                   2.0e-52
E value
```

138 Match length % identity 77

(AC004793) ESTs gb_T20423, gb_AA712864, gb_H76323 and NCBI Description gb Z25560 come from this gene. [Arabidopsis thaliana]

133801

92034 1.R1010 Contig ID

5'-most EST jC-atXLIB327430P1a07a1

133802 Seq. No.

Seq. No.

Contig ID 92043 1.R1010



jC-atXLIB327432P1d10a1 5'-most EST BLASTN Method g2462264 NCBI GI BLAST score 41 1.0e-13 E value Match length 53 % identity Cucumis sativus mRNA for patatin-like protein, partial NCBI Description 133803 Seq. No. 92045 1.R1010 Contig ID jC-atXLIB327432P1d11a1 5'-most EST BLASTX Method q3264778 NCBI GI 214 BLAST score E value 5.0e-17 Match length 54 76 % identity (AF072536) H-protein promoter binding factor-1 [Arabidopsis NCBI Description thaliana] 133804 Seq. No. 92052 1.R1010 Contig ID jC-atXLIB327432P1e07a1 5'-most EST 133805 Seq. No. 92073 1.R1010 Contig ID jC-atXLIB327432P1f11a1 5'-most EST BLASTN Method NCBI GI q3510337 110 BLAST score 8.0e-55 E value Match length 348 92 % identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K19E20, complete sequence [Arabidopsis thaliana] Seq. No. 133806 Contig ID 92084 1.R1010 jC-atXLIB327432P1g09a1 5'-most EST Method BLASTX NCBI GI q4115383 BLAST score 181 E value 4.0e-13 Match length 93 38 % identity (AC005967) receptor-like protein kinase [Arabidopsis NCBI Description thaliana] 133807 Seq. No. 92119 1.R1010 Contig ID jC-atXLIB327432P2c10a1 5'-most EST BLASTN Method q3449318 NCBI GI 285 BLAST score 1.0e-159 E value

421

Match length



```
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLF18, complete sequence [Arabidopsis thaliana]
Seq. No.
                  133808
                  92154 1.R1010
Contig ID
                  jC-atXLIB327432P2f06a2
5'-most EST
                  BLASTX
Method
                  g3402683
                  323
```

NCBI GI BLAST score 2.0e-29 E value Match length 157 % identity 49

(AC004697) patatin-like protein [Arabidopsis thaliana] NCBI Description

92156_1.R1010 Contig ID jC-atXLIB327432P2f08a1 5'-most EST Method BLASTN NCBI GI q4567259 BLAST score 296 E value 1.0e-165

Match length 545 99 % identity

Seq. No.

NCBI Description Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

133810 Seq. No.

Contig ID 92175 1.R1010

jC-atXLIB327432P2g10a2 5'-most EST

133809

Method BLASTN NCBI GI q3241926 BLAST score 282 1.0e-157 E value Match length 396 % identity 98

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MSG15, complete sequence [Arabidopsis thaliana]

133811 Seq. No.

Contig ID 92177 1.R1010

jC-atXLIB327432P2g11a2 5'-most EST

Seq. No. 133812

92191 1.R1010 Contig ID

jC-atXLIB327432P3a03a1 5'-most EST

Seq. No. 133813

92194 1.R1010 Contig ID

jC-atXLIB327432P3a05a1 5'-most EST

Method BLASTN NCBI GI g1785673 BLAST score 134 4.0e-69 E value Match length 317 91 % identity

NCBI Description A.thaliana mitochondrial genome, part A



Seq. No. 133814

Contig ID 92200 1.R1010

5'-most EST jC-atXLIB327440P1c12a1

Method BLASTX
NCBI GI g1903034
BLAST score 569
E value 2.0e-58
Match length 157
% identity 67

NCBI Description (X94625) amp-binding protein [Brassica napus]

Seq. No. 133815

Contig ID 92208 1.R1010

5'-most EST jC-atXP4C86D3T7015a1

Method BLASTN
NCBI GI g3063438
BLAST score 140
E value 2.0e-72
Match length 599
% identity 99

NCBI Description Complete sequence of Arabidopsis F22013, complete sequence

[Arabidopsis thaliana]

Seq. No. 133816

Contig ID 92219 1.R1010

5'-most EST jC-atXLIB327432P3b10a1

Method BLASTN
NCBI GI g2244829
BLAST score 240
E value 1.0e-132
Match length 416
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 133817

Contig ID 92223_1.R1010

5'-most EST jC-atXLIB327432P3b12a1

Method BLASTN
NCBI GI g2924732
BLAST score 368
E value 0.0e+00
Match length 497
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUA2, complete sequence [Arabidopsis thaliana]

Seq. No. 133818

Contig ID 92228 1.R1010

5'-most EST jC-atXLIB327432P3c04a1

Method BLASTX
NCBI GI g1046225
BLAST score 1122
E value 1.0e-123
Match length 221
% identity 99



(U21952) ethylene response sensor [Arabidopsis thaliana]

>gi_2623308 (AC002409) ethylene response sensor (ERS)
[Arabidopsis thaliana] >gi 1584365 prf 2122405A ERS gene

[Arabidopsis thaliana]

Seq. No. 133819

NCBI Description

Contig ID 92228 2.R1010

5'-most EST jC-atXP31C145F13T7d2

Method BLASTX
NCBI GI g1046225
BLAST score 784
E value 9.0e-84
Match length 171
% identity 89

NCBI Description (U21952) ethylene response sensor [Arabidopsis thaliana]

>gi_2623308 (AC002409) ethylene response sensor (ERS)
[Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene

[Arabidopsis thaliana]

Seq. No. 133820

Contig ID 92228 3.R1010

5'-most EST jC-atXP31C144G13T7d2

Method BLASTX
NCBI GI g1046225
BLAST score 552
E value 1.0e-56
Match length 132

% identity 83

NCBI Description (U21952) ethylene response sensor [Arabidopsis thaliana]

>gi_2623308 (AC002409) ethylene response sensor (ERS)
[Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene

[Arabidopsis thaliana]

Seq. No. 133821

Contig ID 92248 1.R1010

5'-most EST jC-atXLIB327432P3d04a1

Method BLASTN
NCBI GI g3869069
BLAST score 368
E value 0.0e+00
Match length 562
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 133822

Contig ID 92250 1.R1010

5'-most EST jC-atXLIB327432P3d05a1

Method BLASTX
NCBI GI g2911078
BLAST score 178
E value 8.0e-13
Match length 76
% identity 49

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 133823



Contig ID 92258 1.R1010

5'-most EST jC-atXLIB327432P3d09a1

Method BLASTX
NCBI GI g3033400
BLAST score 127
E value 6.0e-26
Match length 88
% identity 68

NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 133824

Contig ID 92288 1.R1010

5'-most EST jC-atXP92CH4B11T7096d1

Method BLASTN
NCBI GI g1785673
BLAST score 570
E value 0.0e+00
Match length 609
% identity 99

NCBI Description A.thaliana mitochondrial genome, part A

Seq. No. 133825

Contig ID 92288 2.R1010

5'-most EST jC-atXLIB327432P3f02b1

Method BLASTN
NCBI GI g1785673
BLAST score 635
E value 0.0e+00
Match length 742
% identity 92

NCBI Description A.thaliana mitochondrial genome, part A

Seq. No. 133826

Contig ID 92299 1.R1010

5'-most EST jC-atXLIB327432P3f09a1

Method BLASTX
NCBI GI g4467128
BLAST score 812
E value 7.0e-87
Match length 205
% identity 82

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 133827

Contig ID 92305 1.R1010

5'-most EST jC-atXLIB327432P3g01a1

Method BLASTX
NCBI GI g2980785
BLAST score 691
E value 9.0e-73
Match length 147
% identity 93

NCBI Description (AL022198) SERINE CARBOXYPEPTIDASE II - like protein

[Arabidopsis thaliana]

Seq. No. 133828

```
Contig ID
                  92318 1.R1010
5'-most EST
                  jC-atXLIB327432P3g09a1
Method
                  BLASTX
NCBI GI
                  q1653245
BLAST score
                  266
E value
                  4.0e-23
Match length
                  105
% identity
                  50
NCBI Description (D90912) hypothetical protein [Synechocystis sp.]
Seq. No.
                  133829
Contig ID
                  92322 1.R1010
5'-most EST
                  jC-atXLIB327432P3g11a1
```

Seq. No. 133830 Contig ID 92338 1.R1010

5'-most EST jC-atXLIB327440P3d08a1

Method BLASTN NCBI GI q4688614 BLAST score 329 E value 0.0e + 00Match length 414 % identity 95

NCBI Description Arabidopsis thaliana mRNA for D-type cyclin

133831 Seq. No.

Contig ID 92346 1.R1010

5'-most EST jC-atXLIB327432P3h12a1

Seq. No. 133832

Contig ID 92374 1.R1010

5'-most EST jC-atXLIB327432P4b05a1

Method BLASTX g2829885 NCBI GI BLAST score 252 E value 3.0e-47 Match length 102 % identity 94

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

133833 Seq. No.

92380 1.R1010 Contig ID

5'-most EST jC-atXLIB327432P4b08a1

Method BLASTN NCBI GI g2351069 BLAST score 602 E value 0.0e+00 779 Match length 98 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSH12, complete sequence [Arabidopsis thaliana]

Seq. No. 133834

Contig ID 92382 1.R1010

5'-most EST jC-atXLIB327432P4b09a1

Method BLASTX NCBI GI g140372



BLAST score 154 E value 9.0e-10 Match length 79 % identity 43

NCBI Description HYPOTHETICAL 86.0 KD PROTEIN IN GLK1-SRO9 INTERGENIC REGION

>gi_83159_pir__S19367 hypothetical protein YCL039w - yeast

(Saccharomyces cerevisiae)

Seq. No. 133835

Contig ID 92386 1.R1010

5'-most EST jC-atXLIB327432P4b11a1

Method BLASTX
NCBI GI g4454032
BLAST score 436
E value 5.0e-43
Match length 104
% identity 86

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 133836

Contig ID 92390_1.R1010

5'-most EST jC-atXLIB327432P4c01a1

Method BLASTX
NCBI GI g3859715
BLAST score 252
E value 2.0e-21
Match length 119
% identity 43

NCBI Description (AL033501) transketolase I [Candida albicans]

Seq. No. 133837

Contig ID 92392_1.R1010

5'-most EST jC-atXLIB327432P4c02a1

Method BLASTN
NCBI GI g2262155
BLAST score 260
E value 1.0e-144
Match length 395
% identity 100

NCBI Description DNA sequence of Arabidopsis thaliana BAC F5J6 from

chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No. 133838

Contig ID 92394 1.R1010

5'-most EST jC-atXLIB327432P4c03a1

Method BLASTN
NCBI GI g2290120
BLAST score 50
E value 6.0e-19
Match length 66
% identity 94

NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No. 133839

Contig ID 92419 1.R1010

5'-most EST jC-atXLIB327432P4d04a1



```
BLASTN
Method
                  g2462264
NCBI GI
BLAST score
                  45
E value
                  5.0e-16
Match length
                  53
% identity
                  96
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  133840
Seq. No.
Contig ID
                  92425 1.R1010
                  jC-atXLIB327432P4d08a1
5'-most EST
                  BLASTN
Method
                  g4220638
NCBI GI
BLAST score
                   61
                   3.0e-25
E value
Match length
                  227
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIF21, complete sequence [Arabidopsis thaliana]
                   133841
Seq. No.
Contig ID
                   92425 2.R1010
5'-most EST
                   jC-atXP96CH2C6T7b1
                   BLASTN
Method
                   q4220638
NCBI GI
BLAST score
                   77
                   5.0e-35
E value
Match length
                   263
                   84
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MIF21, complete sequence [Arabidopsis thaliana]
                   133842
Seq. No.
                   92429 1.R1010
Contig ID
                   jC-atXLIB327432P4d10a1
5'-most EST
                   BLASTX
Method
                   g2829880
NCBI GI
BLAST score
                   48
                   2.0e-40
E value
Match length
                   93
% identity
                   91
                   (AC002396) glucose-6-phosphate 1-dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   133843
Seq. No.
Contig ID
                   92435_1.R1010
                   jC-at\overline{X}LIB327432P4e01a1
5'-most EST
                   BLASTN
Method
                   g2290120
NCBI GI
BLAST score
                   54
```

2.0e-21 E value Match length 66 % identity 95

HIV-1 strain MO2 from USA, envelope glycoprotein (env) NCBI Description

gene, partial cds

Seq. No. 133844

Match length

% identity

73

92



```
92440 1.R1010
Contig ID
                   jC-atXLIB327432P4e04a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4314355
BLAST score
                   183
E value
                   3.0e-13
Match length
                   125
                   33
% identity
NCBI Description (AC006340) unknown protein [Arabidopsis thaliana]
Seq. No.
                   133845
Contig ID
                   92444 1.R1010
5'-most EST
                   jC-atXLIB327432P4e06a1
Method
                   BLASTN
                   g3047100
NCBI GI
BLAST score
                   374
                   0.0e+00
E value
                   418
Match length
                   97
% identity
NCBI Description Arabidopsis thaliana BAC F6N23
                   133846
Seq. No.
Contig ID
                   92460 1.R1010
                   jC-atXLIB327432P4f04a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3702323
BLAST score
                   265
E value
                   6.0e-23
Match length
                   111
                   54
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                   133847
Contig ID
                   92465 1.R1010
5'-most EST
                   jC-atXP70C221E5T7060a1
Method
                   BLASTN
NCBI GI
                   g3128143
BLAST score
                   297
E value
                   1.0e-166
Match length
                   405
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MTI20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   133848
Contig ID
                   92477 1.R1010
5'-most EST
                   jC-atXLIB327432P4q01a1
                   133849
Seq. No.
                   92479 1.R1010
Contig ID
                   jC-at\overline{X}LIB327432P4g02a1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2290120
BLAST score
                   45
                   6.0e-16
E value
```



NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No. 133850

Contig ID 92508 1.R1010

5'-most EST jC-atXLIB327432P4h08a1

Method BLASTN
NCBI GI g2290120
BLAST score 50
E value 5.0e-19
Match length 58

% identity 97
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No. 133851

Contig ID 92510 1.R1010

5'-most EST jC-atXLIB327432P4h09a1

Method BLASTN
NCBI GI g2351063
BLAST score 242
E value 1.0e-133
Match length 350
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCL19, complete sequence [Arabidopsis thaliana]

Seq. No. 133852

Contig ID 92535 1.R1010

5'-most EST jC-atXLIB327433P1a10a1

Method BLASTN
NCBI GI g2264302
BLAST score 328
E value 0.0e+00
Match length 438
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAC12, complete sequence [Arabidopsis thaliana]

Seq. No. 133853

Contig ID 92552_1.R1010 5'-most EST 92552_1.R1010

Method BLASTX
NCBI GI g3075398
BLAST score 365
E value 1.0e-34
Match length 111
% identity 76

NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]

Seq. No. 133854

Contig ID 92552 2.R1010

5'-most EST jC-atXLIB327433P1b07a1

Method BLASTN
NCBI GI g3075383
BLAST score 305
E value 1.0e-171



Match length 408 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 133855

Contig ID 92556 1.R1010

5'-most EST jC-atXLIB327433P1b09a1

Method BLASTN
NCBI GI g10782
BLAST score 44
E value 2.0e-15
Match length 63
% identity 92

NCBI Description Tetrahymena pyriformis gene for 26S large subunit ribosomal

RNA

Seq. No. 133856

92563 1.R1010 Contig ID g2062913 5'-most EST BLASTN Method NCBI GI q4539331 370 BLAST score 0.0e + 00E value 485 Match length 95 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13

(ESSA project)

Seq. No. 133857

Contig ID 92571 1.R1010

5'-most EST jC-atXLIB327439P3f04a2

Seq. No. 133858

Contig ID 92579 1.R1010

5'-most EST jC-atXLIB327433P1c09a1

Method BLASTN
NCBI GI g4756963
BLAST score 544
E value 0.0e+00
Match length 572
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23

(ESSA project)

Seq. No. 133859

Contig ID 92606 1.R1010

5'-most EST jC-atXLIB327433P1d12a1

Seq. No. 133860

Contig ID 92675_1.R1010

5'-most EST jC-atXLIB327433P1g12a1

Method BLASTN
NCBI GI g2760316
BLAST score 268
E value 1.0e-149
Match length 352



% identity 95

NCBI Description The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 133861

Contig ID 92703 1.R1010

5'-most EST jC-atXLIB327433P2a09a1

Method BLASTX
NCBI GI g4588001
BLAST score 101
E value 4.0e-28
Match length 82
% identity 77

NCBI Description (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 133862

Contig ID 92712 1.R1010

5'-most EST jC-atXLIB327433P2b06a1

Method BLASTN
NCBI GI 94510323
BLAST score 195
E value 1.0e-105
Match length 528
% identity 96

NCBI Description Arabidopsis thaliana BAC T7B11 from chromosome IV near 10

cM, complete sequence

Seq. No. 133863

Contig ID 92714 1.R1010

5'-most EST jC-atXP117C143B7T7a1

Method BLASTN
NCBI GI g2264321
BLAST score 414
E value 0.0e+00
Match length 555
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXM12, complete sequence [Arabidopsis thaliana]

Seq. No. 133864

Contig ID 92714_2.R1010

5'-most EST jC-atX24027Q1E1G11a1

Method BLASTN
NCBI GI g2264321
BLAST score 250
E value 1.0e-138
Match length 324
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXM12, complete sequence [Arabidopsis thaliana]

Seq. No. 133865

Contig ID 92715_1.R1010

5'-most EST jC-atXLIB327433P2b08a1

Method BLASTN NCBI GI g2342717



BLAST score 380 E value 0.0e+00 Match length 464 % identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 133866

Contig ID 92719 1.R1010

5'-most EST jC-atXLIB327433P2b12a1

Seq. No. 133867

Contig ID 92727 1.R1010

5'-most EST jC-atXLIB327433P2c08a1

Method BLASTN
NCBI GI g2191126
BLAST score 271
E value 1.0e-151
Match length 463
% identity 98

NCBI Description Arabidopsis thaliana BAC IG002N01

Seq. No. 133868

Contig ID 92741 1.R1010

5'-most EST jC-atXLIB327433P2d11a1

Seq. No. 133869

Contig ID 92746 1.R1010

5'-most EST jC-atXLIB327433P2e05a1

Method BLASTN
NCBI GI g2351065
BLAST score 400
E value 0.0e+00
Match length 412
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MHF15, complete sequence [Arabidopsis thaliana]

Seq. No. 133870

Contig ID 92759 1.R1010

5'-most EST jC-atXLIB327433P2f06a1

Seq. No. 133871

Contig ID 92784 1.R1010

5'-most EST jC-atXP87CG10A4T7b1

Method BLASTN
NCBI GI g1280610
BLAST score 39
E value 3.0e-12
Match length 39
% identity 100

NCBI Description Arabidopsis thaliana steroid reductase DET2 mRNA, complete

cds

Seq. No. 133872

Contig ID 92900 1.R1010

5'-most EST jC-atXLIB327439P1a09a1



Method BLASTN
NCBI GI g4006885
BLAST score 336
E value 0.0e+00
Match length 434
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 133873

Contig ID 92944 1.R1010

5'-most EST jC-atXLIB327439P1e04a2

Method BLASTX
NCBI GI g4314400
BLAST score 155
E value 4.0e-10
Match length 97
% identity 19

NCBI Description (AC006232) putative selenium-binding protein [Arabidopsis

thaliana]

Seq. No. 133874

Contig ID 92948 1.R1010

5'-most EST jC-atXLIB327439P1e08a1

Method BLASTN
NCBI GI g4454447
BLAST score 176
E value 4.0e-94
Match length 293
% identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC F5H14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 133875

Contig ID 92967 1.R1010

5'-most EST jC-atXLIB327439P1f09a1

Method BLASTN
NCBI GI g2290120
BLAST score 46
E value 2.0e-16
Match length 65
% identity 94

NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No. 133876

Contig ID 92974_1.R1010 5'-most EST 92739659

Method BLASTX
NCBI GI g4200165
BLAST score 270
E value 1.0e-23
Match length 70
% identity 74

NCBI Description (Y16262) neutral invertase [Daucus carota]

Seq. No. 133877



Contig ID 92975 1.R1010

5'-most EST jC-atXLIB327439P1g08a1

Method BLASTN
NCBI GI g2980787
BLAST score 80
E value 7.0e-37
Match length 414
% identity 64

NCBI Description Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2

(ESSAII project)

Seq. No. 133878

Contig ID 93051 1.R1010

5'-most EST jC-atXLIB327440P1a06a1

Seq. No. 133879

Contig ID 93057 1.R1010

5'-most EST jC-atXLIB327440P1a09a1

Method BLASTX
NCBI GI g2688842
BLAST score 281
E value 1.0e-24
Match length 92
% identity 59

NCBI Description (AF004830) serine palmitoyltransferase LCB2 subunit

[Cricetulus griseus]

Seq. No. 133880

Contig ID 93059 1.R1010

5'-most EST jC-atXLIB327440P1a10a1

Method BLASTX
NCBI GI g1755162
BLAST score 96
E value 3.0e-03
Match length 96
% identity 48

NCBI Description (U75192) germin-like protein [Arabidopsis thaliana]

Seq. No. 133881

Contig ID 93068 1.R1010

5'-most EST jC-atXLIB327440P1b04a1

Method BLASTX
NCBI GI g2887288
BLAST score 208
E value 2.0e-16
Match length 58
% identity 67

NCBI Description (AJ001810) mRNA cleavage factor I 25 kDa subunit [Homo

sapiens]

Seq. No. 133882

Contig ID 93077 1.R1010

5'-most EST jC-atXLIB327440P1c11a1

Method BLASTN
NCBI GI g4757395
BLAST score 338
E value 0.0e+00



Match length 406 % identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21L13, complete sequence

Seq. No. 133883

Contig ID 93103_2.R1010

5'-most EST jC-atXLIB327440P1d06a1

Method BLASTX
NCBI GI g3319344
BLAST score 561
E value 1.0e-57
Match length 130
% identity 85

NCBI Description (AF077407) contains similarity to UDP-glucoronosyl and

UDP-glucosyl transferases (Pfam: UDPGT.hmm, score: 85.94)

[Arabidopsis thaliana]

Seq. No. 133884

Contig ID 93106 1.R1010

5'-most EST jC-atXLIB327440Pld08a1

Method BLASTN
NCBI GI g3641843
BLAST score 122
E value 6.0e-62
Match length 122
% identity 100

NCBI Description Arabidopsis thaliana SKOR gene

Seq. No. 133885

Contig ID 93121 1.R1010

5'-most EST jC-atXLIB327440P1e11a1

Method BLASTX
NCBI GI g4539303
BLAST score 281
E value 6.0e-25
Match length 69
% identity 78

NCBI Description (AL049480) putative protein [Arabidopsis thaliana]

Seq. No. 133886

Contig ID 93133 1.R1010

5'-most EST jC-atXLIB327440P1f09a1

Method BLASTN
NCBI GI g2564048
BLAST score 406
E value 0.0e+00
Match length 431
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MKD15, complete sequence [Arabidopsis thaliana]

Seq. No. 133887

Contig ID 93177 1.R1010

5'-most EST jC-atXLIB327440P2b10a1

Seq. No. 133888



Contig ID 93182 1.R1010

5'-most EST jC-atXP118C143H5T7066a1

Method BLASTN
NCBI GI g3600045
BLAST score 309
E value 1.0e-173
Match length 537
% identity 95

NCBI Description Arabidopsis thaliana BAC F2P3

Seq. No. 133889

Contig ID 93182 2.R1010

5'-most EST jC-atXLIB327440P2c04a1

Method BLASTN
NCBI GI g3600045
BLAST score 300
E value 1.0e-168
Match length 447
% identity 93

NCBI Description Arabidopsis thaliana BAC F2P3

Seq. No. 133890

Contig ID 93191 1.R1010

5'-most EST jC-atXLIB327440P2d09a1

Seq. No. 133891

Contig ID 93208 1.R1010

5'-most EST jC-atXLIB327440P2f07a1

Method BLASTX
NCBI GI g2500139
BLAST score 265
E value 5.0e-23
Match length 87
% identity 55

NCBI Description PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1)

>gi_1653916_dbj_BAA18826_ (D90917) peptide chain release

factor [Synechocystis sp.]

Seq. No. 133892

Contig ID 93246 1.R1010

5'-most EST jC-atXLIB327440P4d08a1

Method BLASTX
NCBI GI g4006850
BLAST score 378
E value 2.0e-36
Match length 102
% identity 70

NCBI Description (Z99707) cytochrome like protein [Arabidopsis thaliana]

Seq. No. 133893

Contig ID 93247 1.R1010

5'-most EST jC-atXLIB327440P4d09a1

Method BLASTN
NCBI GI g2290120
BLAST score 40
E value 6.0e-13
Match length 66



% identity 94

NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No. 133894

Contig ID 93250 1.R1010

5'-most EST jC-atXLIB327440P4d11a1

Seq. No. 133895

Contig ID 93281 1.R1010

5'-most EST jC-atXLIB327401P1b02a1

Method BLASTN
NCBI GI g2656030
BLAST score 335
E value 0.0e+00
Match length 414
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUL8

Seq. No. 133896

Contig ID 93282 1.R1010

5'-most EST jC-atXLIB327401P1a04a1

Method BLASTN
NCBI GI g2264314
BLAST score 53
E value 1.0e-20
Match length 196
% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQK4, complete sequence [Arabidopsis thaliana]

Seq. No. 133897

Contig ID 93285_1.R1010

5'-most EST jC-atXLIB327401P1a12a1

Seq. No. 133898

Contig ID 93298 1.R1010

5'-most EST jC-atXLIB327401P1d07a1

Method BLASTX
NCBI GI g1362093
BLAST score 344
E value 3.0e-32
Match length 98
% identity 67

NCBI Description hypothetical protein (clone TPP15) - tomato (fragment)

>gi_924632 (U20595) unknown [Solanum lycopersicum]

Seq. No. 133899

Contig ID 93300_1.R1010

5'-most EST jC-atXLIB327401P1d09a1

Method BLASTX
NCBI GI g2245136
BLAST score 576
E value 2.0e-67
Match length 200
% identity 65



NCBI Description (Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]

Seq. No. 133900

Contig ID 93321_1.R1010

5'-most EST jC-atXLIB327401P4a02a2

Method BLASTX
NCBI GI g3292817
BLAST score 192
E value 2.0e-14
Match length 52
% identity 65

NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No. 133901

Contig ID 93357 1.R1010

5'-most EST jC-atXLIB327401P2e06a1

Seq. No. 133902

Contig ID 93357 3.R1010

5'-most EST jC-atXP95CH2B1T7088d1

Method BLASTX
NCBI GI g2920706
BLAST score 111
E value 3.0e-29
Match length 252
% identity 34

NCBI Description (Y13568) beta-xylosidase [Emericella nidulans]

Seq. No. 133903

Contig ID 93357_4.R1010

5'-most EST g937551
Method BLASTN
NCBI GI g2058275
BLAST score 58
E value 9.0e-24
Match length 128
% identity 90

NCBI Description A.thaliana atran2 gene

Seq. No. 133904

Contig ID 93358 1.R1010

5'-most EST jC-atXLIB327401P2e07a1

Method BLASTX
NCBI GI g112785
BLAST score 214
E value 7.0e-17
Match length 102
% identity 37

NCBI Description DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA

GLYCOSYLASE I, CONSTITUTIVE) (TAG I) >gi_67508_pir__DGECM1

3-methyladenine DNA glycosylase (EC 3.2.2.-) I -

Escherichia coli >gi_43030_emb_CAA27472_ (X03845) TAGI (aa

1-187) [Escherichia coli] $\geq gi_1 \overline{147920}$ (J $\overline{02606}$)

3-methyladenine-DNA glycosylase I (tag) [Escherichia coli] >gi_46687 (U00039) 3-methyladenine DNA glycosylase I, constitutive [Escherichia coli] >gi_1789971 (AE000432)





3-methyl-adenine DNA glycosylase I, constitutive [Escherichia coli]

Seq. No. 133905

Contig ID 93363_1.R1010

5'-most EST jC-atXLIB327401P2f10a1

Method BLASTN
NCBI GI g4218109
BLAST score 224
E value 1.0e-123
Match length 324
% identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16

(ESSAII project)

Seq. No. 133906

Contig ID 93381 1.R1010

5'-most EST jC-atXLIB327401P2h11a1

Method BLASTX
NCBI GI g4531444
BLAST score 289
E value 8.0e-26
Match length 68
% identity 87

NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No. 133907

Contig ID 93475 1.R1010

5'-most EST jC-atXLIB327404P4g02a1

Method BLASTN
NCBI GI g4510338
BLAST score 128
E value 1.0e-65
Match length 271
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC F2H17 genomic

sequence, complete sequence

Seq. No. 133908

Contig ID 93476 1.R1010

5'-most EST jC-atXLIB327404P4g03a1

Method BLASTN
NCBI GI g3128139
BLAST score 132
E value 7.0e-68
Match length 455
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MIK19, complete sequence [Arabidopsis thaliana]

Seq. No. 133909

Contig ID 93484_1.R1010

5'-most EST jC-atXLIB327404P4g08a1

Method BLASTN
NCBI GI g2244747
BLAST score 333
E value 0.0e+00



Match length 376 % identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 133910

Contig ID 93552 1.R1010

5'-most EST jC-atXLIB327405P3a02a1

Seq. No. 133911

Contig ID 93556 1.R1010

5'-most EST jC-atXLIB327405P3a04a1

Method BLASTN
NCBI GI g2462264
BLAST score 53
E value 1.0e-20
Match length 57
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 133912

Contig ID 93558 1.R1010

5'-most EST jC-atXP12C99P1T7031a1

Method BLASTN
NCBI GI g2264312
BLAST score 576
E value 0.0e+00
Match length 635
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOK16, complete sequence [Arabidopsis thaliana]

Seq. No. 133913

Contig ID 93572 1.R1010

5'-most EST jC-atXLIB327405P3a12a1

Method BLASTX
NCBI GI g2388582
BLAST score 401
E value 8.0e-39
Match length 81
% identity 94

NCBI Description (AC000098) Contains similarity to Rattus O-GlcNAc

transferase (gb U76557). [Arabidopsis thaliana]

Seq. No. 133914

Contig ID 93584 1.R1010

5'-most EST jC-atXLIB327405P3b08a1

Method BLASTN
NCBI GI g2623294
BLAST score 329
E value 0.0e+00
Match length 382
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T20B5 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 133915

```
93604 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327405P3c08a1
Method
                  BLASTX
NCBI GI
                  q3687224
BLAST score
                  100
                  2.0e-37
E value
                  103
Match length
% identity
                  83
                  (AC005169) putative N-acetyl-gamma-glutamyl-phosphate
NCBI Description
                  reductase [Arabidopsis thaliana]
                  133916
Seq. No.
Contig ID
                  93609 1.R1010
5'-most EST
                  jC-atXLIB327405P3c11a1
Method
                  BLASTN
NCBI GI
                  g2828278
BLAST score
                  475
E value
                  0.0e + 00
Match length
                  495
% identity
                 - ,99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16
                  (ESSAII project)
Seq. No.
                  133917
Contig ID
                  93628 1.R1010
5'-most EST
                  jC-atXLIB327405P3d10a1
Method
                  BLASTX
NCBI GI
                  q4056441
BLAST score
                  649
E value
                  5.0e-68
Match length
                  136
% identity
                  93
                  (AC005990) Similar to OBP32pep protein qb U37698 from
NCBI Description
                  Arabidopsis thaliana. [Arabidopsis thaliana]
                  133918
Seq. No.
Contig ID
                  93632 1.R1010
5'-most EST
                  jC-atXLIB327405P3d12a1
Seq. No.
                  133919
Contig ID
                  93636 1.R1010
5'-most EST
                  jC-atXLIB327405P3e02a1
Seq. No.
                  133920
Contig ID
                  93638 1.R1010
```

5'-most EST $jC-at\overline{X}LIB327405P3e03a1$

Method BLASTX g2498329 NCBI GI BLAST score 54 E value 2.0e-09 Match length 64 42

% identity

NCBI Description PATTERN FORMATION PROTEIN EMB30 >gi 2129665 pir S65571 pattern-formation protein GNOM - Arabidopsis thaliana >gi_1209633 (U36433) GNOM gene product [Arabidopsis

thaliana] >gi 1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918



[Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana]

Seq. No. 133921

Contig ID 93650 1.R1010

5'-most EST jC-atXLIB327405P3e11a1

Seq. No. 133922

Contig ID 93652 1.R1010

5'-most EST jC-atXLIB327405P3e12a1

Seq. No. 133923

Contig ID 93656 1.R1010

5'-most EST jC-atXLIB327405P3f02a1

Seq. No. 133924

Contig ID 93705 1.R1010

5'-most EST jC-atXLIB327405P3h04a1

Method BLASTN
NCBI GI g2618599
BLAST score 256
E value 1.0e-142
Match length 436
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBD2, complete sequence [Arabidopsis thaliana]

Seq. No. 133925

Contig ID 93718 1.R1010

5'-most EST jC-atXP86CG10B8T7b1

Method BLASTX
NCBI GI g2583124
BLAST score 721
E value 2.0e-76
Match length 137
% identity 100

NCBI Description (AC002387) 5-enolpyruvylshikimate-3-phosphate synthase

(EPSP) [Arabidopsis thaliana]

Seq. No. 133926

Contig ID 93737 1.R1010

5'-most EST jC-atXLIB327405P4b08a1

Method BLASTN
NCBI GI g2462264
BLAST score 54
E value 2.0e-21
Match length 58
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 133927

Contig ID 93740 1.R1010

5'-most EST jC-atXLIB327405P4b10a1

Method BLASTX
NCBI GI g3600035
BLAST score 205



E value 5.0e-16 Match length 135 % identity 79

NCBI Description (AF080119) contains similarity to GTP-binding proteins

[Arabidopsis thaliana]

Seq. No. 133928

Contig ID 93748 1.R1010

5'-most EST jC-atXLIB327405P4c04a1

Method BLASTX
NCBI GI g3201618
BLAST score 180
E value 5.0e-13
Match length 51
% identity 76

NCBI Description (AC004669) Sop2p-like protein [Arabidopsis thaliana]

Seq. No. 133929

Contig ID 93758 1.R1010

5'-most EST jC-atXLIB327428P1g05a2

Method BLASTX
NCBI GI g3033391
BLAST score 345
E value 2.0e-32
Match length 102
% identity 63

NCBI Description (AC004238) putative amino acid transporter [Arabidopsis

thaliana]

Seq. No. 133930

Contig ID 93758 2.R1010

5'-most EST jC-atXLIB327405P4c10a1

Method BLASTX
NCBI GI g3033391
BLAST score 45
E value 7.0e-12
Match length 61
% identity 58

NCBI Description (AC004238) putative amino acid transporter [Arabidopsis

thaliana]

Seq. No. 133931

Contig ID 93774 1.R1010

5'-most EST jC-alX24089Q1E1F03a1

Method BLASTX
NCBI GI g3914468
BLAST score 153
E value 6.0e-10
Match length 88
% identity 35

NCBI Description 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)

>gi_478411_pir__JQ2257 nuclear antigen 21D7 - carrot >gi_217911_dbj_BAA02696_ (D13434) 21D7 antigen [Daucus

carota]

Seq. No. 133932

Contig ID 93794 1.R1010



```
5'-most EST
                  jC-atXLIB327405P4e08a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  52
                  4.0e-20
E value
Match length
                  56
% identity
                  98
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
Seq. No.
                  133933
Contig ID
                  93815 1.R1010
5'-most EST
                  jC-atXLIB327405P4f08a1
Method
                  BLASTX
NCBI GI
                  q2498731
BLAST score
                  170
E value
                  1.0e-13
Match length
                  53
% identity
                  83
NCBI Description
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
                  >gi 1362013 pir S57611 zeta-crystallin homolog -
                  Arabidopsis thaliana >qi 886428 emb CAA89838 (Z49768)
                  zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.
                  133934
Contig ID
                  93817 1.R1010
5'-most EST
                  jC-atXLIB327405P4f09a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  49
                  2.0e-18
E value
Match length
                  53
% identity
                  98
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                  133935
Seq. No.
Contig ID
                  93835 1.R1010
5'-most EST
                  jC-atXLIB327405P4g08a1
                  BLASTN
Method
                  g2462264
NCBI GI
BLAST score
                  53
E value
                  1.0e-20
                  57
Match length
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  133936
                  93868_1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327406P2a08a1
Method
                  BLASTN
```

NCBI GI q1532162 BLAST score 380 0.0e + 00E value Match length 449 99 % identity

Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3, NCBI Description AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14 genes, partial cds, AT.I.24-7, ascorbate peroxidase





(ATHAPX1), EF-1alpha-A1, -A2 and -A3 (EF-1alpha) and AT.I

Seq. No. 133937

Contig ID 93874 1.R1010

5'-most EST jC-atXLIB327406P3a11a2

Method BLASTX
NCBI GI g1706958
BLAST score 517
E value 2.0e-52
Match length 101
% identity 95

NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

Seq. No. 133938

Contig ID 93888 1.R1010

5'-most EST jC-atXP2C75C8T7024a1

Method BLASTX
NCBI GI g1946360
BLAST score 572
E value 7.0e-59
Match length 103
% identity 100

NCBI Description (U93215) elicitor response element binding protein WRKY3

isolog [Arabidopsis thaliana]

Seq. No. - 133939

Contig ID 93911 1.R1010

5'-most EST jC-atXLIB327406P2c11a1

Method BLASTN
NCBI GI g2462264
BLAST score 50
E value 6.0e-19
Match length 54
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 133940

Contig ID 93932 1.R1010

5'-most EST jC-atXLIB327406P2d11a1

Method BLASTX
NCBI GI g119354
BLAST score 680
E value 2.0e-71
Match length 188
% identity 70

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185

phosphopyruvate hydratase (EC 4.2.1.11) - tomato

>gi_19281_emb_CAA41115_ (X58108) enolase [Lycopersicon

esculentum]

Seq. No. 133941

Contig ID 93961 1.R1010

5'-most EST jC-atXLIB327406P2f10a1

Method BLASTX
NCBI GI g1708971
BLAST score 152



E value 1.0e-09
Match length 71
% identity 41

NCBI Description (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR

(HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1) >gi 421871 pir S32156 mandelonitrile lyase (EC 4.1.2.10) -

black cherry >gi 288116 emb CAA51194 (X72617)

mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814) (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus serotina] >gi_1090776 prf_2019441A mandelonitrile lyase

[Prunus serotina]

Seq. No.

Contig ID 93975 1.R1010

5'-most EST jC-atXLIB327406P2g09a1

133942

Method BLASTN
NCBI GI g2462264
BLAST score 54
E value 2.0e-21
Match length 58

Match length 58 % identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 133943

Contig ID 93979 1.R1010

5'-most EST jC-atXLIB327438P4b04b2

Method BLASTX
NCBI GI g2960364
BLAST score 192
E value 2.0e-14
Match length 112
% identity 42

NCBI Description (AJ224986) cinnamoyl CoA reductase [Populus balsamifera

subsp. trichocarpa]

Seq. No. 133944

Contig ID 94132 1.R1010

5'-most EST jC-atXLIB327429P3g05b2

Method BLASTX
NCBI GI g4678233
BLAST score 690
E value 2.0e-72
Match length 169
% identity 80

NCBI Description (AC007265) unknown protein [Arabidopsis thaliana]

Seq. No. 133945

Contig ID 94137 1.R1010

5'-most EST jC-atXLIB327430P2a05a1

Method BLASTN
NCBI GI g4538895
BLAST score 155
E value 1.0e-81
Match length 441
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8

(ESSA project)



```
Seq. No.
                  133946
Contig ID
                  94142 1.R1010
5'-most EST
                  jC-atXLIB327430P2a11a1
Method
                  BLASTX
NCBI GI
                  q529353
BLAST score
                  133
E value
                  2.0e-16
Match length
                  82
% identity
                  (U12757) diphenol oxidase [Acer pseudoplatanus]
NCBI Description
                  133947
Seq. No.
Contig ID
                  94163 1.R1010
5'-most EST
                  jC-atXLIB327430P2c04a1
                  BLASTN
```

Method g2462264 NCBI GI BLAST score 54 2.0e-21 E value

Match length 54 100 % identity

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

133948 Seq. No. Contig ID 94165 1.R1010

5'-most EST jC-atXLIB327430P2c05a1

Method BLASTN NCBI GI q2462264 BLAST score 44 E value 2.0e-15 Match length 56 % identity 95

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 133949

Contig ID 94203 1.R1010

5'-most EST jC-atXLIB327430P2e06a1

Method BLASTN NCBI GI g2281081 BLAST score 320 E value 1.0e-180 Match length 324 % identity 100

Arabidopsis thaliana chromosome II BAC F18019 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

133950 Seq. No.

Contig ID 94213 1.R1010

5'-most EST jC-atXLIB327430P2e12a1

Method BLASTN NCBI GI g2924731 BLAST score 263 1.0e-146 E value Match length 271 99 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MSI17, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                   133951
```

Contig ID 94216 1.R1010

5'-most EST jC-atXLIB327430P1e05a1

Method BLASTN q2290120 NCBI GI BLAST score 56 E value 2.0e-22 Match length 64 97 % identity

NCBI Description HIV-1 strain MO2 from USA, envelope glycoprotein (env)

gene, partial cds

133952 Seq. No.

Contig ID 94216 3.R1010

5'-most EST jC-atXP66C210O11T7062a1

Seq. No. 133953

94252 1.R1010 Contig ID

5'-most EST q936088 Method BLASTX NCBI GI q4220462 BLAST score 674 E value 7.0e-71 Match length 175 % identity 79

NCBI Description (AC006216) Strong similarity to gb Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF 00046

and bZIP PF 00170 domains. [Arabidopsis thaliana]

Seq. No. 133954

Contig ID 94252 2.R1010

5'-most EST iC-atXLIB327439P3f03a2

Method BLASTX g4220462 NCBI GI BLAST score 601 E value 3.0e-62 Match length 111 % identity 100

NCBI Description (AC006216) Strong similarity to gb Z50851 HD-zip (athb-8)

gene from Arabidopsis thaliana containing Homeobox PF 00046

and bZIP PF 00170 domains. [Arabidopsis thaliana]

Seq. No. 133955

Contig ID 94261 1.R1010

5'-most EST jC-atXLIB327439P3d09a2

Method BLASTN NCBI GI g4589430 BLAST score 405 E value 0.0e+00Match length 421 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MLD14, complete sequence

133956 Seq. No.

Contig ID 94497 1.R1010



5'-most EST jC-atX22013Q1E1H01a1

Seq. No. 133957

Contig ID 94558 1.R1010

5'-most EST jC-atXP112C127F2T7a1

Method BLASTX
NCBI GI g4587528
BLAST score 155
E value 5.0e-22
Match length 126
% identity 44

NCBI Description (AC007060) Strong similarity to F19I3.2 gi_3033375 putative

berberine bridge enzyme from Arabidopsis thaliana BAC

gb AC004238. EST gb R90518 comes from this gene

Seq. No. 133958

Contig ID 94558 3.R1010

5'-most EST jC-atXLIB327401P4a03a1

Method BLASTX
NCBI GI g3033375
BLAST score 133
E value 6.0e-18
Match length 116
% identity 41

NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis

thaliana]

Seq. No. 133959

Contig ID 94571 1.R1010

5'-most EST jC-atXLIB327401P4c01a2

Method BLASTX
NCBI GI g3184281
BLAST score 477
E value 2.0e-49
Match length 134
% identity 68

NCBI Description (AC004136) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 133960

Contig ID 94579 1.R1010

5'-most EST jC-atXLIB327401P4c11a2

Method BLASTX
NCBI GI g3805845
BLAST score 184
E value 2.0e-13
Match length 79
% identity 43

NCBI Description (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 133961

Contig ID 94625 1.R1010

5'-most EST jC-atXP122C117N6T7044a1

Seq. No. 133962

Contig ID 94628 1.R1010

5'-most EST jC-atXLIB327406Pla04a1

Method BLASTN



NCBI GI g3702728 BLAST score 34 E value 2.0e-09 Match length 109 % identity 82

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19M13, complete sequence [Arabidopsis thaliana]

Seq. No. 133963

Contig ID 94930 1.R1010

5'-most EST jC-alX24084Q1E1F03a1

Method BLASTN
NCBI GI g4557061
BLAST score 280
E value 1.0e-156
Match length 487
% identity 84

NCBI Description Arabidopsis thaliana chromosome II BAC F23M2 genomic

sequence, complete sequence

Seq. No. 133964

Contig ID 94932 1.R1010

5'-most EST jC-atXLIB327437P3b08a1

Method BLASTN
NCBI GI g3402671
BLAST score 227
E value 1.0e-124
Match length 473
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC T16B24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 133965

Contig ID 95089 1.R1010

5'-most EST jC-atXLIB327437P2g03b2

Method BLASTN
NCBI GI g4191771
BLAST score 241
E value 1.0e-133
Match length 429
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC F3P11 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 133966

Contig ID 95106_1.R1010

5'-most EST jC-atXLIB327430P1a01a1

Method BLASTX
NCBI GI g3236235
BLAST score 299
E value 9.0e-27
Match length 108
% identity 62

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

>qi 4056501 (AC005896) unknown protein [Arabidopsis

thaliana]



```
Seq. No.
                  133967
Contig ID
                  95109 1.R1010
5'-most EST
                  jC-atXLIB327430P1a04a1
Method
                  BLASTX
NCBI GI
                  q4490316
BLAST score
                  453
E value
                  4.0e-45
Match length
                  92
% identity
                  100
NCBI Description
                  (AL035678) nucellin-like protein [Arabidopsis thaliana]
                  133968
Seq. No.
Contig ID
                  95111 1.R1010
5'-most EST
                  jC-atXLIB327430P1c04a1
Method
                  BLASTX
NCBI GI
                  q4263784
BLAST score
                  285
E value
                  2.0e-25
Match length
                  61
% identity
                  (AC006068) putative glycogenin-2 protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  133969
Contig ID
                  95145 1.R1010
5'-most EST
                  jC-atXLIB327430P1c03a1
Seq. No.
                  133970
Contig ID
                  95173 1.R1010
5'-most EST
                  jC-atXLIB327430P1d08a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  54
                  2.0e-21
E value
Match length
                  62
% identity
                  97
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  133971
Seq. No.
                  95196 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327430P1e11a1
Method
                  BLASTN
                  q3228389
NCBI GI
BLAST score
                  346
                  0.0e+00
E value
Match length
                  423
% identity
                  100
                  Genomic sequence for Arabidopsis thaliana BAC F17L21,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
```

Seq. No.

133972

Contig ID 95205 1.R1010

5'-most EST jC-atXLIB327430P1f07a1

Seq. No.

133973

Contig ID 95218 1.R1010

5'-most EST jC-atXLIB327430P1g06a1



```
Method
                  BLASTN
NCBI GI
                  g4063730
BLAST score
                  449
                  0.0e+00
E value
                  453
Match length
% identity
                  66
NCBI Description
                  Arabidopsis thaliana BAC F21J6 from chromosome V,
                  containing KNAT3 and mapping near 60.5 cM, complete
                  sequence [Arabidopsis thaliana]
                  133974
Seq. No.
Contig ID
                  95224 1.R1010
5'-most EST
                  jC-atXLIB327427P1f06a2
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  54
                  3.0e-21
E value
Match length
                  54
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  133975
Seq. No.
                  95238 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327430P1h05a1
Method
                  BLASTX
NCBI GI
                  q3834323
BLAST score
                  177
                  1.0e-12
E value
                  56
Match length
% identity
                  57
NCBI Description (AC005679) F9K20.25 [Arabidopsis thaliana]
                  133976
Seq. No.
Contig ID
                  95245 1.R1010
5'-most EST
                  jC-atXLIB327430P1h09a1
                  133977
Seq. No.
Contig ID
                  95277_1.R1010
5'-most EST
                  jC-atXLIB327401P4a12a2
Method
                  BLASTX
NCBI GI
                  g2760332
BLAST score
                  181
E value
                  3.0e-13
Match length
                  115
% identity
                  34
NCBI Description
                  (AC002130) F1N21.17 [Arabidopsis thaliana]
```

133978 Seq. No.

Contig ID 95289 1.R1010

5'-most EST jC-atXLIB327401P4b07a2

Method BLASTX NCBI GI q3522949 BLAST score 320 E value 2.0e-29 Match length 68 % identity 91

NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]

% identity

97



```
133979
Seq. No.
                  95336 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327406P3c04a2
Method
                  BLASTX
                  q3928543
NCBI GI
BLAST score
                  378
                  9.0e-89
E value
                  213
Match length
% identity
                  76
                  (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  133980
Seq. No.
Contig ID
                  95383 1.R1010
5'-most EST
                  jC-atXLIB327401P4h04a2
                  BLASTX
Method
                  q3128190
NCBI GI
BLAST score
                  449
                  1.0e-44
E value
Match length
                  82
                  100
% identity
                  (AC004521) putative beta-glucosidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  133981
Contig ID
                  95398 1.R1010
                  jC-atXLIB327406P3a01a2
5'-most EST
Method
                  BLASTX
                  q4204281
NCBI GI
BLAST score
                  231
                  9.0e-19
E value
Match length
                  112
% identity
                  40
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  133982
Seq. No.
                  95485 2.R1010
Contig ID
5'-most EST
                  jC-atXP124C121H16T7d1
                  BLASTN
Method
                  g3643588
NCBI GI
BLAST score
                  179
                  6.0e-96
E value
Match length
                  473
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC F17H15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  133983
Seq. No.
Contig ID
                  95509_1.R1010
                  jC-atXLIB327406P3f11a2
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2290120
BLAST score
                  56
E value
                  2.0e-22
Match length
                  64
```

15833

NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)



gene, partial cds

Seq. No. 133984

Contig ID 95513 1.R1010

5'-most EST jC-atXLIB327406P3g01a2

Method BLASTN
NCBI GI g3522932
BLAST score 321
E value 0.0e+00
Match length 379
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F14M4 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 133985

Contig ID 95524_1.R1010

5'-most EST jC-atXLIB327406P3g07a2

Method BLASTN
NCBI GI g2749918
BLAST score 145
E value 1.0e-75
Match length 345
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F3I6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 133986

Contig ID 95592 1.R1010

5'-most EST jC-atXLIB327406P4b11a2

Method BLASTX
NCBI GI g2511574
BLAST score 449
E value 1.0e-44
Match length 89
% identity 99

NCBI Description (Y13176) multicatalytic endopeptidase [Arabidopsis

thaliana] >gi_3421075 (AF043520) 20S proteasome subunit

PAB1 [Arabidopsis thaliana]

Seq. No. 133987

Contig ID 95598_1.R1010

5'-most EST jC-atXLIB327406P4c02a2

Method BLASTN
NCBI GI g3859113
BLAST score 404
E value 0.0e+00
Match length 432
% identity 98

NCBI Description Arabidopsis thaliana MS5-like protein mRNA, partial cds

Seq. No. 133988

Contig ID 95603_1.R1010

5'-most EST jC-atXLIB327406P4c05a2

Method BLASTX
NCBI GI g2252860
BLAST score 539
E value 4.0e-55



Match length 105 % identity 100

NCBI Description (AF013294) No definition line found [Arabidopsis thaliana]

Seq. No. 133989

Contig ID 95605 2.R1010

5'-most EST jC-atXLIB327406P4c06a2

Method BLASTN
NCBI GI g2252848
BLAST score 313
E value 1.0e-175
Match length 498
% identity 95

NCBI Description Arabidopsis thaliana BAC TM018A10

Seq. No. 133990

Contig ID 95612 1.R1010

5'-most EST jC-atXLIB327406P4c11a2

Method BLASTN
NCBI GI g3337347
BLAST score 460
E value 0.0e+00
Match length 464
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F13P17 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 133991

Contig ID 95648 1.R1010

5'-most EST jC-atXLIB327406P4e10a2

Method BLASTX
NCBI GI g2462754
BLAST score 256
E value 6.0e-22
Match length 127
% identity 40

NCBI Description (AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No. 133992

Contig ID 95650 1.R1010

5'-most EST jC-atXLIB327406P4e11a2

Method BLASTN
NCBI GI g2290120
BLAST score 53
E value 1.0e-20
Match length 60
% identity 98

NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No. 133993

Contig ID 95652_1.R1010

5'-most EST jC-atXP25C125G4T7078a1

Method BLASTX
NCBI GI g4091080
BLAST score 251
E value 3.0e-21



Match length % identity 69 (AF045571) nucleic acid binding protein [Oryza sativa] NCBI Description Seq. No. 133994 Contig ID 95656 1.R1010 5'-most EST jC-atXLIB327406P4f02a2 Method BLASTX NCBI GI q1665817 BLAST score 228 E value 1.0e-18 Match length 97 % identity 48 NCBI Description (D87466) Similar to S.cerevisiae hypothetical protein L3111 (S59316) [Homo sapiens] Seq. No. 133995 Contig ID 95660 1.R1010 5'-most EST jC-atXLIB327406P4f05a2 Method BLASTN NCBI GI g2182287 BLAST score 299 E value 1.0e-167 Match length 363 % identity 99 NCBI Description Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana] 133996 Seq. No. Contig ID 95663 1.R1010 5'-most EST jC-atXLIB327406P4f08a2 Method BLASTN NCBI GI q3985949 BLAST score 269 E value 1.0e-149 Match length 457 % identity 100 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MOB24, complete sequence [Arabidopsis thaliana] 133997 Seq. No. 95665 1.R1010 Contig ID 5'-most EST jC-atXLIB327406P4f09a2 Method BLASTX NCBI GI g4469014 BLAST score 279 E value 1.0e-24

Match length 84 % identity 68

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 133998

95667 1.R1010 Contig ID

5'-most EST iC-atXLIB327406P4f10a2

BLASTN Method NCBI GI g3643588 BLAST score 133



E value 2.0e-68 Match length 401 % identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 133999

Contig ID 95675_1.R1010

5'-most EST jC-atXLIB327406P4g03a2

Method BLASTX
NCBI GI g2304971
BLAST score 166
E value 2.0e-11
Match length 84
% identity 48

NCBI Description (U82828) ATM [Homo sapiens]

Seq. No. 134000

Contig ID 95688 1.R1010

5'-most EST jC-atXP26C128K22T7047a1

Method BLASTX
NCBI GI g3395432
BLAST score 550
E value 3.0e-56
Match length 108
% identity 100

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 134001

Contig ID 95697 1.R1010

5'-most EST jC-atXLIB327406P4h08a2

Seq. No. 134002

Contig ID 95705_1.R1010

5'-most EST jC-atXLIB327407P1a01a2

Method BLASTN
NCBI GI g2244788
BLAST score 374
E value 0.0e+00
Match length 457
% identity 94

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 134003

Contig ID 95709 1.R1010

5'-most EST jC-atXLIB327407P1a03a2

Method BLASTN
NCBI GI g2351069
BLAST score 170
E value 2.0e-90
Match length 359
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSH12, complete sequence [Arabidopsis thaliana]

Seq. No. 134004

```
95721 1.R1010
Contig ID
                  jC-atXLIB327407P1a09a2
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4680765
BLAST score
                  135
E value
                  1.0e-69
Match length
                  207
% identity
                  91
                  Arabidopsis thaliana BAC F14I23 from chromosome V near 69
NCBI Description
                  cM, complete sequence
                  134005
Seq. No.
Contig ID
                  95728 1.R1010
5'-most EST
                  jC-atXLIB327407P1b01a2
Seq. No.
                  134006
Contig ID
                  95736 1.R1010
5'-most EST
                  jC-atXLIB327407P1b06a2
Method
                  BLASTX
NCBI GI
                  q4406761
BLAST score
                  513
E value
                  7.0e-52
Match length
                  97
% identity
                  98
                  (AC006836) putative ubiquinone biosynthesis protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  134007
Contig ID
                  95742 1.R1010
5'-most EST
                  jC-atXLIB327407P1b09a2
                  BLASTX
Method
                  q3668075
NCBI GI
BLAST score
                  73
                  5.0e-50
E value
Match length
                  102
% identity
                  99
                  (AC004667) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  134008
Contig ID
                  95753 1.R1010
5'-most EST
                  jC-atXLIB327407P1c03a2
                  BLASTN
Method
NCBI GI
                  q3985952
BLAST score
                  312
                  1.0e-175
E value
Match length
                  399
```

% identity 99

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.

134009

Contig ID 95755 1.R1010 5'-most EST g2048296

Seq. No. Contig ID 134010

95760 2.R1010

5'-most EST $jC-at\overline{X}P12C103E16T7063a1$



Method BLASTX
NCBI GI g4567197
BLAST score 123
E value 5.0e-36
Match length 171
% identity 51

NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]

Seq. No. 134011

Contig ID 95760 3.R1010

5'-most EST jC-atXLIB327407P1c07a2

Method BLASTN
NCBI GI g531828
BLAST score 52
E value 4.0e-20
Match length 56
% identity 98

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 134012

Contig ID 95768 1.R1010

5'-most EST jC-atXLIB327407P1c11a2

Seq. No. 134013

Contig ID 95770 1.R1010

5'-most EST jC-atXLIB327407P1c12a2

Method BLASTX
NCBI GI g2462739
BLAST score 545
E value 7.0e-56
Match length 100
% identity 100

NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 134014

Contig ID 95772_1.R1010

5'-most EST jC-atXP86CG9G10T7b1

Method BLASTX
NCBI GI g4689328
BLAST score 377
E value 6.0e-36
Match length 130
% identity 58

NCBI Description (AF132552) BcDNA.GM01838 [Drosophila melanogaster]

Seq. No. 134015

Contig ID 95783 1.R1010

5'-most EST jC-atXLIB327407P1d09a2

Method BLASTX
NCBI GI g2688822
BLAST score 194
E value 1.0e-14
Match length 58
% identity 59

NCBI Description (U93272) pyrophosphate-dependent phosphofructo-1-kinase

[Prunus armeniaca]



Seq. No. 134016

Contig ID 95785 1.R1010

5'-most EST jC-atXLIB327407P1d10a2

Method BLASTX NCBI GI g3335372 BLAST score 350 E value 6.0e-33 Match length 117 % identity 57

NCBI Description (AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No. 134017

Contig ID 95795 1.R1010

5'-most EST jC-atXLIB327407P1e04a2

Method BLASTX NCBI GI q4220524 BLAST score 239 E value 6.0e-20 Match length 65 % identity 65

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 134018

95803 1.R1010 Contig ID

5'-most EST jC-atXLIB327407P1e08a2

84

Method BLASTN NCBI GI q4199934 BLAST score 64 E value 3.0e-27 Match length 199

% identity NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 134019

Contig ID 95814 1.R1010

5'-most EST jC-atXLIB327407P1f03a2

Method BLASTX NCBI GI g4587685 BLAST score 603 E value 1.0e-62 Match length 117 % identity 100

(AC007197) putative methylmalonate semi-aldehyde NCBI Description

dehydrogenase [Arabidopsis thaliana]

Seq. No. 134020

Contig ID 95819 1.R1010

5'-most EST jC-atXLIB327407P1f05a2

Seq. No. 134021

Contig ID 95842 1.R1010

5'-most EST jC-atXLIB327407P1g06a2

Method BLASTN NCBI GI g4432829 BLAST score 265 E value 1.0e-147



Match length 395 % identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134022

Contig ID 95853 1.R1010 5'-most EST 91517306

Seq. No. 134023

Contig ID 95855 1.R1010

5'-most EST jC-atXLIB327407P1h01a2

Method BLASTX
NCBI GI g3115852
BLAST score 313
E value 2.0e-28
Match length 72
% identity 89

NCBI Description (AL022023) putative protein [Arabidopsis thaliana]

Seq. No. 134024

Contig ID 95855 2.R1010

5'-most EST g906093
Method BLASTX
NCBI GI g3115852
BLAST score 436
E value 8.0e-50
Match length 128
% identity 85

NCBI Description (AL022023) putative protein [Arabidopsis thaliana]

Seq. No. 134025

Contig ID 95858 1.R1010

5'-most EST jC-atXLIB327407P1h03a2

Method BLASTN
NCBI GI g3150396
BLAST score 321
E value 1.0e-180
Match length 419
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134026

Contig ID 95862 1.R1010

5'-most EST jC-atXLIB327407P1h06a2

Method BLASTN
NCBI GI g2462264
BLAST score 48
E value 8.0e-18
Match length 52
% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 134027

Contig ID 95864 1.R1010

5'-most EST jC-atXP15C106M4T7028a1



Method BLASTX NCBI GI g2245107 BLAST score 422 E value 3.0e-41Match length 126 % identity 39 NCBI Description (297343) thioesterase homolog [Arabidopsis thaliana] 134028 Seq. No. 95864 2.R1010 Contig ID 5'-most EST jC-atXLIB327407P1h08a2 134029 Seq. No. Contig ID 95899 1.R1010 5'-most EST jC-atXLIB327414P4b06a2 Method BLASTX NCBI GI g3335345 BLAST score 229 E value 9.0e-19 Match length 155 % identity 38 NCBI Description (AC004512) Contains similarity to ABC transporter gb_1651790 from Synechocystis sp. gb_D90900. [Arabidopsis thaliana] 134030 Seq. No. 96027 1.R1010 Contig ID 5'-most EST $jC-at\overline{X}P117C143A5T7a1$ Method BLASTX NCBI GI g3953458 BLAST score 116 E value 4.0e-75 Match length 179 % identity 86 NCBI Description (AC002328) F20N2.3 [Arabidopsis thaliana] Seq. No. 134031 Contig ID 96069 1.R1010 5'-most EST $g1755\overline{4}$ Method BLASTX NCBI GI g1086989 BLAST score 345 E value 3.0e-32 Match length 82 % identity 84

NCBI Description (S79323) plasma membrane H(+)-ATPase [Vicia faba, Otafuku,

abaxial epidermis, guard cell protoplasts, Peptide, 963 aa]

[Vicia faba]

Seq. No. 134032

Contig ID 96115 1.R1010

5'-most EST jC-atXLIB327415P2e03a2

Seq. No. 134033

Contig ID 96136 1.R1010

5'-most EST jC-atXLIB327415P2f02a2

Method BLASTX



NCBI GI g4490332 BLAST score 157 E value 2.0e-10 Match length 48 % identity 62

NCBI Description (AL035656) putative protein [Arabidopsis thaliana]

Seq. No.

134034

Contig ID

96201 1.R1010

5'-most EST

jC-atXLIB327419P1a05a2

Seq. No.

134035

Contig ID

96217 1.R1010

5'-most EST

jC-atXLIB327419P3a12a2

Seq. No.

134036

Contig ID

96238 1.R1010

5'-most EST

 $jC-at\overline{X}LIB327419P3b12a2$

Method BLASTX
NCBI GI g1706103
BLAST score 289
E value 1.0e-25
Match length 198
% identity 41

NCBI Description

CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT) >gi 1363022 pir A56351

cleavage and polyadenylation specificity factor 100K chain - bovine >gi_599683_emb_CAA53535_ (X75931) Cleavage and Polyadenylation specificity factor (CPSF) 100kD subunit

[Bos taurus]

Seq. No.

134037

Contig ID

96283 1.R1010

5'-most EST

jC-atXLIB327419P3e03a2

Seq. No.

134038

Contig ID

96285 1.R1010

5'-most EST

jC-atXLIB327419P3e04a2

Method BLASTX
NCBI GI g4510396
BLAST score 352
E value 3.0e-33
Match length 126
% identity 55

NCBI Description (AC006587) hypothetical protein [Arabidopsis thaliana]

Seq. No.

134039

Contig ID

96289_1.R1010

5'-most EST

jC-atXLIB327419P3e06a2

Method BLASTN
NCBI GI g2462264
BLAST score 56
E value 2.0e-22
Match length 56

% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial



Seq. No. 134040

Contig ID 96289_3.R1010 5'-most EST g2047731

Seq. No. 134041

Contig ID 96304 1.R1010

5'-most EST jC-atXP62C201M15T7067a1

Method BLASTN
NCBI GI g2244788
BLAST score 401
E value 0.0e+00
Match length 551
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 134042

Contig ID 96318 1.R1010

5'-most EST jC-atXLIB327419P3f11a2

Method BLASTX
NCBI GI 94335714
BLAST score 397
E value 2.0e-38
Match length 81
% identity 100

NCBI Description (AC006248) putative glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 134043

Contig ID 96320 1.R1010

5'-most EST jC-atXLIB327419P3f12a2

Method BLASTN
NCBI GI g3702732
BLAST score 386
E value 0.0e+00
Match length 418
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGF10, complete sequence [Arabidopsis thaliana]

Seq. No. 134044

Contig ID 96362 1.R1010

5'-most EST jC-atXLIB327422P2a06a2

Method BLASTN
NCBI GI g531828
BLAST score 56
E value 1.0e-22
Match length 60
% identity 98

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 134045

Contig ID 96372 1.R1010

5'-most EST jC-atXLIB327422P2a11a2

Method BLASTX
NCBI GI g3402714
BLAST score 339



E value 1.0e-31 Match length 87 % identity 89

NCBI Description (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No. 134046

Contig ID 96381 1.R1010

5'-most EST jC-atXLIB327422P2b08a2

Method BLASTN
NCBI GI g4589445
BLAST score 219
E value 1.0e-119
Match length 614
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWL2, complete sequence

Seq. No. 134047

Contig ID 96439 1.R1010

5'-most EST jC-atXLIB327422P2e12a2

Method BLASTX
NCBI GI g1730588
BLAST score 150
E value 2.0e-09
Match length 75
% identity 41

NCBI Description HYPOTHETICAL 108.7 KD PROTEIN C14B1.5 IN CHROMOSOME III

Seq. No. 134048

Contig ID 96470 1.R1010

5'-most EST jC-atXLIB327422P3g05a2

Method BLASTX
NCBI GI g1076579
BLAST score 635
E value 4.0e-66
Match length 170
% identity 66

NCBI Description alcohol dehydrogenase homolog ADH3a - tomato

Seq. No. 134049

Contig ID 96472 1.R1010

5'-most EST jC-atXLIB327422P2g06a2

Method BLASTX
NCBI GI g4371293
BLAST score 274
E value 7.0e-24
Match length 101
% identity 64

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 134050

Contig ID 96472 2.R1010

5'-most EST jC-atXLIB327427P1h07a2

Method BLASTX
NCBI GI g4371293
BLAST score 169
E value 1.0e-11



Match length % identity 74

(AC006260) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 134051

Contig ID 96498 1.R1010

5'-most EST iC-atXLIB327422P2h10a2

Method BLASTX NCBI GI q2344889 BLAST score 476 E value 1.0e-47 Match length 110 % identity

NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 134052

Contig ID 96534 1.R1010

5'-most EST jC-atXLIB327422P3c02a2

BLASTN Method NCBI GI q531828 BLAST score 44 2.0e-15 E value Match length 52 % identity 96

Cloning vector pSport1, complete cds NCBI Description

Seq. No. 134053

Contig ID 96560 1.R1010

5'-most EST $jC-at\overline{X}LIB327422P3d04a2$

Method BLASTN NCBI GI q2462264 BLAST score 46 E value 1.0e-16 Match length 54 % identity 96

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

134054 Seq. No.

Contig ID 96566 1.R1010

5'-most EST jC-atXLIB327422P3d08a2

Method BLASTN NCBI GI q4589440 BLAST score 206 E value 1.0e-112 Match length 364 % identity 90

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MSD21, complete sequence

134055 Seq. No.

96588 1.R1010 Contig ID

5'-most EST jC-atX25013Q1E1D06a1

Method BLASTX NCBI GI g3024898 BLAST score 416 E value 2.0e-40 Match length 97



% identity 72

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE KIAA0224 (HA4657) >gi_1504028_dbj_BAA13213_ (D86977) similar to putative ATP-dependent RNA helicase K03H1.2 of C.elegans(S41025) [Homo sapiens] >gi 3123906

(AF038391) pre-mRNA splicing factor [Homo sapiens]

Seq. No.

Contig ID 96599 1.R1010

5'-most EST jC-atXLIB327422P3f04a2

134056

Method BLASTN
NCBI GI g2462264
BLAST score 46
E value 2.0e-16
Match length 54

Match length 54 % identity 96

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 134057

Contig ID 96673 1.R1010

5'-most EST jC-atXP4C88H7T7070a1

Method BLASTN
NCBI GI g4235150
BLAST score 578
E value 0.0e+00
Match length 614

Match length 614 % identity 99

NCBI Description Arabidopsis thaliana chromosome I BAC T25B24 genomic

sequence, complete sequence

Seq. No. 134058

Contig ID 96781 1.R1010

5'-most EST jC-atXLIB327427P3h01a2

Method BLASTN
NCBI GI g2462264
BLAST score 50
E value 6.0e-19
Match length 50
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 134059

Contig ID 96815 1.R1010

5'-most EST jC-atXLIB327427P3h07a2

Method BLASTN
NCBI GI g4691223
BLAST score 310
E value 1.0e-174
Match length 425
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15

(ESSA project)

Seq. No. 134060

Contig ID 96834_1.R1010

5'-most EST jC-atXLIB327427P4a07a2

Method BLASTN

E value

Match length

NCBI Description

% identity

0.0e + 00

440

47



```
NCBI GI
                  q2264307
BLAST score
                  240
                  1.0e-132
E value
Match length
                  436
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MED24, complete sequence [Arabidopsis thaliana]
                  134061
Seq. No.
Contig ID
                  96840 1.R1010
5'-most EST
                  jC-atXLIB327427P4a10a2
                  BLASTN
Method
NCBI GI
                  g531828
BLAST score
                  52
E value
                  4.0e-20
Match length
                  52
                  100
% identity
NCBI Description Cloning vector pSport1, complete cds
                  134062
Seq. No.
                  96880 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327427P4c06a2
Method
                  BLASTX
                  q2880049
NCBI GI
BLAST score
                  356
E value
                  1.0e-33
Match length
                  98
% identity
                  73
                  (AC002340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  134063
                  96898 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327427P4d05a2
                  BLASTX
Method
NCBI GI
                  g4006853
BLAST score
                  439
E value
                  2.0e-43
Match length
                  84
                  100
% identity
NCBI Description
                  (Z99707) cytochrome P450-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  134064
Contig ID
                  96900 1.R1010
5'-most EST
                  jC-atXLIB327427P4d06a2
Seq. No.
                  134065
Contig ID
                  96913 1.R1010
5'-most EST
                  jC-atXLIB327427P4f01a2
Method
                  BLASTN
NCBI GI
                  q2264321
BLAST score
                  396
```

15848

MXM12, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



Seq. No. 134066 Contig ID 96923_1.R1010

5'-most EST jC-atXLIB327427P4e06a2

Method BLASTN
NCBI GI 94757662
BLAST score 390
E value 0.0e+00
Match length 434
% identity 97

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10B6 from

chromosome I, complete sequence

Seq. No. 134067

Contig ID 96928 1.R1010

5'-most EST jC-atXLIB327427P4e10a2

Method BLASTN
NCBI GI g2244870
BLAST score 212
E value 1.0e-115
Match length 550
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 134068

Contig ID 96938 1.R1010

5'-most EST jC-atXLIB327427P4f03a2

Seq. No. 134069

Contig ID 96940_1.R1010

5'-most EST jC-atXLIB327427P4f04a2

Method BLASTN
NCBI GI 94325340
BLAST score 354
E value 0.0e+00
Match length 415
% identity 100

NCBI Description Arabidopsis thaliana BAC T1J1

Seq. No. 134070

Contig ID 96948 1.R1010

5'-most EST jC-atXLIB327427P4f08a2

Method BLASTN
NCBI GI g3510345
BLAST score 283
E value 1.0e-158
Match length 394
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No. 134071

Contig ID 97077_1.R1010 5'-most EST g2723090 Method BLASTX NCBI GI g4580389

```
BLAST score
E value
                  2.0e-41
Match length
                  93
% identity
                  87
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.
                  134072
                  97163 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327429P4d09a2
Method
                  BLASTN
NCBI GI
                  g3269280
BLAST score
                  515
E value
                  0.0e+00
Match length
                  580
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22
                  (ESSAII project)
Seq. No.
                  134073
Contig ID
                  97213 1.R1010
                  jC-atXLIB327429P4h05b2
                  BLASTX
                  g4314401
                  382
                  1.0e-36
```

5'-most EST Method NCBI GI BLAST score E value Match length 73 % identity 99

NCBI Description (AC006232) putative beta-1,3-glucanase [Arabidopsis

thaliana]

Seq. No. 134074 Contig ID 97215 1.R1010 5'-most EST jC-atXLIB327429P4h06b2

Method BLASTN NCBI GI g4159709

BLAST score 423 E value 0.0e+00Match length 423 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MLN21, complete sequence

134075 Seq. No. Contig ID 97224 1.R1010

5'-most EST jC-atXLIB327432P2a02a2

Method BLASTX NCBI GI g3540184 BLAST score 509 E value 1.0e-51 Match length 105 % identity 92

(AC004122) Similar to endoxylanases [Arabidopsis thaliana] NCBI Description

Seq. No.

134076

Contig ID 97239 1.R1010

5'-most EST jC-atXLIB327432P2a10a2

Method BLASTN



NCBI GI g3789706 BLAST score 607 E value 0.0e+00 Match length 611 % identity 100

NCBI Description Arabidopsis thaliana chromosome 1 BAC F15K9 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 134077

Contig ID 97245 1.R1010

5'-most EST jC-atXLIB327432P2b01a2

Method BLASTX
NCBI GI g2642433
BLAST score 540
E value 3.0e-55
Match length 107
% identity 100

NCBI Description (AC002391) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 134078

Contig ID 97259 1.R1010

5'-most EST jC-atXLIB327432P2b09a2

Method BLASTN
NCBI GI g2618677
BLAST score 199
E value 1.0e-108
Match length 396
% identity 94

NCBI Description Arabidopsis thaliana BAC F21B7 chromosome 1, complete

sequence [Arabidopsis thaliana]

Seq. No. 134079

Contig ID 97274 1.R1010

5'-most EST jC-atXLIB327432P2c06a2

Method BLASTN
NCBI GI g4519195
BLAST score 133
E value 1.0e-68
Match length 258
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MQC12, complete sequence

Seq. No. 134080

Contig ID 97286 1.R1010

5'-most EST jC-atXLIB327432P2c12b2

Method BLASTN
NCBI GI g1785729
BLAST score 337
E value 0.0e+00
Match length 377
% identity 91

NCBI Description A.thaliana mitochondrial genome, part B

Seq. No. 134081

Contig ID 97300 1.R1010



```
5'-most EST
                  jC-atXLIB327419P1f06a2
Seq. No.
                  134082
Contig ID
                  97300 2.R1010
                  jC-atXLIB327432P2d11a2
5'-most EST
Seq. No.
                  134083
Contig ID
                  97363 1.R1010
5'-most EST
                  jC-atXLIB327432P2h08a2
Seq. No.
                  134084
Contig ID
                  97367 1.R1010
5'-most EST
                  jC-atXLIB327432P2h11a2
Method
                  BLASTX
NCBI GI
                  q3142300
                  108
BLAST score
                  5.0e-19
E value
Match length
                  98
                  58
% identity
                  (AC002411) Contains similarity to pre-mRNA processing
NCBI Description
                  protein PRP39 gb L29224 from S. cerevisiae. ESTs gb R64908
                  and qb T88158, qb N38703 and qb AA651043 come from this
                  gene. [Arabidopsis thaliana]
                  134085
Seq. No.
Contig ID
                  97418 1.R1010
5'-most EST
                  jC-atXLIB327437P2c12b2
Method
                  BLASTN
NCBI GI
                  g2290120
BLAST score
                  52
E value
                  2.0e-20
Match length
                  72
                  93
% identity
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)
                  gene, partial cds
                  134086
Seq. No.
Contig ID
                  97604 1.R1010
5'-most EST
                  jC-atXLIB327437P3g05a2
Method
                  BLASTN
NCBI GI
                  g2760171
BLAST score
                  123
E value
                  2.0e-62
Match length
                  372
% identity
                  87
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MPA24, complete sequence [Arabidopsis thaliana]
                  134087
```

Seq. No.

Contig ID 97662 1.R1010

5'-most EST jC-atXP53C183019T7091d1

Method BLASTX NCBI GI q3386614 BLAST score 398 1.0e-38 E value Match length 133 % identity 49



NCBI Description (AC004665) putative transcription factor SF3 [Arabidopsis thaliana]

Seq. No. 134088

Contig ID 97774 1.R1010

5'-most EST jC-atXLIB327438P4b09b2

Method BLASTN
NCBI GI g3985950
BLAST score 285
E value 1.0e-159
Match length 353
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MPI10, complete sequence [Arabidopsis thaliana]

Seq. No. 134089

Contig ID 97859 1.R1010

5'-most EST jC-atXLIB327438P4g06b2

Method BLASTN
NCBI GI g2351069
BLAST score 326
E value 0.0e+00
Match length 510
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSH12, complete sequence [Arabidopsis thaliana]

Seq. No. 134090

Contig ID 98080 1.R1010

5'-most EST jC-atXLIB327418P3d07a2

Method BLASTN
NCBI GI g3738313
BLAST score 332
E value 0.0e+00
Match length 422
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T29E15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134091

Contig ID 98103 2.R1010

5'-most EST g560139
Method BLASTX
NCBI GI g4741197
BLAST score 180
E value 3.0e-13
Match length 83
% identity 41

NCBI Description (AL049746) aldose 1-epimerase-like protein [Arabidopsis

thaliana]

Seq. No. 134092

Contig ID 98104_1.R1010

5'-most EST jC-atXLIB327418P3f11a2

Method BLASTX
NCBI GI g3851586
BLAST score 301



E value 3.0e-27 Match length 75 % identity 76

NCBI Description (AF092564) chromosome-associated protein-C [Homo sapiens]

Seq. No. 134093

Contig ID 98127 1.R1010

5'-most EST jC-atXLIB327419P1a02a2

Method BLASTN
NCBI GI 94006885
BLAST score 408
E value 0.0e+00
Match length 428
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 134094

Contig ID 98132 1.R1010

5'-most EST jC-atXLIB327419P1a08a2

Method BLASTN
NCBI GI g2264304
BLAST score 355
E value 0.0e+00
Match length 449
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBG8, complete sequence [Arabidopsis thaliana]

Seq. No. 134095

Contig ID 98134 1.R1010

5'-most EST jC-atXLIB327419P1a10a2

Method BLASTX
NCBI GI g3522961
BLAST score 246
E value 8.0e-21
Match length 70
% identity 71

NCBI Description (AC004411) putative pto kinase [Arabidopsis thaliana]

Seq. No. 134096

Contig ID 98140_1.R1010

5'-most EST jC-atXLIB327419P1b04a2

Method BLASTX
NCBI GI g549975
BLAST score 182
E value 2.0e-13
Match length 35
% identity 97

NCBI Description (U12858) nucleosome assembly protein I-like protein;

similar to mouse nap I, PIR Accession Number JS0707

[Arabidopsis thaliana]

Seq. No. 134097

Contig ID 98143 1.R1010

5'-most EST jC-atXLIB327419P1b07a2

Method BLASTX



NCBI GI g3219815 BLAST score 143 E value 1.0e-08 Match length 57 % identity 49

NCBI Description MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT

TIM22 HOMOLOG >gi 2104453 emb CAB08780 (Z95397) unknown

[Schizosaccharomyces pombe]

Seq. No. 134098

Contig ID 98144 1.R1010

5'-most EST jC-atXP112C129M21T7a1

Method BLASTX
NCBI GI g4510406
BLAST score 236
E value 2.0e-19
Match length 73
% identity 63

NCBI Description (AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No. 134099

Contig ID 98145 1.R1010

5'-most EST jC-atXLIB327419P1b10a2

Seq. No. 134100

Contig ID 98149 1.R1010

5'-most EST jC-atXLIB327419P1c02a2

Method BLASTN
NCBI GI g3402671
BLAST score 37
E value 5.0e-11
Match length 45
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC T16B24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134101

Contig ID 98152 2.R1010

5'-most EST jC-atXLIB327419P1c05a2

Method BLASTX
NCBI GI g4206122
BLAST score 367
E value 7.0e-35
Match length 114
% identity 64

NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum

crystallinum]

Seq. No. 134102

Contig ID 98173 1.R1010

5'-most EST g2047\(\overline{5}\)11

Method BLASTN

NCBI GI g2351073

BLAST score 197

E value 1.0e-106

Match length 578

% identity 97



Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No. 134103

NCBI Description

Contig ID 98173 3.R1010

5'-most EST jC-atXLIB327419P1e04a2

Method BLASTN
NCBI GI g2351073
BLAST score 256
E value 1.0e-142
Match length 423
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No. 134104

Contig ID 98177 1.R1010

5'-most EST jC-atXLIB327419P1e09a2

Method BLASTN
NCBI GI g3293583
BLAST score 393
E value 0.0e+00
Match length 429
% identity 98

NCBI Description Arabidopsis thaliana BAC T27D20

Seq. No. 134105

Contig ID 98186 1.R1010

5'-most EST jC-atXLIB327419P1f07a2

Method BLASTN
NCBI GI g4220510
BLAST score 102
E value 6.0e-50
Match length 358
% identity 91

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18

(ESSAII project)

Seq. No. 134106

Contig ID 98187 1.R1010

5'-most EST jC-atXLIB327419P1f08a2

Method BLASTN
NCBI GI 94589433
BLAST score 370
E value 0.0e+00
Match length 422
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNI5, complete sequence

Seq. No. 134107

Contig ID 98188_1.R1010

5'-most EST jC-atXLIB327419P1f09a2

MethodBLASTXNCBI GIg584867BLAST score428E value4.0e-42



Match length 106 % identity 74

NCBI Description CYTOCHROME P450 77A2 (CYPLXXVIIA2) (P-450EG5)

>gi_481959_pir__S40266 gene CYP77A2 protein - eggplant
>gi_542071_pir__S41598 cytochrome P450 77A2 - eggplant
>gi_438241_emb_CAA50646_ (X71655) CYP77A2 [Solanum

melongena]

Seq. No. 134108

Contig ID 98189 1.R1010

5'-most EST jC-atXLIB327419P1f10a2

Method BLASTX
NCBI GI g1361974
BLAST score 213
E value 2.0e-23
Match length 116
% identity 50

NCBI Description cysteine proteinase - clove pink (fragment) >gi_595986

(U17135) cysteine proteinase [Dianthus caryophyllus]

Seq. No. 134109

Contig ID 98195_1.R1010

5'-most EST jC-atXLIB327419P1g04a2

Method BLASTX
NCBI GI g4056465
BLAST score 283
E value 4.0e-25
Match length 78
% identity 67

NCBI Description (AC005990) F508.40 [Arabidopsis thaliana]

Seq. No. 134110

Contig ID 98197_1.R1010

5'-most EST jC-atXP25C123H15T7059a1

Method BLASTN
NCBI GI g2462264
BLAST score 52
E value 5.0e-20
Match length 52
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 134111

Contig ID 98197 2.R1010

5'-most EST jC-atXLIB327419P1g06a2

Seq. No. 134112

Contig ID 98200 1.R1010

5'-most EST jC-atXLIB327419P1g09a2

Method BLASTN
NCBI GI g4589430
BLAST score 303
E value 1.0e-170
Match length 502
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MLD14, complete sequence



134113

Seq. No.

```
98203 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327419P1g12a2
Seq. No.
                   134114
Contig ID
                   98207 1.R1010
5'-most EST
                   jC-atXLIB327419P1h05a2
Seq. No.
                   134115
                   98211 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327419P1h09a2
Seq. No.
                   134116
Contig ID
                   98335 1.R1010
5'-most EST
                   iC-atXP83C241A21T7065a1
Method
                   BLASTX
NCBI GI
                   q3980396
BLAST score
                   454
E value
                   3.0e-45
Match length
                   82
                   98
% identity
NCBI Description
                  (AC004561) putative C-4 sterol methyl oxidase [Arabidopsis
                   thaliana]
Seq. No.
                   134117
Contig ID
                   98343 1.R1010
5'-most EST
                   jC-atXLIB327419P4e08a2
Method
                   BLASTX
NCBI GI
                   g4544449
BLAST score
                   104
                   2.0e-57
E value
Match length
                   126
% identity
                   98
NCBI Description (AC006592) putative peroxidase [Arabidopsis thaliana]
Seq. No.
                   134118
                   98359 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327419P4g10a2
Method
                  BLASTX
NCBI GI
                   g4512651
BLAST score
                   232
E value
                   5.0e-19
Match length
                   77
% identity
                   53
NCBI Description
                  (AC007048) putative tyrosine transaminase [Arabidopsis
                   thaliana]
Seq. No.
                   134119
                   98368 1.R1010
Contig ID
5'-most EST
                   jC-at\overline{X}P9C93M5T7s1
Method
                  BLASTN
                   g4662628
NCBI GI
BLAST score
                  193
E value
                   1.0e-104
Match length
                   365
% identity
                   95
```



NCBI Description Arabidopsis thaliana chromosome II BAC F27010 genomic sequence, complete sequence

Seq. No. 134120

Contig ID 98375 1.R1010

5'-most EST jC-atXLIB327420P2a05a2

Method BLASTN
NCBI GI g2290120
BLAST score 58
E value 9.0e-24
Match length 62
% identity 98

NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No. 134121

Contig ID 98378 1.R1010

5'-most EST jC-atXLIB327420P2a08a2

Method BLASTN
NCBI GI g3868723
BLAST score 269
E value 1.0e-149
Match length 383
% identity 93

NCBI Description Arabidopsis thaliana chromosome V map 60.5 cM, complete

sequence [Arabidopsis thaliana]

Seq. No. 134122

Contig ID 98383 1.R1010

5'-most EST jC-atXLIB327420P2b03a2

Method BLASTX
NCBI GI g2245029
BLAST score 551
E value 1.0e-56
Match length 115
% identity 90

NCBI Description (Z97341) limonene cyclase homolog [Arabidopsis thaliana]

Seq. No. 134123

Contig ID 98384 1.R1010

5'-most EST jC-atXLIB327420P2b04a2

Method BLASTX
NCBI GI g2129471
BLAST score 260
E value 2.0e-22
Match length 59
% identity 83

NCBI Description glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)

precursor - Scotch pine >gi 1100223 (L32560)

glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]

Seq. No. 134124

Contig ID 98389 1.R1010

5'-most EST jC-atXLIB327420P2b08a2

Method BLASTX NCBI GI g3328231 BLAST score 296



E value 1.0e-26
Match length 117
% identity 51

NCBI Description (AF051784) 14S cohesin SMC1 subunit; SMC protein [Xenopus

laevis]

Seq. No. 134125

Contig ID 98390 1.R1010

5'-most EST jC-atXLIB327420P2b09a2

Method BLASTX
NCBI GI g4544387
BLAST score 566
E value 2.0e-58
Match length 109
% identity 94

NCBI Description (AC007047) putative purple acid phosphatase precursor

[Arabidopsis thaliana]

Seq. No. 134126

Contig ID 98392 1.R1010

5'-most EST jC-atXLIB327420P2b11a2

Method BLASTN
NCBI GI g2245073
BLAST score 227
E value 1.0e-124
Match length 373
% identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 134127

Contig ID 98400_1.R1010

5'-most EST jC-atXLIB327420P2c07a2

Method BLASTN
NCBI GI g3228389
BLAST score 270
E value 1.0e-150
Match length 431
% identity 98

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17L21,

complete sequence [Arabidopsis thaliana]

Seq. No. 134128

Contig ID 98415 1.R1010

5'-most EST jC-atXLIB327420P2d09a2

Method BLASTN
NCBI GI g2264312
BLAST score 295
E value 1.0e-165
Match length 468
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOK16, complete sequence [Arabidopsis thaliana]

Seq. No. 134129

Contig ID 98430 1.R1010

5'-most EST jC-atXLIB327420P2e12a2



Method BLASTN
NCBI GI g4519193
BLAST score 397
E value 0.0e+00
Match length 417
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC11, complete sequence

Seq. No. 134130

Contig ID 98445 1.R1010

5'-most EST jC-atXLIB327420P2g04a2

Method BLASTN
NCBI GI g2642152
BLAST score 205
E value 1.0e-111
Match length 418
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T517 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134131

Contig ID 98464 1.R1010

5'-most EST jC-atXLIB327420P2h12a2

Method BLASTX
NCBI GI g399028
BLAST score 179
E value 6.0e-13
Match length 77
% identity 45

NCBI Description ALLIIN LYASE PRECURSOR (ALLIINASE) (CYSTEINE SULPHOXIDE

LYASE) >gi_419808_pir__ S29302 alliin lyase (EC 4.4.1.4) precursor - garlic >gi_16109_emb_CAA78268_ (Z12622)

precursor alliinase [Allium sativum]

Seq. No. 134132

Contig ID 98594 1.R1010

5'-most EST jC-atXP37C156F24T7d2

Method BLASTX
NCBI GI g3451078
BLAST score 261
E value 1.0e-42
Match length 140
% identity 72

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 134133

Contig ID 98594 2.R1010

5'-most EST jC-atXP37C156F24T7s2

Method BLASTN
NCBI GI g3451055
BLAST score 335
E value 0.0e+00
Match length 404
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20

(ESSAII project)



```
134134
Seq. No.
Contig ID
                  98670 1.R1010
5'-most EST
                   jC-atXLIB327427P1a07a2
                  BLASTN
Method
NCBI GI
                  q4376087
BLAST score
                  307
E value
                  1.0e-172
Match length
                  416
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                  fragment No
Seq. No.
                  134135
                  98676_1.R1010
Contig ID
                  jC-atXLIB327427P1b01a2
5'-most EST
Method
                  BLASTN
NCBI GI
                  g540252
BLAST score
                  33
                  7.0e-09
E value
Match length
                  33
                  100
% identity
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
Seq. No.
                  134136
Contig ID
                   98684 1.R1010
5'-most EST
                   jC-atXLIB327427P1b09a2
Method
                  BLASTX
NCBI GI
                  q4006872
BLAST score
                  525
E value
                  2.0e-53
Match length
                  100
                   99
% identity
NCBI Description
                  (Z99707) methionyl aminopeptidase-like protein [Arabidopsis
                  thaliana]
                  134137
Seq. No.
                   98691 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327427P1c05a2
Method
                  BLASTX
NCBI GI
                   a4544454
BLAST score
                   170
E value
                   7.0e-12
Match length
                  88
% identity
                   58
NCBI Description
                  (AC006592) putative DNAJ protein [Arabidopsis thaliana]
Seq. No.
                   134138
Contig ID
                   98695 2.R1010
5'-most EST
                   jC-atXP28C135H20T7s1
Method
                  BLASTX
```

NCBI GI q3386595 BLAST score 485 1.0e-48 E value Match length 98 97 % identity

NCBI Description (AC004665) hypothetical protein [Arabidopsis thaliana]



>gi_3702345 (AC005397) hypothetical protein [Arabidopsis
thaliana]

Seq. No. 134139

Contig ID 98696_1.R1010

5'-most EST jC-atXLIB327427P1c10a2

Method BLASTN
NCBI GI g2477521
BLAST score 230
E value 1.0e-126
Match length 492
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134140

Contig ID 98702 1.R1010

5'-most EST jC-atXLIB327427P1d04a2

Method BLASTN
NCBI GI g2584827
BLAST score 394
E value 0.0e+00
Match length 414
% identity 99

NCBI Description Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 134141

Contig ID 98703 1.R1010

5'-most EST jC-atXLIB327427P1d05a2

Method BLASTN
NCBI GI 94220645
BLAST score 221
E value 1.0e-121
Match length 440
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYA6, complete sequence [Arabidopsis thaliana]

Seq. No. 134142

Contig ID 98707 1.R1010

5'-most EST jC-atXLIB327427P1d09a2

Seq. No. 134143

Contig ID 98708 1.R1010

5'-most EST jC-atXLIB327427P1d10a2

Seq. No. 134144

Contig ID 98723 1.R1010

5'-most EST jC-atXLIB327427P1f02a2

Method BLASTN
NCBI GI g1871173
BLAST score 421
E value 0.0e+00
Match length 442
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC T06D20 genomic

·,*



sequence, complete sequence

```
Seq. No.
                  134145
                  98725 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327427P1f04a2
Method
                  BLASTX
NCBI GI
                  g4512660
                  195
BLAST score
                  9.0e-15
E value
Match length
                  81
                  51
% identity
NCBI Description
                  (AC006931) hypothetical protein [Arabidopsis thaliana]
                  >gi 4544467 gb AAD22374.1 AC006580 6 (AC006580)
                  hypothetical protein [Arabidopsis thaliana]
                  134146
Seq. No.
Contig ID
                  98726 1.R1010
5'-most EST
                  jC-atXLIB327427P1f05a2
                  134147
Seq. No.
Contig ID
                  98728 1.R1010
5'-most EST
                  jC-atXLIB327427P1f07a2
Seq. No.
                  134148
Contig ID
                  98737 1.R1010
5'-most EST
                  jC-atXLIB327427P1g04a2
                  BLASTN
Method
                  g2462264
NCBI GI
BLAST score
                  54
                  2.0e-21
E value
Match length
                  54
% identity
                  100
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  134149
Contig ID
                  98742 1.R1010
5'-most EST
                  jC-atXLIB327427P1g12a2
Method
                  BLASTX
NCBI GI
                  q2961388
BLAST score
                  294
E value
                  2.0e-26
Match length
                  82
% identity
                  84
NCBI Description
                  (AL022141) putative protein [Arabidopsis thaliana]
                  134150
Seq. No.
Contig ID
                  98751 1.R1010
5'-most EST
                  jC-atXLIB327427P1h10a2
Method
                  BLASTN
NCBI GI
                  q540252
BLAST score
                  34
                  2.0e-09
E value
Match length
                  34
% identity
                  100
```

Seq. No. 134151

15864

NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds



Contig ID 98804 1.R1010

5'-most EST jC-atXP112C129H2T7a1

Method BLASTN
NCBI GI g4159707
BLAST score 590
E value 0.0e+00
Match length 695
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MJK13, complete sequence

Seq. No. 134152

Contig ID 98806 1.R1010

5'-most EST jC-atXLIB327429P3a07a2

Method BLASTX
NCBI GI g2980805
BLAST score 108
E value 8.0e-52
Match length 147
% identity 87

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 134153

Contig ID 98851 1.R1010

5'-most EST jC-atXLIB327429P3d08a2

Seq. No. 134154

Contig ID 98922 1.R1010

5'-most EST jC-atXLIB327403P3a07a2

Method BLASTX
NCBI GI g2462753
BLAST score 573
E value 7.0e-59
Match length 128
% identity 77

NCBI Description (AC002292) putative polygalacturonase [Arabidopsis

thaliana]

Seq. No. 134155

Contig ID 98938 1.R1010

5'-most EST jC-atXLIB327403P3c02a2

Method BLASTN
NCBI GI g3449330
BLAST score 46
E value 1.0e-16
Match length 150
% identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No. 134156

Contig ID 98941 1.R1010

5'-most EST jC-atXLIB327403P3c06a2

Seq. No. 134157

Contig ID 98955 1.R1010

5'-most EST jC-atXLIB327403P3e01a2



Method BLASTN
NCBI GI g2656028
BLAST score 229
E value 1.0e-126
Match length 350
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNF13

Seq. No. 134158

Contig ID 98970_1.R1010

5'-most EST jC-atXLIB327403P3f06a2

Method BLASTN
NCBI GI g3327922
BLAST score 213
E value 1.0e-116
Match length 426
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T31E10 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134159

Contig ID 98983_1.R1010

5'-most EST jC-at \overline{X} LIB327403P3g11a2

Method BLASTX
NCBI GI g3287696
BLAST score 507
E value 3.0e-66
Match length 157
% identity 75

NCBI Description (AC003979) Strong similarity to phosphoribosylanthranilate

transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region.

[Arabidopsis thaliana]

Seq. No. 134160

Contig ID 98985 1.R1010 5'-most EST g2047966

Seq. No. 134161

Contig ID 98995 1.R1010

5'-most EST jC-atXLIB327404P3a05a1

Method BLASTN
NCBI GI g2914688
BLAST score 501
E value 0.0e+00
Match length 558
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F24L7 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134162

Contig ID 99026 1.R1010

5'-most EST jC-atXLIB327404P3d12a1

Method BLASTX NCBI GI g3033392

BLAST score 43



E value 3.0e-25 Match length 75 77 % identity

NCBI Description (AC004238) putative translation initiation factor

EIF-2B-epsilon subunit [Arabidopsis thaliana]

134163 Seq. No.

Contig ID 99035 1.R1010

5'-most EST jC-atXLIB327404P3f03a1

Method BLASTX NCBI GI g3047124 BLAST score 179 E value 9.0e-13 57 Match length % identity 65

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 134164

Contig ID 99037 1.R1010

5'-most EST jC-atXLIB327404P3f06a1

Method BLASTX NCBI GI q4587570 BLAST score 560 E value 2.0e-57 Match length 130 % identity 89

NCBI Description (AC006550) Strong similarity to gi_2244833 centromere

> protein homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97337. ESTs gb_T20765 and gb_AA586277 come from

this gene

Seq. No. 134165

Contig ID 99043 1.R1010

5'-most EST $jC-at\overline{X}LIB327404P3g02a1$

Method BLASTX NCBI GI q4432844 BLAST score 276 E value 3.0e-24Match length 107 % identity 46

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 134166

Contig ID 99046 1.R1010

5'-most EST jC-atXP44C170L2T7062a1

Method BLASTX NCBI GI g4585989 BLAST score 144 1.0e-08 E value Match length 114 % identity 39

(AC005287) Hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 134167

Contig ID

99050 1.R1010

5'-most EST jC-atXLIB327404P3g09a1

Seq. No. 134168 Contig ID 99052 1.R1010 5'-most EST jC-atXLIB327404P3h12a1 BLASTX Method NCBI GI g4539399 BLAST score 509 E value 2.0e-51 Match length 128 % identity 79 NCBI Description (AL035526) ras-like GTP-binding protein [Arabidopsis thaliana] 134169 Seq. No. Contig ID 99059 1.R1010 5'-most EST jC-atXLIB327404P3h07a1 BLASTN Method NCBI GI q3176695 BLAST score 304 E value 1.0e-170 Match length 437 % identity 96 NCBI Description Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana] 134170 Seq. No. Contig ID 99061 1.R1010 5'-most EST jC-atXP2C77E7T7059a1 Method BLASTX NCBI GI q4586044 BLAST score 361 4.0e-34 E value Match length 92 % identity 75 (AC007020) putative receptor protein kinase [Arabidopsis NCBI Description thaliana] Seq. No. 134171 Contig ID 99068 1.R1010 jC-atXLIB327405P2a08a1 5'-most EST

Method BLASTX
NCBI GI g4567260
BLAST score 424
E value 1.0e-41
Match length 82
% identity 100

NCBI Description (AC006841) putative NADPH dependent mannose 6-phosphate

reductase [Arabidopsis thaliana]

>gi_4582440_gb_AAD24825.1_AC007142_3 (AC007142) putative
NADPH-dependent mannose-6-phosphate reductase [Arabidopsis

thaliana]

Seq. No.

134172 99073 2.R1010

Contig ID 99073_2.R1010

5'-most EST $g5020\overline{8}0$

Seq. No. 134173



Contig ID 99101 1.R1010

5'-most EST jC-atXLIB327405P2d10a1

Method BLASTX
NCBI GI g4325345
BLAST score 250
E value 3.0e-21
Match length 73
% identity 23

NCBI Description (AF128393) similar to thioredoxin-like proteins (Pfam:

PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42,

N=1) [Arabidopsis thaliana]

Seq. No. 134174

Contig ID 99112 1.R1010

5'-most EST jC-atXLIB327405P2e10a1

Method BLASTN
NCBI GI g3063690
BLAST score 400
E value 0.0e+00
Match length 515
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11

(ESSAII project)

Seq. No. 134175

Contig ID 99124 1.R1010

5'-most EST jC-atXLIB327405P2f10a1

Seq. No. 134176

Contig ID 99128 1.R1010

5'-most EST jC-atXLIB327405P2g03a1

Method BLASTN
NCBI GI g4406776
BLAST score 58
E value 1.0e-23
Match length 204
% identity 82

NCBI Description Arabidopsis thaliana chromosome II BAC F14H2O genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134177

Contig ID 99134 1.R1010

5'-most EST jC-atXLIB327405P2g10a1

Method BLASTN
NCBI GI g2462264
BLAST score 50
E value 6.0e-19
Match length 50
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 134178

Contig ID 99153 1.R1010

5'-most EST jC-atXLIB327428P1a03a2

Method BLASTN NCBI GI g3059018



BLAST score 442 E value 0.0e+00 Match length 454 % identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12

(ESSAII project)

Seq. No. 134179

Contig ID 99200_1.R1010

5'-most EST jC-atXLIB327428P1c06a2

Method BLASTX
NCBI GI 94262147
BLAST score 255
E value 8.0e-22
Match length 94
% identity 53

NCBI Description (AC005275) putative homolog of transport inhibitor response

1 [Arabidopsis thaliana]

Seq. No. 134180

Contig ID 99238_1.R1010

5'-most EST jC-atXLIB327428P1e03a2

Method BLASTX
NCBI GI g4097543
BLAST score 349
E value 7.0e-33
Match length 68
% identity 87

NCBI Description (U64904) ATFP1 [Arabidopsis thaliana]

Seq. No. 134181

Contig ID 99242 1.R1010

5'-most EST jC-atXLIB327428P1e05a2

Method BLASTN
NCBI GI g2564049
BLAST score 103
E value 1.0e-50
Match length 239
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MLE2, complete sequence [Arabidopsis thaliana]

Seq. No. 134182

Contig ID 99251 1.R1010

5'-most EST jC-atXLIB327428P1e10a2

Method BLASTN
NCBI GI g4589420
BLAST score 398
E value 0.0e+00
Match length 428
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K3G17, complete sequence

Seq. No. 134183

Contig ID 99253 1.R1010

5'-most EST jC-atXLIB327428P1e11a2



```
Method
                   BLASTX
NCBI GI
                   q2493321
BLAST score
                   274
E value
                   2.0e-67
Match length
                   226
                   56
% identity
NCBI Description
                  L-ASCORBATE OXIDASE PRECURSOR (ASCORBASE) (ASO)
                   >gi_2129952 pir S66353 L-ascorbate oxidase (EC 1.10.3.3)
                   precursor - common tobacco >gi_599594_dbj_BAA07734_
                   (D43624) ascorbate oxidase precursor [Nicotiana tabacum]
Seq. No.
                   134184
Contig ID
                   99253 2.R1010
5'-most EST
                   jC-atXP17C110F23T7s3
Method
                   BLASTN
NCBI GI
                   q2208902
BLAST score
                   422
E value
                   0.0e + 00
Match length
                   458
% identity
                  Arabidopsis thaliana mRNA for ascorbate oxidase, partial
NCBI Description
Seq. No.
                   134185
Contig ID
                   99257 1.R1010
5'-most EST
                   jC-atXLIB327428P1f02a2
Method
                   BLASTN
NCBI GI
                   q4544381
BLAST score
                   208
E value
                   1.0e-113
Match length
                   423
% identity
                   97
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F16F14 genomic
                   sequence, complete sequence
Seq. No.
                   134186
Contig ID
                   99285 1.R1010
5'-most EST
                   jC-atXLIB327428P1g06a2
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                   43
E value
                   4.0e-15
Match length
                   47
% identity
                   98
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  134187
Contig ID
                   99289 1.R1010
5'-most EST
                   jC-at\overline{X}LIB327428P1g09a2
Method
                  BLASTN
NCBI GI
                  g4092471
```

BLAST score 120 E value 9.0e-61 Match length 339 85 % identity

NCBI Description Arabidopsis thaliana BAC F9M13 from chromosome IV near 21.5

cM, complete sequence



```
Seq. No.
                  134188
Contig ID
                  99307 1.R1010
                  jC-atXLIB327428P1h06a2
5'-most EST
                  BLASTN
Method
NCBI GI
                  q540252
BLAST score
                  50
                  6.0e-19
E value
                  50
Match length
                  100
% identity
NCBI Description Cloning vector pSVSport1 beta-lactamase gene, complete cds
Seq. No.
                  134189
Contig ID
                  99310 1.R1010
5'-most EST
                  jC-atXLIB327428P1h09a2
Method
                  BLASTN
NCBI GI
                  q3449312
BLAST score
                  371
                  0.0e+00
E value
                  505
Match length
% identity
                  96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K16L22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  134190
Contig ID
                  99316 1.R1010
5'-most EST
                  jC-atXLIB327428P4a01a2
Method
                  BLASTN
NCBI GI
                  q4519195
BLAST score
                  401
E value
                  0.0e+00
Match length
                  425
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MQC12, complete sequence
Seq. No.
                  134191
                  99317 2.R1010
Contig ID
                  jC-at\overline{X}LIB327428P4a02a2
5'-most EST
Seq. No.
                  134192
                  99346 1.R1010
Contig ID
5'-most EST
                  jC-atXP34C149G13T7a1
Method
                  BLASTX
NCBI GI
                  g4678332
BLAST score
                  290
                  1.0e-25
E value
Match length
                  135
% identity
                  49
NCBI Description
                  (AL049658) putative peptide transporter [Arabidopsis
                  thaliana]
```

Seq. No. 134193 Contig ID

99347 1.R1010 5'-most EST jC-atXLIB327428P4g12a2

Method BLASTX NCBI GI g2462763



BLAST score 303 E value 2.0e-27 Match length 61 % identity 100

NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 134194

Contig ID 99349_1.R1010

5'-most EST jC-atXLIB327428P4g07a2

Method BLASTN
NCBI GI g17686
BLAST score 174
E value 7.0e-93
Match length 252
% identity 98

NCBI Description A.thaliana telomere associated sequence DNA

Seq. No. 134195

Contig ID 99356 1.R1010

5'-most EST jC-atXLIB327428P4d10a2

Method BLASTX
NCBI GI g4006896
BLAST score 585
E value 3.0e-60
Match length 124
% identity 91

NCBI Description (Z99708) SCARECROW-like protein [Arabidopsis thaliana]

Seq. No. 134196

Contig ID 99361 1.R1010

5'-most EST jC-atXLIB327428P4e04a2

Method BLASTX
NCBI GI g3763932
BLAST score 288
E value 1.0e-25
Match length 71
% identity 77

NCBI Description (AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No. 134197

Contig ID 99371_1.R1010

5'-most EST jC-atXLIB327428P4f02a2

Method BLASTN
NCBI GI g3789706
BLAST score 397
E value 0.0e+00
Match length 429
% identity 98

NCBI Description Arabidopsis thaliana chromosome 1 BAC F15K9 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 134198

Contig ID 99372 1.R1010

5'-most EST jC-atXLIB327428P4f03a2

Method BLASTN NCBI GI g2264311



BLAST score E value 0.0e + 00Match length 452 99 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MLN1, complete sequence [Arabidopsis thaliana]

134199 Seq. No.

99375 1.R1010 Contig ID

5'-most EST jC-atXLIB327428P4f06a2

Seq. No. 134200

Contig ID 99376 1.R1010

jC-atXLIB327428P4f07a2 5'-most EST

Method BLASTN NCBI GI g2462264 BLAST score 52 E value 4.0e-20 Match length 52

% identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

134201 Seq. No.

Contig ID 99378 1.R1010

5'-most EST jC-atXLIB327428P4f09a2

100

Method BLASTX g3928543 NCBI GI 380 BLAST score E value 2.0e-36 Match length 104 % identity

(AB016819) UDP-glucose glucosyltransferase [Arabidopsis NCBI Description

thaliana]

134202 Seq. No.

Contig ID 99389 1.R1010

5'-most EST jC-atXLIB327428P4g08a2

Method BLASTX NCBI GI q3355470 BLAST score 274 5.0e-24 E value Match length 98 % identity 54

NCBI Description (AC004218) putative lysophospholipase [Arabidopsis

thaliana]

Seq. No. 134203

Contig ID 99400 1.R1010

5'-most EST jC-atXLIB327428P4h09a2

Method BLASTN NCBI GI g3176701 BLAST score 340 E value 0.0e + 00Match length 474 % identity 97

Arabidopsis thaliana chromosome II BAC T20K24 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                   134204
                   99415 1.R1010
Contig ID
                   jC-at\overline{X}P39C161F15T7s1
5'-most EST
                   BLASTN
Method
                   g2262097
NCBI GI
BLAST score
                   584
                   0.0e + 00
E value
                   604
Match length
                   99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome IV BAC T19F6 genomic
                   sequence, complete sequence
                   134205
Seq. No.
                   99425 1.R1010
Contig ID
                   q735942
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2392894
BLAST score
                   138
                   2.0e-71
E value
Match length
                   376
% identity
                   96
NCBI Description Arabidopsis thaliana brassinosteroid insensitive 1 (BRI1)
                  gene, complete cds
                   134206
Seq. No.
Contig ID
                   99434 1.R1010
5'-most EST
                   jC-atXLIB327438P3d12b1
                   134207
Seq. No.
                   99434 2.R1010
Contig ID
5'-most EST
                   jC-atXP31C144K1T7s1
Seq. No.
                   134208
Contig ID
                   99444 1.R1010
5'-most EST
                   jC-atXLIB327438P3e11b1
Method
                   BLASTX
NCBI GI
                   q4097505
BLAST score
                   588
E value
                   6.0e-61
Match length
                   116
% identity
                   97
NCBI Description
                  (U63020) D1 protein [Magnolia pyramidata]
Seq. No.
                   134209
                   99444 2.R1010
Contig ID
5'-most EST
                   g2747932
Method
                  BLASTX
NCBI GI
                  g4097505
BLAST score
                   46
E value
                   3.0e-18
Match length
                   58
```

NCBI Description (U63020) D1 protein [Magnolia pyramidata] Seq. No. 134210

% identity

Contig ID 99581_1.R1010

100



```
jC-atXLIB327439P1h02a2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4115383
BLAST score
                  43
E value
                  4.0e-25
Match length
                  159
% identity
                  47
                  (AC005967) receptor-like protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  134211
Seq. No.
Contig ID
                  99731 1.R1010
5'-most EST
                  jC-atXLIB327403P3h04b2
Method
                  BLASTN
NCBI GI
                  q4510360
BLAST score
                  192
E value
                  1.0e-103
Match length
                  437
% identity
                  99
NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic
                  sequence, complete sequence
                  134212
Seq. No.
Contig ID
                  99743 1.R1010
5'-most EST
                  jC-atXP70C220P10T7054a1
Method
                  BLASTN
NCBI GI
                  g4589445
BLAST score
                  222
                  1.0e-121
E value
Match length
                  379
% identity
                  92
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWL2, complete sequence
                  134213
Seq. No.
Contig ID
                  99749 1.R1010
5'-most EST
                  jC-atXLIB327405P1a10a2
Method
                  BLASTN
NCBI GI
                  q4757395
BLAST score
                  415
E value
                  0.0e + 00
Match length
                  415
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K21L13, complete sequence
Seq. No.
                  134214
                  99759 1.R1010
Contig ID
                  jC-atXLIB327405P1b07a2
5'-most EST
Method
                  BLASTX
```

 \tilde{x}_{i}

NCBI GI q728868 BLAST score 95 2.0e-21 E value Match length 111 % identity 48

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) NCBI Description >gi 99824_pir__S16748 proline-rich protein - rape





(fragment) >gi 22597 emb CAA42924 (X60376) proline-rich protein [Brassica napus]

Seq. No. 134215

Contig ID 99761 1.R1010

5'-most EST jC-atXLIB327405P1b08a2

Method BLASTN NCBI GI g2351073 BLAST score 356 0.0e + 00E value Match length 400 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No. 134216

Contig ID 99766 1.R1010

5'-most EST jC-atXLIB327405P1c01a2

Method BLASTX g2388580 NCBI GI BLAST score 425 9.0e-42 E value Match length 96 % identity 74

NCBI Description (AC000098) Similar to Sequence 10 from patent 5477002

(gb 1253956). [Arabidopsis thaliana]

Seq. No. 134217

Contig ID 99768 1.R1010

5'-most EST jC-atXLIB327405P1c02a2

Method BLASTX NCBI GI g2827659 BLAST score 467 E value 1.0e-46 Match length 95 % identity 97

NCBI Description (AL021637) putative protein [Arabidopsis thaliana]

Seq. No. 134218

99771 1.R1010 Contig ID

5'-most EST jC-atXLIB327405P1c04a2

Method BLASTN NCBI GI g4455229 BLAST score 209 1.0e-114 E value 418 Match length % identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23

(ESSAII project)

134219 Seq. No.

99778 1.R1010 Contig ID

5'-most EST jC-atXLIB327405P1c09a2

Method BLASTX NCBI GI g4455293 BLAST score 67

E value 3.0e-11



Match length 70 % identity 67

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 134220

Contig ID 99786_1.R1010

5'-most EST jC-atXLIB327405P1d03a2

Method BLASTN
NCBI GI g2262155
BLAST score 354
E value 0.0e+00
Match length 527
% identity 96

NCBI Description DNA sequence of Arabidopsis thaliana BAC F5J6 from

chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No. 134221

Contig ID 99786 2.R1010

Method BLASTN
NCBI GI g2262155
BLAST score 273
E value 1.0e-152
Match length 595
% identity 99

NCBI Description DNA sequence of Arabidopsis thaliana BAC F5J6 from

chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No. 134222

Contig ID 99788 1.R1010

5'-most EST jC-atXLIB327405P1d05a2

Method BLASTN
NCBI GI g2462264
BLAST score 57
E value 4.0e-23
Match length 57
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 134223

Contig ID 99810 1.R1010

5'-most EST jC-atXLIB327405P1e08a2

Method BLASTN
NCBI GI g2564049
BLAST score 229
E value 1.0e-126
Match length 431
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MLE2, complete sequence [Arabidopsis thaliana]

Seq. No. 134224

Contig ID 99819 1.R1010

5'-most EST jC-atXLIB327405P1f01a2

Method BLASTN NCBI GI g3128137

BLAST score 54



E value 2.0e-21 Match length 130 % identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9I9, complete sequence [Arabidopsis thaliana]

Seq. No. 134225

Contig ID 99830 1.R1010

5'-most EST jC-atXLIB327405P1f09a2

Seq. No. 134226

Contig ID 99834 1.R1010

5'-most EST jC-atXLIB327405P1f11a2

Method BLASTN
NCBI GI g2335089
BLAST score 331
E value 0.0e+00
Match length 413
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T11A7 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134227

Contig ID 99838_1.R1010

5'-most EST jC-atXP19C113B6T7072a1

Method BLASTN
NCBI GI g3785992
BLAST score 362
E value 0.0e+00
Match length 548
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC T6A23 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134228

Contig ID 99851 1.R1010

5'-most EST jC-atXLIB327405P1h04a2

Method BLASTN
NCBI GI g4454587
BLAST score 430
E value 0.0e+00
Match length 512
% identity 100

NCBI Description Arabidopsis thaliana BAC F21A20 from chromosome V near 61

cM, complete sequence [Arabidopsis thaliana]

Seq. No. 134229

Contig ID 99870 1.R1010

5'-most EST jC-atXLIB327405P2b01b2

Method BLASTN
NCBI GI g3869068
BLAST score 370
E value 0.0e+00
Match length 370
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC16, complete sequence [Arabidopsis thaliana]



```
134230
Seq. No.
Contig ID
                  100024 1.R1010
                  jC-atXLIB327439P2d04a2
5'-most EST
                  BLASTN
Method
NCBI GI
                  g2264312
BLAST score
                  264
E value
                  1.0e-146
                  404
Match length
                  91
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOK16, complete sequence [Arabidopsis thaliana]
Seq. No.
                  134231
                  100032 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P2e04a2
                  134232
Şeq. No.
                  100035 1.R1010
Contig ID
                  jC-atXLIB327439P2e10a2
5'-most EST
Method
                  BLASTX
                  g4006918
NCBI GI
BLAST score
                  407
E value
                  1.0e-39
Match length
                  81
% identity
                  100
                  (Z99708) peroxidase like protein [Arabidopsis thaliana]
NCBI Description
                  134233
Seq. No.
Contig ID
                  100042 1.R1010
5'-most EST
                  jC-atXLIB327439P2f08a2
Method
                  BLASTN
NCBI GI
                  g2656029
BLAST score
                  311
                  1.0e-174
E value
Match length
                  398
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQB2
                  134234
Seq. No.
Contig ID
                  100064 1.R1010
5'-most EST
                  jC-atXLIB327439P2h10a2
Method
                  BLASTX
NCBI GI
                  q3033384
BLAST score
                  288
E value
                  1.0e-25
Match length
                  62
% identity
NCBI Description
                  (AC004238) putative CTP synthase [Arabidopsis thaliana]
```

Seq. No. 134235

100067 1.R1010 Contig ID

5'-most EST g773535 Method BLASTN g4376087 NCBI GI BLAST score 114



E value 4.0e-57

Match length 122
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No. 134236

Contig ID 100091_1.R1010
5'-most EST jC-atXLIB327439P3b07a2

5'-most EST jC-atXLIB3274

Method BLASTX

NCBI GI g4406756

BLAST score 608

E value 4.0e-63

E value 4.06
Match length 145
% identity 77

NCBI Description (AC006836) putative integral membrane protein A3

[Arabidopsis thaliana]

Seq. No. 134237

Contig ID 100111 1.R1010

5'-most EST jC-atXLIB327439P3c11a2

Method BLASTN
NCBI GI g4220643
BLAST score 230
E value 1.0e-126
Match length 338
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 134238

Contig ID 100114_1.R1010

5'-most EST jC-atXLIB327439P3d04a2

Method BLASTN
NCBI GI g4519194
BLAST score 264
E value 1.0e-146
Match length 411
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MHM17, complete sequence

Seq. No. 134239

Contig ID 100121 1.R1010

5'-most EST jC-atXLIB327439P3d10a2

Seq. No. 134240

Contig ID 100125 1.R1010

5'-most EST jC-atXLIB327439P3e01a2

Method BLASTX
NCBI GI g2688828
BLAST score 405
E value 2.0e-39
Match length 118
% identity 64

NCBI Description (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus

armeniaca]



```
Seq. No.
                  134241
                  100130 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P3e05a2
Seq. No.
                  134242
Contig ID
                  100157 1.R1010
5'-most EST
                  jC-atXLIB327439P3g03a2
                  134243
Seq. No.
Contig ID
                  100161 1.R1010
5'-most EST
                  jC-atX\overline{L}IB327439P3g05a2
Method
                  BLASTX
                  g4115377
NCBI GI
BLAST score
                  337
                  2.0e-31
E value
Match length
                  96
                  65
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
                  134244
Seq. No.
Contig ID
                  100162_1.R1010
5'-most EST
                   jC-atXLIB327439P3g06a2
Method
                  BLASTX
NCBI GI
                   q3688598
BLAST score
                   510
                  1.0e-51
E value
Match length
                  127
% identity
                  72
NCBI Description (AB009029) Cycloartenol Synthase [Panax ginseng]
Seq. No.
                   134245
                   100166 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327439P3g09a2
Seq. No.
                   134246
Contig ID
                   100306 1.R1010
                   jC-atXP73CF3D8T7b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   a2507097
BLAST score
                   189
E value
                   1.0e-13
Match length
                   180
                   36
% identity
NCBL Description PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP)
Seq. No.
                   134247
Contig ID
                   100311 1.R1010
5'-most EST
                   jC-atXP73CF3A11T7b1
Method
                   BLASTX
NCBI GI
                   q4587589
BLAST score
                   56
                   3.0e-14
E value
Match length
                   66
```

% identity 61
NCBI Description (AC007232) hypothetical protein [Arabidopsis thaliana]



```
Seq. No.
                   134248
                   100348 1.R1010
Contig ID
                   jC-atXP73C224E2T7b1
5'-most EST
Method
                   BLASTX
                   g4587525
NCBI GI
BLAST score
                   596
                   2.0e-61
E value
Match length
                   240
% identity
                   49
NCBI Description
                   (AC007060) Contains the PF 00650 CRAL/TRIO
                   phosphatidyl-inositol-transfer protein domain. ESTs
                   gb_T76582, gb_N06574 and gb_Z25700 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   134249
Contig ID
                   100349 1.R1010
5'-most EST
                   jC-atXP73C224D8T7b1
Method
                   BLASTX
NCBI GI
                   q1651907
BLAST score
                   220
E value
                   9.0e-41
Match length
                   174
% identity
                   52
NCBI Description
                   (D90901) spore germination protein c2 [Synechocystis sp.]
Seq. No.
                   134250
                   100354 1.R1010
Contig ID
5'-most EST
                   iC-atXP73C224B4T7d2
Method
                   BLASTX
NCBI GI
                   g547706
BLAST score
                   219
E value
                   2.0e-17
Match length
                   126
% identity
                   40
                   INSULIN-DEGRADING ENZYME (INSULYSIN) (INSULINASE) (INSULIN PROTEASE) >gi 347022 pir S29509 insulinase (EC 3.4.99.45)
NCBI Description
                   - rat >gi 56492 emb CAA47689 (X67269) insulin-degrading
                   enzyme [Rattus norvegicus]
                   134251
Seq. No.
                   100362 1.R1010
Contig ID
                   jC-atXP73C223K9T7d2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3080427
BLAST score
                   1045
E value
                   1.0e-114
                   294
Match length
% identity
                   67
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
```

134252 Seq. No.

100364 1.R1010 Contig ID 5'-most EST $jC-atX\overline{P}73C223K12T7b1$

Method BLASTN g3249094 NCBI GI BLAST score 822 E value 0.0e + 00



Match length 860 % identity 99

NCBI Description Arabidopsis thaliana chromosome 1 BAC T12M4 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 134253

Contig ID 100378_1.R1010

5'-most EST jC-atXP73C223F20T7b1

Method BLASTX
NCBI GI g2618699
BLAST score 1149
E value 1.0e-126
Match length 266
% identity 83

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 134254

Contig ID 100388 1.R1010 5'-most EST jC-atXP91CH1G5T7b1

Method BLASTN
NCBI GI g3869069
BLAST score 58
E value 1.0e-23
Match length 331
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 134255

Contig ID 100400_1.R1010 5'-most EST jC-atXP91CH1D7T7b1

Method BLASTX
NCBI GI g4220523
BLAST score 297
E value 1.0e-26
Match length 148
% identity 39

NCBI Description (AL035356) putative alliin lyase [Arabidopsis thaliana]

Seq. No. 134256

Contig ID 100423_1.R1010 5'-most EST jC-atXP91CG6H6T7b1

Method BLASTX
NCBI GI g4176531
BLAST score 150
E value 3.0e-09
Match length 84
% identity 42

NCBI Description (AL035263) weak similarity to chick phosphatidylcholine-ste

rol acetyltransferase [Schizosaccharomyces pombe]

Seq. No. 134257

Contig ID 100425_1.R1010 5'-most EST jC-atXP91CG6G8T7b1

Method BLASTX NCBI GI g1698548 BLAST score 404



E value 5.0e-39
Match length 131
% identity 63

NCBI Description (U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No. 134258

Contig ID 100426_1.R1010 5'-most EST jC-atXP91C247K7T7b1

Method BLASTN
NCBI GI g3241916
BLAST score 219
E value 1.0e-120
Match length 374
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K15N18, complete sequence [Arabidopsis thaliana]

Seq. No. 134259

Contig ID 100428_1.R1010 5'-most EST jC-atXP91C247K19T7b1

Method BLASTN
NCBI GI g3047100
BLAST score 346
E value 0.0e+00
Match length 346
% identity 100

NCBI Description Arabidopsis thaliana BAC F6N23

Seq. No. 134260

Contig ID 100434_1.R1010 5'-most EST jC-atXP91C247J10T7b1

Method BLASTX
NCBI GI g3582340
BLAST score 246
E value 2.0e-20
Match length 91
% identity 57

NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 134261

Contig ID 100435_1.R1010 5'-most EST jC-atXP91C247I6T7b1

Method BLASTX
NCBI GI g4587546
BLAST score 591
E value 5.0e-61
Match length 155
% identity 81

NCBI Description (AC006577) Belongs to the PF_00011 Hsp20/alpha crystallin

family. EST gb_W4312 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 134262

Contig ID 100441_1.R1010 5'-most EST jC-atXP91C247G24T7b1

Method BLASTX NCBI GI g4490297



```
BLAST score
E value
                  2.0e-26
Match length
                  170
                   39
% identity
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                  134263
                  100445 1.R1010
Contig ID
5'-most EST
                  jC-atXP91C247G14T7b1
Seq. No.
                  134264
Contig ID
                  100447 1.R1010
5'-most EST
                  jC-atXP91C247E4T7b1
                  134265
Seq. No.
                  100513 1.R1010
Contig ID
5'-most EST
                   jC-atXP73CF2F2T7d2
Method
                  BLASTN
                                          -112
                  g3461810
NCBI GI
                   577
BLAST score
                  0.0e+00
E value
Match length
                  743
% identity
                   96
                  Arabidopsis thaliana chromosome II BAC T17M13 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   134266
Seq. No.
                   100569 1.R1010
Contig ID
5'-most EST
                   jC-atXP118C155K3T7024a1
                   BLASTN
Method
NCBI GI
                   q3046855
BLAST score
                   82
E value
                   7.0e-38
Match length
                   321
% identity
                   88
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MSL1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134267
                   100574 1.R1010
Contig ID
5'-most EST
                   q2759178
Method
                   BLASTN
                   g4544435
NCBI GI
BLAST score
                   487
                   0.0e+00
E value
                   605
Match length
% identity
                   95
                  Arabidopsis thaliana chromosome II BAC F14M13 genomic
NCBI Description
                   sequence, complete sequence
                   134268
Seq. No.
```

 Seq. No.
 134268

 Contig ID
 100574_4.R1010

 5'-most EST
 g2597355

 Method
 BLASTN

 NCBI GI
 g4544435

 BLAST score
 320

 E value
 1.0e-180



Match length % identity 99

Arabidopsis thaliana chromosome II BAC F14M13 genomic NCBI Description

sequence, complete sequence

134269 Seq. No.

100609 1.R1010 Contig ID

jC-atXP118C146F12T7029d2 5'-most EST

Method BLASTX g3128201 NCBI GI BLAST score 761 E value 1.0e-132 Match length 246 % identity 92

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

134270 Seq. No.

100618 1.R1010 Contig ID

5'-most EST - jC-atXP118C145M5T7005a1

Method BLASTX q4337187 NCBI GI 874 BLAST score E value 3.0e-94 Match length 167 % identity 96

(AC006403) putative prolylcarboxypeptidase, 5' partial NCBI Description

[Arabidopsis thaliana]

Seq. No. 134271

100618 2.R1010 Contig ID

5'-most EST $g34503\overline{2}8$ BLASTN Method NCBI GI q4337186 BLAST score 265 E value 1.0e-147 Match length 305 % identity 98

Arabidopsis thaliana chromosome II BAC T28I24 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134272

100633 1.R1010 Contig ID

jC-atXP118C144M20T7046a1 5'-most EST

Method BLASTN NCBI GI q2462264 BLAST score 58 E value 1.0e-23 Match length 58 % identity 100

Cucumis sativus mRNA for patatin-like protein, partial NCBI Description

Seq. No. 134273

100633 2.R1010 Contig ID

5'-most EST g2393488

Seq. No. 134274

100659 1.R1010 Contig ID

5'-most EST jC-atXP119C209B10T7031a1 Method BLASTX q1542941 NCBI GI 794 BLAST score 9.0e-85 E value 198 Match length % identity 77 (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus] NCBI Description 134275 Seq. No. Contig ID 100661_1.R1010 5'-most EST jC-atXP118C144B3T7075d2 Method BLASTN a2213606 NCBI GI 208 BLAST score 1.0e-113 E value 694 Match length 98 % identity Genomic sequence for Arabidopsis thaliana BAC F21J9, NCBI Description complete sequence [Arabidopsis thaliana] 134276 Seq. No. Contig ID 100670 1.R1010 jC-atXP118C143N23T7027d2 5'-most EST BLASTN q4589437 545 0.0e + 00716

Method NCBI GI BLAST score E value Match length 97 % identity

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MPN9, complete sequence

Seq. No. 134277

100671 1.R1010 Contig ID

5'-most EST jC-atXP118C143N23T7027a1

Method BLASTN NCBI GI q4589437 BLAST score 604 E value 0.0e + 00Match length 680 74 % identity

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MPN9, complete sequence

134278 Seq. No.

100682 1.R1010 Contig ID

jC-atXP118C143H5T7066d2 5'-most EST

BLASTN Method q3600045 NCBI GI 270 BLAST score 1.0e-150 E value 552 Match length 93 % identity

NCBI Description Arabidopsis thaliana BAC F2P3

Seq. No. 134279



Contig ID 100686 1.R1010

5'-most EST jC-atXP118C143G21T7058d2

Method BLASTX
NCBI GI g322752
BLAST score 354
E value 4.0e-33
Match length 130
% identity 53

NCBI Description auxin-independent growth promoter - Nicotiana tabacum

>gi 559921 emb CAA56570 (X80301) axi 1 [Nicotiana tabacum]

Seq. No. 134280

Contig ID 100709 1.R1010

5'-most EST jC-atXP118C142N22T7035d2

Method BLASTX
NCBI GI g3236241
BLAST score 310
E value 4.0e-28
Match length 86
% identity 63

NCBI Description (AC004684) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 134281

Contig ID 100713 1.R1010

5'-most EST jC-atXP118C142N16T7050a1

Method BLASTX
NCBI GI g3513739
BLAST score 534
E value 2.0e-54
Match length 113
% identity 88

NCBI Description (AF080118) Similar to uridine diphosphate glucose

epimerase; F8M12.10 [Arabidopsis thaliana]

Seq. No. 134282

Contig ID 100722 1.R1010

Method BLASTX
NCBI GI g2924784
BLAST score 713
E value 2.0e-97
Match length 185
% identity 61

NCBI Description (AC002334) similar to jasmonate inducible protein

[Arabidopsis thaliana]

Seq. No. 134283

Contig ID 100740 1.R1010

5'-most EST jC-atXP113C228M12T7031a1

Seq. No. 134284

Contig ID 100740 4.R1010

5'-most EST $g94807\overline{6}$

Seq. No. 134285

Contig ID 100742_2.R1010

% identity

NCBI Description

99



```
5'-most EST
                   jC-atXP113C230D23T7095a1
Method
                   BLASTX
NCBI GI
                   q3641252
BLAST score
                   178
                   8.0e-13
E value
                   90
Match length
% identity
                   48
                   (AF053127) leucine-rich receptor-like protein kinase [Malus
NCBI Description
                   domestica]
Seq. No.
                   134286
Contig ID
                   100744 1.R1010
5'-most EST
                   jC-atXP113C133N20T7067a1
Method
                   BLASTN
                   q4589437
NCBI GI
BLAST score
                   217
                   1.0e-118
E value
Match length
                   393
% identity
                   90
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MPN9, complete sequence
                   134287
Seq. No.
Contig ID
                   100744 4.R1010
                   jC-atXP113C223D5T7070a1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4589437
BLAST score
                   227
E value
                   1.0e-124
Match length
                   338
% identity
                   92
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MPN9, complete sequence
                   134288
Seq. No.
Contig ID
                   100749 1.R1010
                   jC-atXP113C125G5T7029a1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4757388
BLAST score
                   636
E value
                   0.0e + 00
Match length
                   716
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   F15L12, complete sequence
Seq. No.
                   134289
Contig ID
                   100752 2.R1010
                   jC-atXP39C161H12T7s1
5'-most EST
Method
                   BLASTN
                   g3337347
NCBI GI
BLAST score
                   422
                   0.0e + 00
E value
                   450
Match length
```

15890

Arabidopsis thaliana chromosome II BAC F13P17 genomic

sequence, complete sequence [Arabidopsis thaliana]



```
134290
Seq. No.
Contig ID
                  100756 1.R1010
                  jC-atXP113C21706T7037a2
5'-most EST
                  BLASTN
Method
NCBI GI
                  g3212846
BLAST score
                  210
E value
                  1.0e-114
Match length
                  630
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  134291
Contig ID
                  100775 1.R1010
                  jC-atXP113C133N23T7075a2
5'-most EST
                  BLASTN
Method
                  g4519195
NCBI GI
BLAST score
                  251
                  1.0e-138
E value
                  826
Match length
% identity
                  97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MQC12, complete sequence
                  134292
Seq. No.
                  100808 1.R1010
Contig ID
                  jC-atXP79CF4H9T7d2
5'-most EST
                  BLASTN
Method
NCBI GI
                  g4725940
BLAST score
                  301
E value
                  1.0e-168
Match length
                  377
                  96
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T1P17
NCBI Description
                   (ESSA project)
Seq. No.
                  134293
                  100808 2.R1010
Contig ID
                   jC-atXP79CF4H9T7b1
5'-most EST
                  BLASTX
Method
                  q112717
NCBI GI
BLAST score
                   381
E value
                   3.0e-36
Match length
                  162
                   46
% identity
NCBI Description
                  21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi 82050 pir S10911
                  hypothetical protein precursor - carrot
                   >gi_18312_emb_CAA36642_ (X52395) precursor polypeptide (AA
                   -22 to 171) [Daucus carota]
                   134294
Seq. No.
```

Contig ID 100810_1.R1010 5'-most EST jC-atXP79CF4H7T7b1

Method BLASTX
NCBI GI g4689473
BLAST score 515



E value 5.0e-52 Match length 124 % identity 79

NCBI Description (AC007213) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 134295

Contig ID 100810_2.R1010 5'-most EST jC-atXP79CF4G9T7d2

Method BLASTX
NCBI GI g4689473
BLAST score 817
E value 2.0e-87
Match length 201
% identity 78

NCBI Description (AC007213) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 134296

Contig ID 100830_1.R1010 5'-most EST jC-atXP79C239E2T7b1

Method BLASTX
NCBI GI g4567225
BLAST score 424
E value 2.0e-41
Match length 80
% identity 99

NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]

Seq. No. 134297

Contig ID 100842_1.R1010 5'-most EST jC-atXP79C237B2T7b1

Method BLASTX
NCBI GI g629692
BLAST score 674
E value 1.0e-70
Match length 223
% identity 62

NCBI Description hypothetical protein - common tobacco

>gi_506471_emb_CAA56189_ (X79794) unnamed protein product

[Nicotiana tabacum]

Seq. No. 134298

Contig ID 100842_2.R1010

NCBI Description hypothetical protein - common tobacco

>qi 506471 emb CAA56189 (X79794) unnamed protein product

[Nicotiana tabacum]

Seq. No. 134299

Contig ID 100844_1.R1010



```
jC-atXP79C231J2T7b1
5'-most EST
Method
                  BLASTN
                  q4539415
NCBI GI
BLAST score
                  449
                  0.0e+00
E value
                  551
Match length
                  55
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA
                  project)
                  134300
Seq. No.
                  100845 1.R1010
Contig ID
5'-most EST
                  jC-atXP79C231I16T7b1
Method
                  BLASTX
                  g135483
NCBI GI
BLAST score
                  649
                  1.0e-82
E value
                  167
Match length
                  92
% identity
                  TUBULIN BETA CHAIN >gi_84364_pir__B30309 tubulin beta chain
NCBI Description
                  - Euplotes crassus (SGC9) >gi 290685 (J04534) beta-tubulin
                   [Euplotes crassus]
                  134301
Seq. No.
Contig ID
                  100856 1.R1010
5'-most EST
                  jC-atXP79C231F8T7b1
Method
                  BLASTN
                  g2351063
NCBI GI
BLAST score
                  533
E value
                  0.0e + 00
                  716
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCL19, complete sequence [Arabidopsis thaliana]
                   134302
Seq. No.
Contig ID
                   100861 1.R1010
                   jC-atXP79C231E7T7b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4589451
BLAST score
                   305
                   1.0e-171
E value
Match length
                   550
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   T32G24, complete sequence
                   134303
Seq. No.
Contig ID
                   100884 1.R1010
                   jC-atXP20C115H1T7063a1
5'-most EST
Method
                   BLASTX
```

NCBI GI q4008006 BLAST score 379 E value 4.0e-69 Match length 240 % identity 53

NCBI Description (AF084034) receptor-like protein kinase [Arabidopsis

E value

Match length

% identity

5.0e-31 140

54



thaliana] 134304 Seq. No. 100892 1.R1010 Contig ID 5'-most EST jC-atXP85CG8A6T7b1 Method BLASTX g2809246 NCBI GI BLAST score 646 1.0e-67 E value 188 Match length % identity 74 (AC002560) F2401.15 [Arabidopsis thaliana] NCBI Description Seq. No. 134305 100898 1.R1010 Contig ID 5'-most EST jC-atXP85CG7H9T7b1BLASTX Method NCBI GI g3894191 BLAST score 326 6.0e-30 E value Match length 146 48 % identity NCBI Description (AC005662) unknown protein [Arabidopsis thaliana] Seq. No. 134306 Contig ID 100904 1.R1010 $jC-atX\overline{P}85CG7H10T7b1$ 5'-most EST Method BLASTX NCBI GI q4678262 703 BLAST score 3.0e-74 E value Match length 169 % identity 86 NCBI Description (AL049657) argininosuccinate synthase-like protein [Arabidopsis thaliana] Seq. No. 134307 Contig ID 100912 1.R1010 5'-most EST jC-atXP85CG7F11T7b1 Method BLASTN NCBI GI q2582640 BLAST score 71 E value 2.0e-31 Match length 71 % identity 100 Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 Seq. No. 134308 Contig ID 100931 1.R1010 jC-atXP85C241H16T7b1 5'-most EST Method BLASTX q2129956 NCBI GI 170 BLAST score



```
NCBI Description photoassimilate-responsive protein PAR-1c precursor -
                   common tobacco >gi_871489_emb_CAA58732_ (X83852) mRNA
                   inducible by sucrose and salicylic acid and potato virus Y
                   expressed in sugar-accumulating plants [Nicotiana tabacum]
                   134309
Seq. No.
                   100931 2.R1010
Contig ID
5'-most EST
                   q2759097
                   134310
Seq. No.
                   100931 3.R1010
Contig ID
5'-most EST
                   g27588<del>9</del>3
                   BLASTX
Method
                   g2129957
NCBI GI
BLAST score
                   318
                   2.0e-29
E value
                   124
Match length
                   51
% identity
                   photoassimilate-responsive protein precursor (clone PAR-1a)
NCBI Description
                   - common tobacco
                   134311
Seq. No.
                   100939 1.R1010
Contig ID
                   jC-atX\overline{P}85C241F8T7b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3236253
                   548
BLAST score
                   5.0e-56
E value
                   182
Match length
                   57
% identity
                   (AC004684) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   134312
Seq. No.
                   100942 1.R1010
Contig ID
                   jC-atX\overline{P}85C241F21T7b1
5'-most EST
Method
                   BLASTX
                   g2529663
NCBI GI
                   484
BLAST score
E value
                   1.0e-113
                   247
Match length
                   85
% identity
                   (AC002535) putative lysophospholipase [Arabidopsis
NCBI Description
                   thaliana] >gi 3738277 (AC005309) putative lysophospholipase
                   [Arabidopsis thaliana]
                   134313
Seq. No.
                   100945 1.R1010
Contig ID
```

jC-atXP85C241E4T7b15'-most EST

BLASTN Method NCBI GI q2760164 BLAST score 173 E value 4.0e-92 Match length 181 99 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K18P6, complete sequence [Arabidopsis thaliana]

E value

Match length

% identity

0.0e+00

700

98



```
134314
Seq. No.
                   100945 2.R1010
Contig ID
5'-most EST
                   g1520690
                   BLASTN
Method
                   g2760164
NCBI GI
BLAST score
                   65
E value
                   7.0e-28
                   139
Match length
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K18P6, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134315
                   100946 1.R1010
Contig ID
                   jC-atXP85C241E2T7b1
5'-most EST
                   BLASTN
Method
                   g3800746
NCBI GI
                   42
BLAST score
                   5.0e-14
E value
                   50
Match length
% identity
                   96
                   Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA,
NCBI Description
                   complete cds
                   134316
Seq. No.
                   100949 1.R1010
Contig ID
                   jC-atX\overline{P}85C241D9T7b1
5'-most EST
                   BLASTN
Method
                   g3075383
NCBI GI
BLAST score
                   577
                   0.0e+00
E value
                   667
Match length
                   96
% identity
                   Arabidopsis thaliana chromosome II BAC T1D16 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134317
                   100975 1.R1010
Contig ID
                   jC-atX\overline{P}82C240P20T7b1
5'-most EST
Method
                   BLASTX
                   g3283893
NCBI GI
                   236
BLAST score
                   2.0e-19
E value
Match length
                   77
% identity
                   56
                   (AF070626) unknown [Homo sapiens]
NCBI Description
Seq. No.
                   134318
                   101020 1.R1010
Contig ID
5'-most EST
                   jC-atXP82CG2B2T7d3
Method
                   BLASTN
NCBI GI
                   q4455168
BLAST score
                   438
```



NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No. 134319

Contig ID 101026 1.R1010

5'-most EST jC-atXP83CG3D10T7085d1

Method BLASTN
NCBI GI g3063438
BLAST score 458
E value 0.0e+00
Match length 597
% identity 98

NCBI Description Complete sequence of Arabidopsis F22013, complete sequence

[Arabidopsis thaliana]

Seq. No. 134320

Contig ID 101106_1.R1010 5'-most EST jC-atXP82CG1E11T7b1

Method BLASTX
NCBI GI g3287693
BLAST score 419
E value 7.0e-41
Match length 153
% identity 58

NCBI Description (AC003979) Similar to LIM17 gene product gb_1653769 from

the genome of Synechocystis sp. gb_D90916. [Arabidopsis

thaliana]

Seq. No. 134321

Contig ID 101130_1.R1010 5'-most EST jC-atXP82C241A2T7b1

Method BLASTN
NCBI GI g2656024
BLAST score 188
E value 1.0e-101
Match length 689
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K15E6

Seq. No. 134322

Contig ID 101156_1.R1010

5'-most EST g2048347
Method BLASTN
NCBI GI g3449330
BLAST score 95
E value 2.0e-45
Match length 1018
% identity 76

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No. 134323

Contig ID 101225 1.R1010

5'-most EST jC-atXP95CH2A5T7048d1

Method BLASTX NCBI GI g2102691

E value

Match length

% identity

0.0e+00

433 94



```
BLAST score
                  3.0e-34
E value
                  102
Match length
                  68
% identity
NCBI Description (U64817) fructokinase [Lycopersicon esculentum]
Seq. No.
                  134324
                  101225 2.R1010
Contig ID
5'-most EST
                  jC-atXP89C245B20T7s1
                  {\tt BLASTX}
Method
                  g2102691
NCBI GI
BLAST score
                  122
                  3.0e-27
E value
                  116
Match length
% identity
                  61
                  (U64817) fructokinase [Lycopersicon esculentum]
NCBI Description
                  134325
Seq. No.
                  101242 1.R1010
Contig ID
5'-most EST
                  jC-atXP98CH8E5T7064d1
                  BLASTN
Method
                  g2244950
NCBI GI
BLAST score
                  317
                  1.0e-178
E value
                  456
Match length
% identity
                  98
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  134326
Seq. No.
                  101243 1.R1010
Contig ID
5'-most EST
                  jC-atXP86CG9H5T7d2
                  134327
Seq. No.
                  101246 1.R1010
Contig ID
5'-most EST
                  jC-atXP58C192P1T7s3
                  134328
Seq. No.
                  101246 2.R1010
Contig ID
5'-most EST
                  jC-atXP95CG12G6T7029d1
                  BLASTN
Method
                  q4467358
NCBI GI
BLAST score
                  41
                  1.0e-13
E value
Match length
                  49
                  96
% identity
NCBI Description Arabidopsis thaliana mRNA for Phosphatidylinositol 4-Kinase
Seq. No.
                  134329
Contig ID
                  101266 1.R1010
                  jC-atXP95CG12F3T7028b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4325340
BLAST score
                  350
```



NCBI Description Arabidopsis thaliana BAC T1J1

Seq. No. 134330

Contig ID 101274_1.R1010

5'-most EST jC-atXP95CG12E8T7091d1

Seq. No. 134331

Contig ID 101276 1.R1010

5'-most EST jC-atXP95CG12E5T7083d1

Seq. No. 134332

Contig ID 101283 1.R1010

5'-most EST jC-atXP95CG12E1T7051d1

Method BLASTX
NCBI GI g4582436
BLAST score 485
E value 1.0e-48
Match length 198
% identity 56

NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]

Seq. No. 134333

Contig ID 101283_3.R1010

5'-most EST g2393386
Method BLASTX
NCBI GI g4582436
BLAST score 145
E value 5.0e-09
Match length 59
% identity 47

NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]

Seq. No. 134334

Contig ID 101298 1.R1010

5'-most EST jC-atXP95CG12D11T7035d1

Method BLASTN
NCBI GI g3985950
BLAST score 514
E value 0.0e+00
Match length 673
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MPI10, complete sequence [Arabidopsis thaliana]

Seq. No. 134335

Contig ID 101298_2.R1010 5'-most EST jC-atXP84CG5F12T7b1

Method BLASTN
NCBI GI g3985950
BLAST score 444
E value 0.0e+00
Match length 578
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MPI10, complete sequence [Arabidopsis thaliana]

Seq. No. 134336



```
101306 1.R1010
Contig ID
5'-most EST
                   q25807\overline{3}6
                   BLASTN
Method
                   q1871173
NCBI GI
BLAST score
                   392
                   0.0e + 00
E value
Match length
                   424
% identity
                   100
NCBI Description Arabidopsis thaliana chromosome II BAC T06D20 genomic
                   sequence, complete sequence
                   134337
Seq. No.
Contig ID
                   101306_2.R1010
5'-most EST
                   g2580922
                   BLASTN
Method
                   g1871173
NCBI GI
BLAST score
                   378
E value
                   0.0e+00
Match length
                   400
                   98
% identity
                  Arabidopsis thaliana chromosome II BAC T06D20 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   134338
                   101335 1.R1010
Contig ID
                   jC-atX\overline{P}95CG11H2T7079d1
5'-most EST
                   BLASTX
Method
                   q1653702
NCBI GI
BLAST score
                   230
                   2.0e-64
E value
                   271
Match length
% identity
                   52
                   (D90915) dihydrolipoamide acetyltransferase component (E2)
NCBI Description
                   of pyruvate dehydrogenase complex [Synechocystis sp.]
Seq. No.
                   134339
                   101341 1.R1010
Contig ID
                   jC-atXP95CG11H10T7087d1
5'-most EST
Seq. No.
                   134340
                   101343 1.R1010
Contig ID
                   jC-atXP95CG11G8T7039d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3885330
BLAST score
                   333
                   6.0e - 31
E value
Match length
                   117
% identity
                   55
                   (AC005623) putative cytochrome p450 protein [Arabidopsis
NCBI Description
                   thaliana]
                   134341
Seq. No.
                   101360 1.R1010
Contig ID
                   jC-atXP95CG11F8T7054d1
5'-most EST
```

15900

134342

101364 1.R1010

Seq. No.

Contig ID



```
jC-atXP95CG11F5T7038d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2911058
BLAST score
                  192
                  2.0e-14
E value
Match length
                  89
                  40
% identity
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  134343
                  101378 1.R1010
Contig ID
                   jC-atXP95CG11E8T7077d1
5'-most EST
Method
                  BLASTN
                   g4415905
NCBI GI
BLAST score
                   384
E value
                   0.0e+00
Match length
                   436
% identity
                   97
                  Arabidopsis thaliana chromosome II BAC F13K3 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134344
                   101419 1.R1010
Contig ID
                   jC-atXP94CH4F4T7027d1
5'-most EST
                   BLASTX
Method
                   g2341041
NCBI GI
BLAST score
                   77
                   2.0e-32
E value
                   145
Match length
% identity
                   62
                   (AC000104) Arabidopsis thaliana putative ethylene receptor
NCBI Description
                   (ERS2) gene (gb AF047976). EST gb_W43451 comes from this
                   gene. [Arabidopsis thaliana] >gi_3687656 (AF047976)
                   putative ethylene receptor; ERS2 [Arabidopsis thaliana]
                   134345
Seq. No.
                   101422 1.R1010
Contig ID
                   jC-atXP94CH4F11T7059d1
5'-most EST
                   BLASTN
Method
                   q4467358
NCBI GI
BLAST score
                   35
                   6.0e-10
E value
                   39
Match length
                   97
% identity
NCBI Description Arabidopsis thaliana mRNA for Phosphatidylinositol 4-Kinase
                   134346
Seq. No.
                   101429 1.R1010
Contig ID
                   jC-atXP94CG12A1T7090d1
5'-most EST
                   134347
Seq. No.
                   101444 1.R1010
Contig ID
```

jC-atXP94CG11C7T7015d1 5'-most EST

Method BLASTN q1070003 NCBI GI BLAST score 40

6.0e-13 E value



Match length % identity 100

B.napus mRNA for biotin carboxyl carrier protein (pBP3) NCBI Description

>qi 3715065 emb A59874.1 A59874 Sequence 3 from Patent

WO9707222

134348 Seq. No.

101446 1.R1010 Contig ID

jC-atXP94CG11C5T7094d1 5'-most EST

Method BLASTX NCBI GI q4415931 BLAST score 323 E value 1.0e-29 Match length 147 50 % identity

(AC006418) unknown protein [Arabidopsis thaliana] NCBI Description

>gi 4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown

protein [Arabidopsis thaliana]

134349 Seq. No.

101459 2.R1010 Contig ID

jC-atXP94CG11B12T7054d1 5'-most EST

BLASTX Method NCBI GI q4454039 BLAST score 276 4.0e-24E value 73 Match length 79 % identity

(AL035394) putative Na+/H+-exchanging protein [Arabidopsis NCBI Description

thaliana]

134350 Seq. No.

Contig ID 101459_3.R1010

5'-most EST q506597 BLASTN Method NCBI GI q4454022 BLAST score 371 0.0e + 00E value 465 Match length % identity 97

Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 NCBI Description

(ESSAII project)

134351 Seq. No.

101462 1.R1010 Contig ID

jC-atXP94CG11A8T7045d1 5'-most EST

Method BLASTX NCBI GI q4759286 BLAST score 65 2.0e-14 E value 85 Match length 47 % identity

uncoupling protein 4 >gi 4324701_gb_AAD16995_ (AF110532) NCBI Description

uncoupling protein UCP-4 [Homo sapiens]

134352 Seq. No.

101465_1.R1010 Contig ID



```
iC-atXP94CG11A2T7005d1
5'-most EST
                  BLASTX
Method
                  g1652678
NCBI GI
                  49
BLAST score
                  6.0e-12
E value
                  103
Match length
                  48
% identity
                  (D90907) amidase [Synechocystis sp.]
NCBI Description
                  134353
Seq. No.
                  101466 1.R1010
Contig ID
                  jC-atXP94CG11A12T7077d1
5'-most EST
                  BLASTX
Method
                  g3047104
NCBI GI
BLAST score
                  256
                  7.0e-22
E value
                  118
Match length
                  51
% identity
                  (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
                  134354
Seq. No.
                   101474_1.R1010
Contig ID
                   jC-atXP89CG6E6T7094d1
5'-most EST
                   BLASTN
Method
                   g2696018
NCBI GI
                   274
BLAST score
                   1.0e-152
E value
                   443
Match length
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134355
Contig ID
                   101495 2.R1010
                   jC-atXP89CG6B5T7013d1
5'-most EST
                   134356
Seq. No.
Contig ID
                   101510 1.R1010
                   jC-atXP89C245C6T7063d1
5'-most EST
                   134357
Seq. No.
                   101518 1.R1010
Contig ID
                   jC-atXP89C245B2T7036d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3877655
BLAST score
                   218
                   3.0e-17
E value
                   73
Match length
% identity
                   56
                   (Z72511) possible zinc finger protein; cDNA EST EMBL:M89115
NCBI Description
                   comes from this gene; cDNA EST EMBL:D71533 comes from this
```

gene; cDNA EST EMBL:D72314 comes from this gene; cDNA EST EMBL: D75164 comes from this gene; cDNA EST EMBL: C1

Seq. No. 134358

101520 1.R1010 Contig ID

jC-atXP89C245B19T7060d1 5'-most EST



Method BLASTX
NCBI GI g1565227
BLAST score 433
E value 2.0e-42
Match length 156
% identity 63

NCBI Description (X95573) salt-tolerance zinc finger protein [Arabidopsis

thaliana]

Seq. No. 134359

Contig ID 101524_1.R1010

5'-most EST jC-atXP89C245A15T7020d1

Method BLASTX
NCBI GI g2244896
BLAST score 1077
E value 1.0e-118
Match length 227
% identity 94

NCBI Description (Z97338) similar to HSR201 protein N.tabacum [Arabidopsis

thaliana]

Seq. No. 134360

Contig ID 101526_1.R1010

5'-most EST jC-atXP89C244P2T7035d1

Method BLASTX
NCBI GI g4467096
BLAST score 578
E value 8.0e-79
Match length 157
% identity 71

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 134361

Contig ID 101531_1.R1010

5'-most EST jC-atXP89C244P16T7059d1

Seq. No. 134362

Contig ID 101538_1.R1010

5'-most EST jC-atXP89C244M23T7082d1

Method BLASTN
NCBI GI g3046851
BLAST score 318
E value 1.0e-179
Match length 488
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No. 134363

Contig ID 101540_1.R1010



NCBI Description Arabidopsis thaliana BAC T3H13

134364 Seq. No. 101540 2.R1010 Contig ID 5'-most EST g1269450 BLASTN Method NCBI GI g3367500 BLAST score 444 0.0e + 00E value 460 Match length 99 % identity

NCBI Description REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1

TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No. 134365

Contig ID 101542 1.R1010

5'-most EST jC-atXP89C244L13T7050d1

Method BLASTX
NCBI GI g2506938
BLAST score 566
E value 3.0e-58
Match length 154
% identity 75

NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4, CHLOROPLAST

Seq. No. 134366

Contig ID 101564_1.R1010 5'-most EST jC-atXP87CG8H1T7b1

Method BLASTX
NCBI GI g3355464
BLAST score 185
E value 1.0e-13
Match length 147
% identity 40

NCBI Description (AC004218) putative ATP-binding-cassette protein, 3'

partial [Arabidopsis thaliana]

Seq. No. 134367

Contig ID 101586_1.R1010 5'-most EST jC-atXP87CG8E10T7b1

Method BLASTX
NCBI GI g3402672
BLAST score 335
E value 4.0e-31
Match length 100
% identity 64

NCBI Description (AC004697) putative white protein [Arabidopsis thaliana]

Seq. No. 134368

Contig ID 101596_1.R1010 5'-most EST jC-atXP87CG10H7T7b1

Seq. No. 134369

Contig ID 101598_1.R1010

5'-most EST $g50701\overline{3}$ Method BLASTX NCBI GI g267120



BLAST score 174 E value 9.0e-23 Match length 85 % identity 67

NCBI Description THIOREDOXIN F-TYPE PRECURSOR (TRX-F) >gi_100070_pir__S20929

thioredoxin f precursor - garden pea

>gi_20907_emb_CAA45098_ (X63537) thioredoxin F [Pisum

satīvum] >gi_1388086 (U35830) thioredoxin f [Pisum satīvum]

Seq. No. 134370

Contig ID 101600_1.R1010

5'-most EST jC-atXP87CG10H11T7b1

Method BLASTN
NCBI GI g3212102
BLAST score 458
E value 0.0e+00
Match length 465
% identity 100

NCBI Description Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM,

complete sequence [Arabidopsis thaliana]

Seq. No. 134371

Contig ID 101605 1.R1010

5'-most EST g2393148
Method BLASTN
NCBI GI g2264312
BLAST score 537
E value 0.0e+00
Match length 594
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOK16, complete sequence [Arabidopsis thaliana]

Seq. No. 134372

Contig ID 101606_1.R1010 5'-most EST jC-atXP87CG10G11T7b1

Method BLASTX
NCBI GI g4262167
BLAST score 625
E value 3.0e-65
Match length 124
% identity 96

NCBI Description (AC005275) putative LRR receptor-linked protein kinase

[Arabidopsis thaliana]

Seq. No. 134373

Contig ID 101611_1.R1010 5'-most EST jC-atX24061Q1E1C10a1

Method BLASTN
NCBI GI g2264318
BLAST score 379
E value 0.0e+00
Match length 591
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUP24, complete sequence [Arabidopsis thaliana]



Seq. No. 134374 Contig ID 101629 1.R1010 $jC-atX\overline{P}87C244H11T7b1$ 5'-most EST BLASTN Method g3080430 NCBI GI BLAST score 521 0.0e+00E value Match length 521 100 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19 (ESSAII project) 134375 Seq. No. 101642 1.R1010 Contig ID 5'-most EST jC-atXP87C244C12T7b1 BLASTX Method NCBI GI g2498069 BLAST score 215

E value 2.0e-21 118 Match length 51 % identity

NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE (NDK) (NDP KINASE) >gi_1353658 (U41267) Ndk [Pseudomonas aeruginosa]

Seq. No. 134376

101658_1.R1010 Contig ID jC-atXP84CG5G4T7b1 5'-most EST

BLASTX Method NCBI GI q3023956 BLAST score 58 3.0e-08 E value Match length 157 % identity

NCBI Description VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 >gi 607003 (L28125) beta transducin-like protein [Podospora anserina]

Seq. No. 134377

101658 2.R1010 Contig ID

5'-most EST q2048795 Method BLASTX NCBI GI q1346729 BLAST score 132 E value 2.0e-11 Match length 195 % identity 11

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA >gi_886024 NCBI Description (U23820) protein kinase PkwA [Thermomonospora curvata]

134378 Seq. No.

101681 1.R1010 Contiq ID jC-atXP84CG5D5T7b1 5'-most EST

BLASTN Method g4519791 NCBI GI 49 BLAST score 2.0e-18 E value 73 Match length 92 % identity



```
NCBI Description Arabidopsis thaliana mRNA for Aspl, complete cds
Seq. No.
                  134379
                  101693 1.R1010
Contig ID
                  jC-atXP84CG5B4T7b1
5'-most EST
                  BLASTN
Method
                  g416352
NCBI GI
                  36
BLAST score
                  1.0e-10
E value
                  44
Match length
                  95
% identity
                  Drosophila melanogaster C/EBP gene, complete cds
NCBI Description
                  134380
Seq. No.
                  101700 2.R1010
Contig ID
                  g2749613
5'-most EST
                  BLASTX
Method
                  g1103322
NCBI GI
                  205
BLAST score
                   6.0e-16
E value
                  63
Match length
                  71
% identity
                  (X78820) casein kinase I [Arabidopsis thaliana]
NCBI Description
                   134381
Seq. No.
                   101726 1.R1010
Contig ID
                   jC-atXP83CG3H2T7040a1
5'-most EST
                   BLASTX
Method
                   g1706130
NCBI GI
                   174
BLAST score
                   3.0e-12
E value
                   61
Match length
                   62
% identity
                  CDPK-RELATED PROTEIN KINASE (PK421) >gi_2129917_pir__S60052
NCBI Description
                   calcium-dependent protein kinase homolog - carrot
                   >gi_1103386_emb_CAA58750_ (X83869) CDPK-related protein
                   kinase [Daucus carota]
                   134382
Seq. No.
Contig ID
                   101734 1.R1010
                   jC-atXP83CG3G3T7071a1
5'-most EST
                   BLASTX
Method
                   g4185133
NCBI GI
                   525
BLAST score
                   2.0e-53
E value
                   147
Match length
                   73
% identity
                   (AC005724) putative zinc finger protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   134383
                   101775 1.R1010
Contig ID
                   jC-atXP2C78F1T7079a1
```

5'-most EST BLASTX Method g3873707 NCBI GI

BLAST score 216 7.0e-17 E value



Match length 147 % identity 38

NCBI Description (Z73102) Similarity to B. subtilis DNAJ protein

(SW:DNAJ_BACSU); cDNA EST yk437a1.5 comes from this gene

[Caenorhabditis elegans]

Seq. No. 134384

Contig ID 101778_1.R1010

5'-most EST g1268724

Seq. No. 134385

Contig ID 101783_1.R1010

5'-most EST jC-atXP83CG3D1T7029a1

Method BLASTN

NCBI GI g2833627

BLAST score 386

E value 0.0e+00

Match length 386
% identity 100

NCBI Description Arabidopsis thaliana chromosome 1 BAC F1707 complete

sequence [Arabidopsis thaliana]

Seq. No. 134386

Contig ID 101796_1.R1010

5'-most EST jC-atXP83CG3C4T7084d1

Seq. No. 134387

Contig ID 101799_1.R1010

5'-most EST jC-atXP83CG3C2T7076al

Method BLASTX
NCBI GI g2739376
BLAST score 551
E value 2.0e-56
Match length 112

Match length 112 % identity 96

NCBI Description (AC002505) putative permease [Arabidopsis thaliana]

Seq. No. 134388

Contig ID 101814 1.R1010

5'-most EST jC-atXP83CG3B10T7060a1

Method BLASTN
NCBI GI g4519193
BLAST score 462
E value 0.0e+00
Match length 466
% identity 53

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC11, complete sequence

Seq. No. 134389

Contig ID 101819 1.R1010

5'-most EST jC-atXP83CG3A6T7059d1

Method BLASTX
NCBI GI g3746059
BLAST score 804
E value 3.0e-86
Match length 161



% identity 95 NCBI Description (ACC

(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative

cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 134390

Contig ID 101830 1.R1010

5'-most EST jC-atXP83CG2H5T7096d1

Seq. No. 134391

Contig ID 101838_1.R1010

5'-most EST jC-atXP83CG2G7T7048a1

Method BLASTN
NCBI GI g4159708
BLAST score 405
E value 0.0e+00
Match length 439
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MKP6, complete sequence

Seq. No. 134392

Contig ID 101840 1.R1010

5'-most EST jC-atXP83CG2G11T7072a1

Method BLASTN
NCBI GI 94071007
BLAST score 36
E value 1.0e-10
Match length 40
% identity 97

NCBI Description Strongylocentrotus purpuratus stage specific activator

protein mRNA, complete cds

Seq. No. 134393

Contig ID 101897_1.R1010 5'-most EST jC-atXP78CF6D5T7b1

Seq. No. 134394

Contig ID 101956_1.R1010 5'-most EST jC-atXP78C229O4T7b1

Method BLASTX
NCBI GI g4490743
BLAST score 55
E value 2.0e-41
Match length 159
% identity 77

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 134395

Contig ID 101962_1.R1010 5'-most EST jC-atXP78C229L4T7b1

Seq. No. 134396

Contig ID 101997 1.R1010

5'-most EST jC-atXP70C221D24T7052a1

Method BLASTX NCBI GI g4512683



BLAST score 552 E value 1.0e-56 Match length 103 % identity 98

NCBI Description (AC006931) putative lipase [Arabidopsis thaliana]

>gi 4559323 gb AAD22985.1 AC007087_4 (AC007087) putative

lipase [Arabidopsis thaliana]

Seq. No. 134397

Contig ID 102030_1.R1010

5'-most EST jC-atXP70C220K21T7021a1

Method BLASTX
NCBI GI g4585907
BLAST score 414
E value 9.0e-79
Match length 153
% identity 99

NCBI Description (AC006298) unknown protein [Arabidopsis thaliana]

Seq. No. 134398

Contig ID 102033 1.R1010

5'-most EST jC-atXP70C220K15T7019a1

Method BLASTN
NCBI GI 94263813
BLAST score 168
E value 2.0e-89
Match length 215
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T13P21 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134399

Contig ID 102039 1.R1010

5'-most EST jC-atXP70C220H22T7058a1

Method BLASTX
NCBI GI g4335749
BLAST score 353
E value 2.0e-33
Match length 80
% identity 93

NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 134400

Contig ID 102049 1.R1010

5'-most EST jC=atXP70C220D2T7049a1

Method BLASTN
NCBI GI g2564050
BLAST score 344
E value 0.0e+00
Match length 384
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUA22, complete sequence [Arabidopsis thaliana]

Seq. No. 134401

Contig ID 102056 1.R1010

5'-most EST jC-atXP69C220G13T7092d1



```
Method BLASTN
NCBI GI g3451055
BLAST score 264
E value 1.0e-146
Match length 730
% identity 98
```

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20

(ESSAII project)

Seq. No. 134402

Contig ID 102068 1.R1010

5'-most EST jC-atXP69C219M8T7047a1

Method BLASTN
NCBI GI g4455168
BLAST score 558
E value 0.0e+00
Match length 931
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10

(ESSAII project)

Seq. No. 134403

Contig ID 102068 2.R1010

5'-most EST jC-atXP69C219O8T7087a1

Method BLASTN
NCBI GI g3763944
BLAST score 362
E value 0.0e+00
Match length 594
% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23

(ESSAII project)

Seq. No. 134404

Contig ID 102084_1.R1010

5'-most EST jC-atXP69C219I4T7062a1

Method BLASTN
NCBI GI g4159706
BLAST score 291
E value 1.0e-162
Match length 755
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGL6, complete sequence

Seq. No. 134405

Contig ID 102108 1.R1010

5'-most EST jC-atXP69C218L18T7066a1

Method BLASTN
NCBI GI g2582640
BLAST score 38
E value 1.0e-11
Match length 38
% identity 100

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40



Seq. No. 134406 102117 1.R1010 Contig ID 5'-most EST jC-atXP69C217N5T7028a1 Method BLASTN NCBI GI g3869072 BLAST score 425 0.0e+00E value Match length 767 % identity 94 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MJB24, complete sequence [Arabidopsis thaliana] 134407 Seq. No. Contig ID 102129 1.R1010 5'-most EST jC-atXP25C125G6T7086a1 BLASTN Method NCBI GI g2351066 BLAST score 440 0.0e + 00E value Match length 523 % identity 96 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MOP9, complete sequence [Arabidopsis thaliana] 134408 Seq. No. Contig ID 102134 1.R1010 5'-most EST jC-atXP69C217E19T7057a1 Method BLASTN NCBI GI g3800746 BLAST score 39 4.0e-12 E value Match length 39 100 % identity Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, NCBI Description complete cds 134409 Seq. No. 102144 1.R1010 Contig ID $jC-atX\overline{P}67C214I6T7060a1$ 5'-most EST Method BLASTX q3360289 NCBI GI BLAST score 339 2.0e-31 E value Match length 85 % identity 78 NCBI Description 1 [Zea mays]

(AF023164) leucine-rich repeat transmembrane protein kinase

Seq. No. 134410

Contig ID 102188 1.R1010

5'-most EST jC-atXP67C213F20T7021a1

Method BLASTX NCBI GI q4454009 BLAST score 497 E value 9.0e-71 Match length 157 % identity 89



NCBI Description (AL035396) putative protein [Arabidopsis thaliana]

Seq. No. 134411

Contig ID 102196 1.R1010

Method BLASTN
NCBI GI g1707006
BLAST score 381
E value 0.0e+00
Match length 453
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC T1B8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134412

Contig ID 102212 1.R1010

5'-most EST jC-atXP67C212C9T7042a1

Method BLASTN
NCBI GI g2244788
BLAST score 124
E value 5.0e-63
Match length 544
% identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 134413

Contig ID 102231_1.R1010

5'-most EST jC-atXP66C211C6T7016a1

Method BLASTN
NCBI GI g531828
BLAST score 53
E value 1.0e-20
Match length 67
% identity 96

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 134414

Contig ID 102247 1.R1010

5'-most EST jC-atXP66C210M14T7014a1

Method BLASTN
NCBI GI g4415905
BLAST score 229
E value 1.0e-125
Match length 675
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC F13K3 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134415

Contig ID 102249 1.R1010

5'-most EST jC-atXP66C210L23T7006a1

Method BLASTN
NCBI GI g3702731
BLAST score 407
E value 0.0e+00
Match length 467



```
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFC19, complete sequence [Arabidopsis thaliana]
                  134416
Seq. No.
                  102251 1.R1010
Contig ID
5'-most EST
                  jC-atXP66C210L14T7077a1
                  134417
Seq. No.
                  102251_2.R1010
Contig ID
5'-most EST
                  g458782
Seq. No.
                  134418
Contig ID
                  102254 2.R1010
5'-most EST
                  jC-atXP66C210K13T7045a1
                  BLASTX
Method
                  g3176726
NCBI GI
BLAST score
                  289
E value
                  8.0e-26
                  94
Match length
                  62
% identity
                  (AC002392) putative serine proteinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  134419
Contig ID
                  102265 1.R1010
5'-most EST
                  jC-atXP66C210G6T7012a1
                  BLASTN
Method
NCBI GI
                  g3402695
BLAST score
                  65
E value
                  6.0e-28
Match length
                  125
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T3K9 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  134420
Contig ID
                  102274 1.R1010
5'-most EST
                  jC-atXP19C109K2T7053a1
Method
                  BLASTN
NCBI GI
                  a3869064
BLAST score
                  81
E value
                  3.0e-37
Match length
                  141
% identity
                  90
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K1013, complete sequence [Arabidopsis thaliana]
Seq. No.
                  134421
                  102274 2.R1010
Contig ID
                  g1158495
5'-most EST
```

Method BLASTX
NCBI GI g3047104
BLAST score 312
E value 2.0e-28
Match length 89
% identity 66



NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 134422

Contig ID 102281 1.R1010

Seq. No. 134423

Contig ID 102304_1.R1010

5'-most EST jC-atXP66C208N19T7089a1

Method BLASTN
NCBI GI g4756963
BLAST score 255
E value 1.0e-141
Match length 443
% identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23

(ESSA project)

Seq. No. 134424

Contig ID 102319 2.R1010

5'-most EST jC-atXP62C204A22T7071a1

Method BLASTN
NCBI GI g2760316
BLAST score 260
E value 1.0e-144
Match length 435
% identity 96

NCBI Description The sequence of BAC F1N21 from Arabidopsis thaliana

chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 134425

Contig ID 102341 1.R1010

5'-most EST jC-atXP62C203B4T7061a1

Method BLASTX
NCBI GI g3169175
BLAST score 179
E value 5.0e-13
Match length 40
% identity 82

NCBI Description (AC004401) putative serine carboxypeptidase I [Arabidopsis

thaliana]

Seq. No. 134426

Contig ID 102354 1.R1010

5'-most EST jC-atXP62C202M10T7066a1

Method BLASTX
NCBI GI g2244888
BLAST score 349
E value 1.0e-32
Match length 155
% identity 45

NCBI Description (Z97338) similarity to cytochrome P450 [Arabidopsis

thaliana]

Seq. No. 134427

Contig ID 102356_1.R1010

5'-most EST g1054301



```
BLASTX
Method
NCBI GI
                   q1064883
                   234
BLAST score
                   2.0e-19
E value
Match length
                   136
                   40
% identity
NCBI Description (X92976) ZAP1 [Arabidopsis thaliana]
                   134428
Seq. No.
                   102361 1.R1010
Contig ID
                   jC-atX\overline{P}81C240M6T7s1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2494140
                   333
BLAST score
                   1.0e-30
E value
                   127
Match length
                   51
% identity
NCBI Description
                   (AC003002) R29515 1 [Homo sapiens] >gi 3068727 (AF058918)
                   unknown [Homo sapiens]
                   134429
Seq. No.
                   102364 1.R1010
Contig ID
                   jC-atX\overline{P}62C202H21T7057a1
5'-most EST
Method
                   BLASTX
                   a2829925
NCBI GI
                   1048
BLAST score
                   1.0e-114
E value
                   221
Match length
% identity
                   94
                   (AC002291) Similar to dnaj-like protein, gp Y11969 2230757
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                   134430
                   102381 1.R1010
Contig ID
5'-most EST
                   jC-atXP62C201N13T7091a1
Method
                   BLASTX
NCBI GI
                   g3402699
BLAST score
                   499
E value
                   2.0e-50
Match length
                   89
 % identity
                   100
NCBI Description (AC004261) unknown protein [Arabidopsis thaliana]
Seq. No.
                   134431
                   102391 1.R1010
Contig ID
                   jC-atXP60C200E12T7077d1
 5'-most EST
Method
                   BLASTX
NCBI GI
                   q400483
BLAST score
                   515
                   4.0e-52
E value
                   203
Match length
                   51
% identity
```

NCBI Description BACTERIOPHAGE N4 ADSORPTION PROTEIN B

>gi_538730_pir__A49351 bacteriophage N4 adsorption inner

membrane protein nfrB - Escherichia coli >gi_290459

(L16945) GTG start codon [Escherichia coli]

>gi 1651237 dbj BAA35203 (D90699) Bacteriophage n4



adsorption inner membrane protein NfrB. [Escherichia coli] >gi_1778484 (U82598) bacteriophage N4 adsorption protein B precursor [Escherichia coli] >gi_1786781 (AE000161) bacteriophage N4 receptor, outer membrane protein [Escherichia coli]

Seq. No. 134432

Contig ID 102393_1.R1010

5'-most EST jC-atXP60C198B24T7059d1

Method BLASTX
NCBI GI g4027895
BLAST score 300
E value 2.0e-31
Match length 104
% identity 60

NCBI Description (AF049352) alpha-expansin precursor [Nicotiana tabacum]

Seq. No. 134433

Contig ID 102394 1.R1010

5'-most EST jC-atXP60C200D4T7069a1

Method BLASTX
NCBI GI g1040877
BLAST score 220
E value 9.0e-18
Match length 62
% identity 63

NCBI Description (U30460) expansin S2 precursor [Cucumis sativus]

Seq. No. 134434

Contig ID 102405_1.R1010

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 134435

Contig ID 102405 2.R1010

5'-most EST jC-atXP60C200A22T7045d1

Method BLASTN
NCBI GI g2244901
BLAST score 279
E value 1.0e-155
Match length 407
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 134436

Contig ID 102412_1.R1010

 5'-most EST
 g1054196

 Method
 BLASTX

 NCBI GI
 g2979562



BLAST score 289 E value 7.0e-26 Match length 98 % identity 59

NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]

>gi_3386623 (AC004665) unknown protein [Arabidopsis

thaliana]

Seq. No. 134437

Contig ID 102412_2.R1010

5'-most EST jC-atXP60C199K22T7084d1

Method BLASTX
NCBI GI g2979562
BLAST score 154
E value 7.0e-10
Match length 52
% identity 60

NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]

>qi 3386623 (AC004665) unknown protein [Arabidopsis

thaliana]

Seq. No. 134438

Contig ID 102428 1.R1010

5'-most EST g1053435
Method BLASTN
NCBI GI g2262097
BLAST score 478
E value 0.0e+00
Match length 675
% identity 99

NCBI Description Arabidopsis thaliana chromosome IV BAC T19F6 genomic

sequence, complete sequence

Seq. No. 134439

Contig ID 102432 1.R1010

5'-most EST jC-atXP60C199F15T7080d1

Seq. No. 134440

Contig ID 102441 1.R1010

5'-most EST jC-at $\overline{XP}60C198020T7064d1$

Method BLASTX
NCBI GI g3152568
BLAST score 300
E value 4.0e-49
Match length 118
% identity 96

NCBI Description (AC002986) Similar to hypothetical protein product

gb Z97337 from A. thaliana. EST gb_H76597 comes from this

gene. [Arabidopsis thaliana]

Seq. No. 134441

Contig ID 102479_1.R1010

5'-most EST jC-atXP60C198H14T7086d1

Method BLASTX
NCBI GI g4335773
BLAST score 212
E value 9.0e-17



```
Match length
% identity
                   62
                  (AC006284) unknown protein [Arabidopsis thaliana]
NCBI Description
                  134442
Seq. No.
Contig ID
                  102488 1.R1010
5'-most EST
                  jC-atXP60C198F3T7014a1
                  134443
Seq. No.
Contig ID
                  102512 1.R1010
5'-most EST
                  q1053548
Method
                  BLASTN
```

NCBI GI q4249393 BLAST score 317 1.0e-178 E value 414 Match length % identity

Arabidopsis thaliana chromosome II BAC T9J23 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

134444 Seq. No.

Contig ID 102519 1.R1010

5'-most EST jC-atXP60C197I20T7050a1

Method BLASTX q2462741 NCBI GI BLAST score 306 1.0e-27 E value 61 Match length % identity 98

(AC002292) Highly similar to auxin-induced protein NCBI Description (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 134445

102529 1.R1010 Contig ID

5'-most EST jC-atXP60C197G24T7049d1

BLASTN Method NCBI GI q531828 BLAST score 51 E value 2.0e-19 Match length 70 % identity 94

NCBI Description Cloning vector pSport1, complete cds

134446 Seq. No.

102529 2.R1010 Contig ID

jC-atXP38C158H22T7d1 5'-most EST

Method BLASTX NCBI GI q4432823 BLAST score 330 1.0e-30 E value Match length 104 59 % identity

NCBI Description (AC006593) hypothetical protein [Arabidopsis thaliana]

134447 Seq. No.

102536 1.R1010 Contig ID

5'-most EST jC-atXP60C196P6T7043d1



Contig ID 102549_1.R1010

5'-most EST jC-atXP25C125F22T7054a1

Method BLASTN
NCBI GI g4757411
BLAST score 187
E value 1.0e-100
Match length 416
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MXC7, complete sequence

Seq. No. 134449

Contig ID 102549 2.R1010

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MXC7, complete sequence

Seq. No. 134450

Contig ID 102551 1.R1010

5'-most EST jC-atXP57C192C1T7080a1

Method BLASTN
NCBI GI g2656025
BLAST score 333
E value 0.0e+00
Match length 422
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCD7

Seq. No. 134451

Contig ID 102552 1.R1010

5'-most EST q958212

Seq. No. 134452

Contig ID 102565 1.R1010

5'-most EST jC-atXP57C192A5T7052a1

Method BLASTN
NCBI GI g2462264
BLAST score 33
E value 8.0e-09
Match length 53
% identity 91

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 134453

Contig ID 102569 1.R1010

5'-most EST jC-atXP43C163P22T7056d1

Method BLASTX NCBI GI g4218991



BLAST score 563 E value 9.0e-58 Match length 118 % identity 95

NCBI Description (AF098632) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 134454

Contig ID 102572 1.R1010

5'-most EST jC-atXP57C192A3T7050a1

Seq. No. 134455

Contig ID 102584 1.R1010

5'-most EST jC-atXP57C190H19T7009a1

Method BLASTN
NCBI GI g2689438
BLAST score 276
E value 1.0e-154
Match length 350
% identity 98

NCBI Description Arabidopsis thaliana BAC F2401 chromosome 1, complete

sequence [Arabidopsis thaliana]

Seq. No. 134456

Contig ID 102605 1.R1010

Method BLASTN
NCBI GI g3449321
BLAST score 279
E value 1.0e-155
Match length 414
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTG10, complete sequence [Arabidopsis thaliana]

Seq. No. 134457

Contig ID 102617 1.R1010

5'-most EST jC-atXP57C190J16T7019a1

Method BLASTN
NCBI GI g2290120
BLAST score 51
E value 2.0e-19
Match length 66
% identity 96

NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No. 134458

Contig ID 102619 1.R1010

5'-most EST jC-atXP57C190I9T7013a1

Method BLASTN
NCBI GI g4587641
BLAST score 416
E value 0.0e+00
Match length 420
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic

sequence, complete sequence

Match length

525 99



```
Seq. No.
                  134459
                  102663 1.R1010
Contig ID
                   jC-atXP54C186H2T7095a1
5'-most EST
                  BLASTN
Method
                  g3869075
NCBI GI
BLAST score
                   98
                  1.0e-47
E value
Match length
                   374
% identity
                   88
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXK3, complete sequence [Arabidopsis thaliana]
                   134460
Seq. No.
                   102675 1.R1010
Contig ID
5'-most EST
                   g2445913
                  BLASTX
Method
NCBI GI
                   g4584257
BLAST score
                   258
                   4.0e-22
E value
                   110
Match length
                  54
% identity
                  (Y18472) SINA2p [Vitis vinifera]
NCBI Description
                   134461
Seq. No.
Contig ID
                   102675 2.R1010
5'-most EST
                   jC-atXP54C186F24T7047d1
Method
                   BLASTX
NCBI GI
                   g4584255
BLAST score
                   521
                   5.0e-53
E value
                   135
Match length
% identity
                   76
NCBI Description
                  (Y18471) SINAlp [Vitis vinifera]
Seq. No.
                   134462
Contig ID
                   102689 1.R1010
                   jC-atXP54C186E19T7038a1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q4539448
BLAST score
                   235
E value
                   1.0e-129
Match length
                   395
% identity
                   91
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23
NCBI Description
                   (ESSA project)
Seq. No.
                   134463
                   102691 2.R1010
Contig ID
                   g2445900
5'-most EST
                   BLASTN
Method
                   q4455348
NCBI GI
BLAST score
                   503
                   0.0e+00
E value
```

% identity 99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8



(ESSAII project)

Seq. No. 134464

Contig ID 102701_1.R1010

5'-most EST jC-atXP54C185N3T7068d1

Method BLASTN
NCBI GI 94580454
BLAST score 107
E value 5.0e-53
Match length 408
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T2G17 genomic

sequence, complete sequence

Seq. No. 134465

Contig ID 102718 1.R1010

5'-most EST jC-atXP54C186B15T7019a1

Method BLASTN
NCBI GI g3860243
BLAST score 209
E value 1.0e-114
Match length 333
% identity 92

NCBI Description Arabidopsis thaliana chromosome II BAC F15K20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134466

Contig ID 102735 1.R1010

5'-most EST jC-atXP54C185P17T7029d1

Method BLASTN
NCBI GI g2961335
BLAST score 207
E value 1.0e-112
Match length 445
% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20

(ESSAII project)

Seq. No. 134467

Contig ID 102736 1.R1010

5'-most EST g957922

Method BLASTX

NCBI GI g4753652

BLAST score 171

E value 8.0e-16

Match length 123

% identity 49

NCBI Description (AL049751) short-chain alcohol dehydrogenase like protein

[Arabidopsis thaliana]

Seq. No. 134468

Contig ID 102750_1.R1010

 5'-most EST
 g2445897

 Method
 BLASTX

 NCBI GI
 g2494749

 BLAST score
 147

 E value
 5.0e-09



Match length % identity 33

GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE) (GS) NCBI Description

>gi 1134886 emb CAA54030 (X76490) glutamine synthetase

[Staphylococcus aureus]

Seq. No. 134469

102763 1.R1010 Contig ID

 $jC-atX\overline{P}54C184P8T7081a1$ 5'-most EST

BLASTN Method q3047100 NCBI GI BLAST score 174 E value 5.0e-93 290 Match length 92 % identity

NCBI Description Arabidopsis thaliana BAC F6N23

Seq. No. 134470

102787 1.R1010 Contig ID

jC-atXP53C185F10T7079a1 5'-most EST

Method BLASTX NCBI GI g3482924 BLAST score 55 E value 6.0e-54 Match length 114 % identity

(AC003970) Highly similar to cinnamyl alcohol NCBI Description

dehydrogenase, gi 1143445 [Arabidopsis thaliana]

134471 Seq. No.

102789 1.R1010 Contig ID

5'-most EST jC-atXP53C185E10T7063a1

Seq. No. 134472

102790 1.R1010 Contig ID

5'-most EST jC-atXP53C185D3T7031d1

Method BLASTN NCBI GI q3941523 BLAST score 50 6.0e-19 E value Match length 50 % identity 100

Arabidopsis thaliana putative transcription factor (MYB92) NCBI Description

mRNA, complete cds

134473 Seq. No.

102806 1.R1010 Contig ID

5'-most EST jC-atXP53C185B13T7092d1

BLASTX Method q1871178 NCBI GI BLAST score 778 3.0e-86 E value 167 Match length % identity 91

NCBI Description (U90439) unknown protein [Arabidopsis thaliana]

Seq. No. 134474

Match length

NCBI Description

% identity

163 66



```
102828 1.R1010
Contig ID
                  jC-atXP53C184J10T7038d1
5'-most EST
Method
                  BLASTX
                  g2281083
NCBI GI
BLAST score
                  254
E value
                  8.0e-72
Match length
                  206
                  73
% identity
                  (AC002333) polygalacturonase isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  102828 2.R1010
Contig ID
5'-most EST
                  jC-atXP90C246F17T7d2
Method
                  BLASTX
NCBI GI
                  q2281083
BLAST score
                   435
E value
                  5.0e-43
Match length
                  156
% identity
                   63
NCBI Description
                  (AC002333) polygalacturonase isolog [Arabidopsis thaliana]
                  134476
Seq. No.
Contig ID
                  102836 1.R1010
5'-most EST
                   jC-atXP53C184H18T7069a1
                  BLASTN
Method
                  a2351063
NCBI GI
BLAST score
                  270
                  1.0e-150
E value
Match length
                   501
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCL19, complete sequence [Arabidopsis thaliana]
                   134477
Seq. No.
                   102892 1.R1010
Contig ID
                   jC-atXP50C180L21T7094d1
5'-most EST
Method
                   BLASTX
                   q419760
NCBI GI
BLAST score
                   268
                   3.0e-23
E value
                   118
Match length
                   24
% identity
                  P-glycoprotein atpgpl - Arabidopsis thaliana
NCBI Description
                   >gi 3849833 emb CAA43646 (X61370) P-glycoprotein
                   [Arabidopsis thaliana]
Seq. No.
                   134478
                   102896 1.R1010
Contig ID
5'-most EST
                   jC-atXP50C180K16T7054d1
Method
                   BLASTX
                   q1730149
NCBI GI
                   399
BLAST score
                   2.0e-45
E value
```

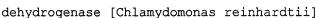
15926

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,

CHLOROPLAST >gi 1181548 (L27668) glyceraldehyde-3-phosphate

E value Match length





Seq. No. 134479 102898 1.R1010 Contig ID jC-atXP50C180J23T7022d1 5'-most EST Method BLASTX NCBI GI g2443876 BLAST score 238 8.0e-20 E value Match length 95 60 % identity (AC002294) Hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 134480 102900 1.R1010 Contig ID 5'-most EST jC-atXP50C180J13T7093d1 134481 Seq. No. Contig ID 102954 1.R1010 jC-atXP50C179E11T7051d1 5'-most EST BLASTX Method g4455217 NCBI GI BLAST score 508 , E value 3.0e-60 Match length 161 77 % identity (AL035440) Avr9 elicitor response like protein [Arabidopsis NCBI Description thaliana] Seq. No. 134482 102956 1.R1010 Contig ID $jC-atX\overline{P}50C179D10T7019d1$ 5'-most EST BLASTX Method NCBI GI q3450842 BLAST score 376 1.0e-40 E value Match length 159 53 % identity NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza satival Seq. No. 134483 Contig ID 102973 1.R1010 5'-most EST jC-atXP45C172B22T7015a1 Seq. No. 134484 Contig ID 102999 1.R1010 5'-most EST g2733772 Seq. No. 134485 103002 1.R1010 Contig ID 5'-most EST jC-atXP45C171L9T7005a1 BLASTN Method NCBI GI g4589434 BLAST score 402

15927

0.0e+00



```
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNJ7, complete sequence
                  134486
Seq. No.
Contig ID
                  103016 1.R1010
5'-most EST
                  jC-atXP45C171I4T7075a1
                  BLASTX
Method
                  g1616787
NCBI GI
BLAST score
                  345
E value
                  2.0e-32
Match length
                  68
% identity
                  96
                  (U71122) pyruvate decarboxylase [Arabidopsis thaliana]
NCBI Description
                  134487
Seq. No.
                  103039 1.R1010
Contig ID
                   jC-atX\overline{P}45C170N11T7002a1
5'-most EST
Method
                  BLASTX
                  q3367522
NCBI GI
BLAST score
                  376
                  9.0e-36
E value
Match length
                  124
% identity
                  53
                  (AC004392) EST gb T04691 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  134488
Seq. No.
Contig ID
                  103055 1.R1010
5'-most EST
                   jC-atXP11C98020T7082d1
Method
                  BLASTX
NCBI GI
                   q4678360
BLAST score
                   944
E value
                   1.0e-102
Match length
                   209
% identity
                   90
                   (AL049659) Cytochrome P450-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   134489
Seq. No.
                   103061 1.R1010
Contig ID
                   jC-atXP11C98K3T7065d1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3702728
BLAST score
                   504
                   0.0e + 00
E value
Match length
                   684
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19M13, complete sequence [Arabidopsis thaliana]
                   134490
Seq. No.
                   103063 1.R1010
Contig ID
```

5'-most EST jC-atXP24C122I20T7068d1

BLASTX Method NCBI GI g2244891 BLAST score 86



E value 1.0e-102 Match length 227 % identity 92

NCBI Description (Z97338) strong similarity to cytochrome P450 [Arabidopsis

thaliana]

Seq. No. 134491

Contig ID 103065_1.R1010

5'-most EST jC-atXP11C98J7T7062d1

Method BLASTX
NCBI GI g2370459
BLAST score 465
E value 4.0e-46
Match length 112
% identity 80

NCBI Description (Y11987) FPF1 protein [Sinapis alba]

Seq. No. 134492

Contig ID 103085 2.R1010

5'-most EST jC-atXP11C97P16T7034d1

Method BLASTX
NCBI GI g2765817
BLAST score 540
E value 2.0e-71
Match length 172
% identity 84

NCBI Description (Z95352) AtMlo-h1 [Arabidopsis thaliana]

>gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1

[Arabidopsis thaliana]

Seq. No. 134493

Contig ID 103097 1.R1010

5'-most EST jC-atXP11C97H2T7012d1

Method BLASTN
NCBI GI g3128141
BLAST score 355
E value 0.0e+00
Match length 863
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQD22, complete sequence [Arabidopsis thaliana]

Seq. No. 134494

Contig ID 103102 1.R1010

5'-most EST jC-atXP11C97E4T7003d1

Method BLASTX
NCBI GI g4586114
BLAST score 105
E value 3.0e-21
Match length 107
% identity 50

NCBI Description (AL049638) putative protein [Arabidopsis thaliana]

Seq. No. 134495

Contig ID 103229_1.R1010

5'-most EST jC-atXP101CE2C10T7015d1



Contig ID 103229_2.R1010 5'-most EST jC-atXP75C225K17T7s1

Method BLASTX
NCBI GI g4467100
BLAST score 363
E value 3.0e-34
Match length 150
% identity 49

NCBI Description (AL035538) MADS-box protein AGL17-like protein [Arabidopsis

thaliana]

Seq. No. 134497

Contig ID 103253 1.R1010

5'-most EST jC-atXP101CE2A12T7061d1

Seq. No. 134498

Contig ID 103271 1.R1010

5'-most EST jC-atXP101CE1G8T7075d1

Method BLASTX
NCBI GI g4490309
BLAST score 422
E value 4.0e-41
Match length 197
% identity 34

NCBI Description (AL035678) peroxidase ATP17a-like protein [Arabidopsis

thaliana]

Seq. No. 134499

Contig ID 103297 1.R1010

5'-most EST jC-atXP101CE1E7T7034d1

Method BLASTX
NCBI GI g4262239
BLAST score 569
E value 1.0e-58
Match length 156
% identity 57

NCBI Description (AC006200) putative membrane transporter [Arabidopsis

thaliana]

Seq. No. 134500

Contig ID 103298_1.R1010 5'-most EST jC-alx25043Q1E1H07a1

Method BLASTN
NCBI GI g4262221
BLAST score 255
E value 1.0e-141
Match length 552
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F10A8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134501

Contig ID 103341_1.R1010 5'-most EST jC-alX22037Q1E1A04a1

Seq. No. 134502



```
Contig ID
                   103371 1.R1010
5'-most EST
                   jC-atX22085Q1E1A09a1
Method
                   BLASTN
                   q3046848
NCBI GI
BLAST score
                   64
                   2.0e-27
E value
Match length
                   236
% identity
                   82
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K18C1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134503
Contig ID
                   103380 1.R1010
                   g23931<del>9</del>8
5'-most EST
Seq. No.
                   134504
Contig ID
                   103382 1.R1010
5'-most EST
                   jC-atXP12C99L17T7019a1
Method
                   BLASTX
NCBI GI
                   g1495366
BLAST score
                   211
                   2.0e-16
E value
Match length
                   120
% identity
                   35
NCBI Description
                  (Z69370) nitrite transporter [Cucumis sativus]
Seq. No.
                   134505
                   103382 3.R1010
Contig ID
5'-most EST
                   jC-atXmonuni10Ab03a1
                   134506
Seq. No.
Contig ID
                   103390 1.R1010
5'-most EST
                   jC-atXmonuni10Bb02a1
Method
                   BLASTX
NCBI GI
                   q4204278
BLAST score
                   568
E value
                   1.0e-58
Match length
                   109
% identity
                   100
NCBI Description
                   (AC004146) putative Cytochrome P450 protein [Arabidopsis
                   thalianal
Seq. No.
                   134507
Contig ID
                   103421 1.R1010
5'-most EST
                   q315779
Method
                   BLASTX
NCBI GI
                   g2980774
BLAST score
                   351
                   2.0e-33
E value
Match length
                   68
% identity
                   99
                   (AL022198) leucyl aminopeptidase - like protein
NCBI Description
                   [Arabidopsis thaliana]
```

103444 1.R1010 Contig ID

5'-most EST jC-atXmonuni10Af02a1



Contig ID 103459_1.R1010 5'-most EST jC-atXmonuni10Bb06a1

Method BLASTN
NCBI GI g2760168
BLAST score 376
E value 0.0e+00
Match length 432
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MEE6, complete sequence [Arabidopsis thaliana]

Seq. No. 134510

Contig ID 103511_1.R1010 5'-most EST jC-alX22043Q1E1H08a1

Method BLASTX
NCBI GI g2894559
BLAST score 218
E value 1.0e-17
Match length 70
% identity 67

NCBI Description (AL021890) putative protein [Arabidopsis thaliana]

Seq. No. 134511

Contig ID 103523_1.R1010

5'-most EST jC-atXmonuni10Dc03a1

Method BLASTX
NCBI GI 94510342
BLAST score 389
E value 8.0e-38
Match length 85
% identity 87

NCBI Description (AC006921) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 134512

Contig ID 103526 1.R1010

5'-most EST g2764195
Method BLASTN
NCBI GI g4376087
BLAST score 483
E value 0.0e+00
Match length 525
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 134513

Contig ID 103557_1.R1010 5'-most EST jC-alX22044Q1E1H02a1

Seq. No. 134514

Contig ID 103599_1.R1010 5'-most EST jC-alX22045Q1E1F09a1

Method BLASTN NCBI GI g4538990



BLAST score 383
E value 0.0e+00
Match length 387
% identity 100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19
(ESSA project)

Seq. No. 134515
Contig ID 103615 1.R1010

Contig ID 103615 1.R1010 5'-most EST g2048276 Method BLASTN

NCBI GI g4262221 BLAST score 37 E value 4.0e-11 Match length 137 % identity 82

NCBI Description Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134516

Contig ID 103629_1.R1010 5'-most EST jC-atXP37C157M20T7d2

Method BLASTX
NCBI GI g3894178
BLAST score 88
E value 1.0e-27
Match length 112
% identity 54

NCBI Description (AC005312) putative nucleic acid binding protein

[Arabidopsis thaliana]

Seq. No. 134517

Contig ID 103636_1.R1010 5'-most EST jC-alX22046Q1E1D01a1

Method BLASTX
NCBI GI g3021279
BLAST score 313
E value 7.0e-29
Match length 67
% identity 93

NCBI Description (AL022347) serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 134518

Contig ID 103667_1.R1010 5'-most EST jC-alX22047Q1E1A11a1

Method BLASTX
NCBI GI g2982437
BLAST score 243
E value 1.0e-20
Match length 70
% identity 70

NCBI Description (AL022224) terpene cyclase like protein [Arabidopsis

thaliana]

Seq. No. 134519

Contig ID 103681_1.R1010 5'-most EST jC-atXmonuni10Df04a1



```
Method
                  BLASTX
NCBI GI
                  q4006818
BLAST score
                   300
E value
                   3.0e-27
                  59
Match length
                  100
% identity
NCBI Description
                  (AC005970) putative translation initiation factor eIF-2B,
                  alpha subunit [Arabidopsis thaliana]
Seq. No.
                  134520
Contig ID
                  103695 1.R1010
5'-most EST
                  q747703
Method
                  BLASTX
NCBI GI
                  q1841355
BLAST score
                  233
E value
                  2.0e-19
Match length
                  53
% identity
                  74
NCBI Description
                  (D85381) cytochrome c oxidase subunit Vb precursor [Oryza
                  sativa]
                  134521
Seq. No.
Contig ID
                  103741_1.R1010
5'-most EST
                  g1269157
Method
                  BLASTN
                  q4757402
NCBI GI
BLAST score
                  262
E value
                  1.0e-145
Match length
                  315
                  96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MIG5, complete sequence
Seq. No.
                  134522
Contig ID
                  103751 1.R1010
5'-most EST
                  jC-a1X22049Q1E1F03a1
Method
                  BLASTX
                  g2618689
NCBI GI
BLAST score
                  310
E value
                  2.0e-28
Match length
                  94
% identity
                   67
NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]
                  134523
Seq. No.
                  103770 1.R1010
Contig ID
5'-most EST
                  jC-alX22050Q1E1B04a1
Method
                  BLASTX
                  g4220485
NCBI GI
                  148
BLAST score
E value
                  2.0e-09
Match length
                   42
% identity
                   60
                  (AC006069) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                  thaliana]
```

NCBI Description

partial cds



```
103783 1.R1010
Contig ID
5'-most EST
                   jC-atXmonuni10Dg08a1
                   BLASTX
Method
                   q1523800
NCBI GI
BLAST score
                   211
                   8.0e-17
E value
Match length
                   69
% identity
                   55
                   (Y07694) MAP kinase kinase alpha protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   134525
Contig ID
                   103784 1.R1010
5'-most EST
                   jC-a1X22050Q1E1E04a1
Method
                   BLASTX
NCBI GI
                   g2961357
BLAST score
                   654
E value
                   2.0e-68
Match length
                   158
                   85
% identity
NCBI Description
                  (AL022140) putative protein [Arabidopsis thaliana]
                   134526
Seq. No.
Contig ID
                   103790 1.R1010
5'-most EST
                   jC-alX22050Q1E1F09a1
Method
                   BLASTN
NCBI GI
                   q3298532
BLAST score
                   380
E value
                   0.0e + 00
Match length
                   408
                   99
% identity
                   Arabidopsis thaliana chromosome II BAC T26B15 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   134527
Seq. No.
Contig ID
                   103798 1.R1010
5'-most EST
                   g2446099
                   BLASTX
Method
NCBI GI
                   g2827544
BLAST score
                   314
E value
                   8.0e-29
Match length
                   61
                   100
% identity
NCBI Description
                   (AL021635) HSP associated protein like [Arabidopsis
                   thaliana]
Seq. No.
                   134528
Contig ID
                   103818 1.R1010
5'-most EST
                   g2723264
Method
                   BLASTN
                   g3822224
NCBI GI
BLAST score
                   286
                   1.0e-160
E value
Match length
                   399
% identity
                   92
```

15935

Arabidopsis thaliana RING-H2 finger protein RHG1a mRNA,



134529

Seq. No.

```
103841 1.R1010
Contig ID
                   jC-a1X\overline{2}2082Q1E1A04a1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4589434
BLAST score
                   369
E value
                   0.0e+00
Match length
                   417
                   97
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MNJ7, complete sequence
                   134530
Seq. No.
                   103842 1.R1010
Contig ID
                   jC-atX22014Q1E1C04a1
5'-most EST
                   BLASTN
Method
                   g1839239
NCBI GI
BLAST score
                   384
                   0.0e + 00
E value
                   479
Match length
% identity
                   95
NCBI Description Arabidopsis thaliana aVps41p (AVPS41) gene, partial cds
Seq. No.
                   134531
                   103849 1.R1010
Contig ID
5'-most EST
                   jC-alX22082Q1E2A08a1
Method
                   BLASTX
NCBI GI
                   q4455341
BLAST score
                   348
E value
                   1.0e-32
Match length
                   80
% identity
NCBI Description
                   (AL035522) O-methyltransferase-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   134532
Contig ID
                   103937 1.R1010
5'-most EST
                   q1216080
Method
                   BLASTN
NCBI GI
                   q2894591
BLAST score
                   296
E value
                   1.0e-166
Match length
                   384
% identity
                   95
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21
NCBI Description
                   (ESSAII project)
                   134533
Seq. No.
                   103976 1.R1010
Contig ID
                   jC-alx\overline{2}4002Q1E1G08a1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4056476
                   39
BLAST score
E value
                   2.0e-12
                   132
Match length
                   86
% identity
```



NCBI Description Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134534

Contig ID 103990_1.R1010 5'-most EST jC-atXF94CH4F11T7b1

Seq. No. 134535

Contig ID 104004_1.R1010

5'-most EST jC-alX24004Q1E1A06a1

Method BLASTN
NCBI GI g3047100
BLAST score 267
E value 1.0e-148
Match length 500
% identity 99

NCBI Description Arabidopsis thaliana BAC F6N23

Seq. No. 134536

Contig ID 104016 1.R1010

5'-most EST jC-alX24004Q1E1D07a1

Seq. No. 134537

Contig ID 104041_1.R1010

5'-most EST jC-atXP34C153D10T7a1

Method BLASTX
NCBI GI g4335719
BLAST score 97
E value 6.0e-13
Match length 72
% identity 50

NCBI Description (AC006248) putative RING-H2 finger protein RHGla

[Arabidopsis thaliana]

Seq. No. 134538

Contig ID 104148_1.R1010 5'-most EST jC-atXP10C95G22T7s2

Method BLASTX
NCBI GI g475719
BLAST score 484
E value 1.0e-48
Match length 116
% identity 46

NCBI Description (U08467) RNA-binding protein 2 [Arabidopsis thaliana]

Seq. No. 134539

Contig ID 104250_1.R1010 5'-most EST jC-atX24009Q1E1G11a1 Method BLASTX

NCBI GI g3335372 BLAST score 560 E value 1.0e-57 Match length 109 % identity 100

NCBI Description (AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No. 134540



Contig ID 104297_1.R1010 5'-most EST jC-alX24077Q1E1A02a1

Method BLASTX
NCBI GI g2191152
BLAST score 660
E value 3.0e-69
Match length 143
% identity 89

NCBI Description (AF007269) A IG002N01.31 gene product [Arabidopsis

thaliana]

Seq. No. 134541

Contig ID 104406_1.R1010

5'-most EST jC-atXL1025Q1B1G06b1

Method BLASTN
NCBI GI g1255986
BLAST score 177
E value 8.0e-95
Match length 209
% identity 96

NCBI Description Arabidopsis thaliana GF14chi isoform (GRF1) gene, complete

cds

Seq. No. 134542

Contig ID 104542_1.R1010

NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic

sequence, complete sequence

Seq. No. 134543

Contig ID 104544 1.R1010

5'-most EST jC-atXP123C119P20T7043a1

Method BLASTX
NCBI GI g2213590
BLAST score 457
E value 3.0e-45
Match length 133
% identity 67

NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No. 134544

Contig ID 104664_1.R1010 5'-most EST jC-alX24089Q1E1F11a1

Seq. No. 134545

Contig ID 104684 1.R1010

5'-most EST jC-atXP25C125A5T7091a1

Seq. No. 134546

Contig ID 104698_1.R1010

5'-most EST $q25966\overline{3}9$



```
Method
                  BLASTX
NCBI GI
                  g2194117
BLAST score
                  267
                  3.0e-23
E value
                  103
Match length
                  54
% identity
                  (AC002062) Strong similarity to Arabidopsis receptor
NCBI Description
                  protein kinase PR5K (gb ATU48698). [Arabidopsis thaliana]
                  134547
Seq. No.
                  104706 1.R1010
Contig ID
                  jC-atX24061Q1E1C06a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2880051
BLAST score
                  234
                  2.0e-19
E value
                  70
Match length
                  67
% identity
                  (AC002340) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  134548
                  104719 1.R1010
Contig ID
5'-most EST
                  g1054203
Method
                  BLASTN
NCBI GI
                  g4220638
BLAST score
                  54
                   4.0e-21
E value
                  225
Match length
                   90
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIF21, complete sequence [Arabidopsis thaliana]
                  134549
Seq. No.
Contig ID
                  104719 2.R1010
                   jC-atXP33C151B13T7s2
5'-most EST
Seq. No.
                   134550
                   104757 1.R1010
Contig ID
5'-most EST
                   jC-alX24093Q1E1A05b1
Seq. No.
                   134551
                   104766 1.R1010
Contig ID
                   jC-a1X\overline{2}4093Q1E1C08a1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q2264305
BLAST score
                   347
E value
                   0.0e + 00
Match length
                   395
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBK23, complete sequence [Arabidopsis thaliana]
```

134552

Contig ID 104801_1.R1010

5'-most EST jC-at $X\overline{2}4063Q1E1E02a1$

Seq. No.

134553



Contig ID 104893 1.R1010 5'-most EST q1103341 134554 Seq. No. 105213 1.R1010 Contig ID $jC-a1X\overline{2}4132Q1E1B03a1$ 5'-most EST Method BLASTX q4007800 NCBI GI BLAST score 159 2.0e-10 E value Match length 54 % identity 48 (AL034463) hypothetical protein [Schizosaccharomyces pombe] NCBI Description 134555 Seq. No. Contig ID 105391 1.R1010 jC-alX\(\overline{2}\)5032Q1E1H03a1 5'-most EST Seq. No. 134556 Contig ID 105405 1.R1010 $jC-a1X\overline{2}5033Q1E1E04a1$ 5'-most EST Method BLASTX NCBI GI g2673910 BLAST score 177 1.0e-12 E value Match length 85 % identity 53 NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana] 134557 Seq. No. Contig ID 105443 1.R1010 5'-most EST jC-alX25036Q1E1F03a1 Method BLASTN NCBI GI g3746057 BLAST score 302 E value 1.0e-169 Match length 456 % identity 100 NCBI Description Arabidopsis thaliana chromosome II BAC T16B12 genomic sequence, complete sequence [Arabidopsis thaliana] 134558 Seq. No. 105476 1.R1010 Contig ID

5'-most EST $jC-a1X\overline{2}5042Q1E1A12a1$

Method BLASTX q4314365 NCBI GI BLAST score 428 2.0e-42 E value Match length 86 100 % identity

(AC006340) putative copia-like retrotransposon Hopscotch NCBI Description

[Arabidopsis thaliana]

134559 Seq. No.

105490 1.R1010 Contig ID 5'-most EST jC-atXmonuni25Ca07b1

Method BLASTN

Match length

% identity

113

7



```
NCBI GI
                   q4454587
BLAST score
                   346
                  0.0e+00
E value
                   497
Match length
                   99
% identity
                  Arabidopsis thaliana BAC F21A20 from chromosome V near 61
NCBI Description
                  cM, complete sequence [Arabidopsis thaliana]
                  134560
Seq. No.
Contig ID
                  105493 1.R1010
                   jC-alx\overline{2}5042Q1E1E01a1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2244950
BLAST score
                   335
E value
                   0.0e + 00
Match length
                   389
                   96
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  134561
Seq. No.
Contig ID
                   105498 1.R1010
5'-most EST
                   jC-atXmonuni25Ac01a1
Method
                  BLASTN
NCBI GI
                   q4455348
BLAST score
                   326
E value
                   0.0e + 00
Match length
                   429
% identity
                   100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8
                   (ESSAII project)
Seq. No.
                   134562
                   105506 1.R1010
Contig ID
5'-most EST
                   jC-atXP4C86H11T7027a1
                  BLASTX
Method
NCBI GI
                  q2160185
BLAST score
                   427
                   8.0e-42
E value
                   142
Match length
                   52
% identity
                   (ACO00132) Similar to S. pombe ISP4 (gb_D83992).
NCBI Description
                   [Arabidopsis thaliana]
                   134563
Seq. No.
                   105507 1.R1010
Contig ID
5'-most EST
                   jC-atXmonuni25Ac11a1
                   134564
Seq. No.
                   105517 1.R1010
Contig ID
5'-most EST
                   jC-a1X\overline{2}5042Q1E1H09a1
Method
                  BLASTX
NCBI GI
                   g4220475
BLAST score
                   114
E value
                   2.0e-05
```



NCBI Description (AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 134565

Contig ID 105518_1.R1010 5'-most EST jC-alX25042Q1E1H11a1

Method BLASTX
NCBI GI g4063755
BLAST score 153
E value 6.0e-10
Match length 70
% identity 49

NCBI Description (AC005851) putative chloroplast nucleoid DNA binding

protein [Arabidopsis thaliana]

Seq. No. 134566

Contig ID 105520_1.R1010 5'-most EST jC-alX25043Q1E1A03a1

Seq. No. 134567

Contig ID 105531_1.R1010

5'-most EST g2413254
Method BLASTN
NCBI GI g4581084
BLAST score 186
E value 1.0e-100
Match length 291
% identity 99

NCBI Description Arabidopsis thaliana chromosome I BAC T30F21 genomic

sequence, complete sequence

Seq. No. 134568

Contig ID 105533 1.R1010

5'-most EST jC-atXP112C126O22T7a1

Method BLASTX
NCBI GI g4056506
BLAST score 322
E value 2.0e-29
Match length 142
% identity 46

NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 134569

Contig ID 105540_1.R1010

5'-most EST jC-atXP44C171C15T7094a1

Method BLASTX
NCBI GI g3928150
BLAST score 568
E value 2.0e-58
Match length 162
% identity 75

NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]

Seq. No. 134570

Contig ID 105548_1.R1010 5'-most EST jC-atXmonuni25Cb02b1

Method BLASTN NCBI GI g2618599



```
BLAST score
E value
                   2.0e-53
Match length
                   175
                   90
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MBD2, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134571
Contig ID
                   105555 1.R1010
5'-most EST
                   jC-a1X\overline{2}5051Q1E1E04a1
Seq. No.
                   134572
Contig ID
                   105564 1.R1010
                   jC-alX25043Q1E1H06a1
5'-most EST
                   BLASTN
Method
NCBI GI
                   a2244829
BLAST score
                   101
E value
                   1.0e-49
Match length
                   230
                   43
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
Seq. No.
                   134573
                   105596 1.R1010
Contig ID
                   jC-atXmonuni25Cb06b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   a1663724
BLAST score
                   248
E value
                   4.0e-21
Match length
                   78
% identity
                   58
NCBI Description
                   (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
Seq. No.
                   134574
                   105600 1.R1010
Contig ID
5'-most EST
                   jC-atXmonuni25Ac08a1
Seq. No.
                   134575
                   105611 1.R1010
Contig ID
5'-most EST
                   jC-a1X25045Q1E1H04a1
Method
                   BLASTN
                   g4490734
NCBI GI
BLAST score
                   238
                   1.0e-131
E value
                   307
Match length
% identity
                   96
                   Arabidopsis thaliana DNA chromosome 4, BAC clone
NCBI Description
                                                                         (ESSA
                   project)
                   134576
Seq. No.
                   105619 1.R1010
Contig ID
5'-most EST
                   jC-a1X\overline{2}5045Q1E1B04a1
```

5'-most EST jC-alX25045Q1E
Method BLASTX
NCBI GI g4056488
BLAST score 157
E value 2.0e-10



Match length 81 % identity 60

NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 134577

Contig ID 105634_1.R1010 5'-most EST jC-atXmonuni25Db01a1

Seq. No. 134578

Contig ID 105638_1.R1010 5'-most EST jC-alX25045Q1E1E07a1

Method BLASTN
NCBI GI g3046853
BLAST score 335
E value 0.0e+00
Match length 360
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRA19, complete sequence [Arabidopsis thaliana]

Seq. No. 134579

Contig ID 105645_1.R1010 5'-most EST jC-alX25045Q1E1G01a1

Method BLASTX
NCBI GI g2129581
BLAST score 211
E value 9.0e-17
Match length 91
% identity 46

NCBI Description envelope Ca2+-ATPase precursor - Arabidopsis thaliana

>gi_471089_dbj_BAA03091_ (D13984) chloroplast envelope

Ca2+-ATPase precursor [Arabidopsis thaliana]

>gi_4165448_emb_CAA49558_ (X69940) envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 134580

Contig ID 105649_1.R1010

5'-most EST jC-atXmonuni25Ac08b1

Seq. No. 134581

Contig ID 105656_1.R1010 5'-most EST jC-alX25046Q1E1A11a1

Method BLASTN
NCBI GI g2191157
BLAST score 388
E value 0.0e+00
Match length 409
% identity 88

NCBI Description Arabidopsis thaliana BAC IG002P16

Seq. No. 134582

Contig ID 105669_1.R1010 5'-most EST jC-atXmonuni25Ce11b1

Method BLASTN
NCBI GI g2979540
BLAST score 330
E value 0.0e+00



Match length 387 % identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134583

Contig ID 105672 1.R1010

5'-most EST jC-atXmonuni25Ce09b1

Method BLASTN
NCBI GI g3702736
BLAST score 198
E value 1.0e-107
Match length 308
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRI1, complete sequence [Arabidopsis thaliana]

Seq. No. 134584

Contig ID 105680 1.R1010

5'-most EST g2062895
Method BLASTX
NCBI GI g2160176
BLAST score 294
E value 2.0e-26
Match length 83
% identity 67

NCBI Description (AC000132) F21M12.25 gene product [Arabidopsis thaliana]

Seq. No. 134585

Contig ID 105693_1.R1010 5'-most EST jC-alX25047Q1E1B01a1

Method BLASTN
NCBI GI g2656026
BLAST score 385
E value 0.0e+00
Match length 413
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDF20

Seq. No. 134586

Contig ID 105704_1.R1010 5'-most EST jC-atXmonuni25Ae06a1

Method BLASTN
NCBI GI g2760169
BLAST score 234
E value 1.0e-129
Match length 401
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MFB13, complete sequence [Arabidopsis thaliana]

Seq. No. 134587

Contig ID 105721_1.R1010 5'-most EST jC-atXmonuni25Cf11b1

Seq. No. 134588



Contig ID 105732_1.R1010 5'-most EST jC-alX25049Q1E1B02a1

Method BLASTN
NCBI GI g2645198
BLAST score 327
E value 0.0e+00
Match length 501
% identity 98

NCBI Description Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134589

Contig ID 105743_1.R1010 5'-most EST jC-atXmonuni25Ce05b1

Method BLASTN
NCBI GI 94589427
BLAST score 324
E value 0.0e+00
Match length 328
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MFG13, complete sequence

Seq. No. 134590

Contig ID 105752_1.R1010 5'-most EST jC-alX25048Q1E1G06a1

Seq. No. 134591

Contig ID 105756 1.R1010

5'-most EST g957476
Method BLASTX
NCBI GI g2493495
BLAST score 513
E value 1.0e-54
Match length 134
% identity 79

NCBI Description SERINE CARBOXYPEPTIDASE-LIKE >qi 2129878 pir S72370

carboxypeptidase - garden pea (fragment)

>gi_1089904_emb_CAA92216_ (Z68130) carboxypeptidase [Pisum sativum] >gi_1587217_prf__2206338A Ser carboxypeptidase

[Pisum sativum]

Seq. No. 134592

Contig ID 105756 2.R1010 5'-most EST jC-alX25048Q1E1G09a1

Method BLASTX
NCBI GI g2493495
BLAST score 324
E value 4.0e-30
Match length 78
% identity 71

NCBI Description SERINE CARBOXYPEPTIDASE-LIKE >qi 2129878 pir S72370

carboxypeptidase - garden pea (fragment)

>gi_1089904_emb_CAA92216_ (Z68130) carboxypeptidase [Pisum sativum] >gi_1587217_prf__2206338A Ser carboxypeptidase

[Pisum sativum]



```
134593
Seq. No.
Contig ID
                  105757 1.R1010
                  jC-alX25048Q1E1H02a1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4006815
BLAST score
                   323
                  0.0e + 00
E value
Match length
                  331
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T6P5 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  134594
Seq. No.
Contig ID
                  105762 1.R1010
5'-most EST
                   jC-alX25048Q1E1H12a1
                  BLASTX
Method
                   q1934730
NCBI GI
                   303
BLAST score
E value
                   1.0e-27
                   82
Match length
                  71
% identity
                  (U95036) germin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   134595
Contig ID
                   105764 1.R1010
5'-most EST
                   jC-atXmonuni25Ad05a1
                   BLASTN
Method
                   g3510338
NCBI GI
BLAST score
                   384
E value
                   0.0e + 00
Match length
                   384
% identity
                   100
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K21I16, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134596
Contig ID
                   105774 1.R1010
                   jC-atXP5C89H23T7038a1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q2462264
BLAST score
                   43
E value
                   1.0e-14
                   51
Match length
                   96
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   134597
Seq. No.
Contig ID
                   105793 1.R1010
5'-most EST
                   jC-atXmonuni25Ae10a1
Method
                   BLASTN
                   g3046854
NCBI GI
BLAST score
                   388
                   0.0e+00
E value
```

15947

MRG7, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

420

98

Match length % identity

NCBI Description



Seq. No. 134598 105795 1.R1010 Contig ID jC-atXmonuni25Ag07a1 5'-most EST BLASTN Method NCBI GI q2351066 BLAST score 332 0.0e + 00E value 372 Match length 99 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana] 134599 Seq. No. 105812 1.R1010 Contig ID 5'-most EST $jC-a1X\overline{2}5049Q1E1G02a1$ Seq. No. 134600 Contig ID 105825 1.R1010 5'-most EST g586966 134601 Seq. No. Contig ID 105826_1.R1010 5'-most EST g2062948 Method BLASTN g4539378 NCBI GI BLAST score 336 0.0e + 00E value Match length 462 % identity 93 Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 NCBI Description (ESSA project) Seq. No. 134602 Contig ID 105837 1.R1010 5'-most EST jC-atX25050Q1E1C03a1 Seq. No. 134603 Contig ID 105844 1.R1010 5'-most EST q453761 Method BLASTX NCBI GI g3328221 BLAST score 203 E value 2.0e-39 94 Match length % identity 90 NCBI Description (AF076920) thioredoxin peroxidase [Secale cereale] 134604 Seq. No. 105847 1.R1010 Contig ID jC-a1X25051Q1E1A03a1 5'-most EST Method BLASTN

Method BLASTN
NCBI GI g4753195
BLAST score 67
E value 3.0e-29
Match length 311
% identity 85



NCBI Description Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No. 134605

Contig ID 105851_1.R1010

5'-most EST jC-atXmonuni25Ag09a1

Method BLASTN
NCBI GI g4589423
BLAST score 322
E value 0.0e+00
Match length 405
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K7B16, complete sequence

Seq. No. 134606

Contig ID 105856_1.R1010 5'-most EST jC-alX25051Q1E1B12a1

Method BLASTX
NCBI GI g3660187
BLAST score 221
E value 5.0e-18
Match length 58
% identity 67

NCBI Description Chain A, E2-C, An Ubiquitin Conjugating Enzyme Required For

The Destruction Of Mitotic Cyclins >gi_3660188_pdb_1E2C_B Chain B, E2-C, An Ubiquitin Conjugating Enzyme Required For The Destruction Of Mitotic Cyclins >gi_3660189_pdb_1E2C_C Chain C, E2-C, An Ubiquitin Conjugating Enzyme Required For The Destruction Of Mitotic Cyclins >gi_4388942_pdb_2E2C_E2-C, An Ubiquitin Conjugating Enzyme Required For The

Destruction Of Mitotic Cyclins

Seq. No. 134607

Contig ID 105861_1.R1010

5'-most EST jC-atXmonuni25Cg07b1

Method BLASTN
NCBI GI g2832667
BLAST score 358
E value 0.0e+00
Match length 553
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14

(ESSAII project)

Seq. No. 134608

Contig ID 105866 1.R1010

5'-most EST jC-atXmonuni25Cg09b1

Seq. No. 134609

Contig ID 105870_1.R1010 5'-most EST jC-atXmonuni25Ah04a1

Method BLASTN
NCBI GI g3510337
BLAST score 209
E value 1.0e-114
Match length 381



% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19E20, complete sequence [Arabidopsis thaliana]

Seq. No. 134610

Contig ID 105880_1.R1010

5'-most EST jC-alX25051Q1E1E10a1

Seq. No. 134611

Contig ID 105889_1.R1010

5'-most EST jC-al $X\overline{2}$ 5052Q1E1A11a1

Method BLASTX
NCBI GI g3297815
BLAST score 244
E value 1.0e-33
Match length 71
% identity 92

NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 134612

Contig ID 105909_1.R1010

5'-most EST jC-atXmonuni25Ch05b1

Method BLASTN
NCBI GI g3510336
BLAST score 344
E value 0.0e+00
Match length 479
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18J17, complete sequence [Arabidopsis thaliana]

Seq. No. 134613

Contig ID 105913_1.R1010 5'-most EST jC-atXmonuni25Dg01a1

Method BLASTN
NCBI GI g3492855
BLAST score 349
E value 0.0e+00
Match length 401
% identity 90

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F20N2,

complete sequence [Arabidopsis thaliana]

Seq. No. 134614

Contig ID 105945_1.R1010 5'-most EST jC-alX25071Q1E1F11a1

Method BLASTN
NCBI GI g2583106
BLAST score 317
E value 1.0e-178
Match length 431
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F4L23 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134615

Contig ID 106271 1.R1010



```
5'-most EST
                  q2763960
Method
                  BLASTN
NCBI GI
                  q3298532
BLAST score
                  354
E value
                  0.0e+00
Match length
                  402
% identity
                  Arabidopsis thaliana chromosome II BAC T26B15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  134616
Contig ID
                  106393 1.R1010
5'-most EST
                  q2722930
                  BLASTN
Method
NCBI GI
                  a2264304
BLAST score
                  164
                  5.0e-87
E value
Match length
                  338
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBG8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  134617
Contig ID
                  106401 1.R1010
5'-most EST
                  q2749256
Method
                  BLASTX
                  q3341672
NCBI GI
BLAST score
                  213
E value
                  6.0e-17
Match length
                  60
                  77
% identity
                   (AC003672) putative heme A: farnesyltransferase, 5' partial
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  134618
                  106422 1.R1010
Contig ID
5'-most EST
                  jC-alX25113Q1E1F11a1
Method
                  BLASTX
NCBI GI
                  g3152557
BLAST score
                  90
                  3.0e-10
E value
Match length
                  80
% identity
                  50
NCBI Description
                   (AC002986) Contains similarity to S. cerevisiae
                  hypothetical protein YOR197w, gb Z75105. EST gb T76227
                  comes from this gene. [Arabidopsis thaliana]
Seq. No.
                  134619
                  106428 1.R1010
Contig ID
                  jC-atXP12C103C7T7052a1
5'-most EST
```

Method BLASTN
NCBI GI g2618605
BLAST score 482
E value 0.0e+00
Match length 482
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:





```
MUK11, complete sequence [Arabidopsis thaliana]
                   134620
Seq. No.
                   106462 1.R1010
Contig ID
5'-most EST
                   q398682
Method
                   BLASTN
NCBI GI
                   q2618605
BLAST score
                   234
                   1.0e-129
E value
                   393
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUK11, complete sequence [Arabidopsis thaliana]
                   134621
Seq. No.
                   106464 1.R1010
Contig ID
5'-most EST
                   jC-alX\overline{2}5114Q1E1G12a1
Seq. No.
                   134622
                   106575_1.R1010
Contig ID
5'-most EST
                   jC-atXmonuni26Ch08a1
Method
                   BLASTX
```

Method BLASTX
NCBI GI g2245107
BLAST score 578
E value 7.0e-60
Match length 111

Match length 111 % identity 59

NCBI Description (Z97343) thioesterase homolog [Arabidopsis thaliana]

Seq. No. 134623

Contig ID 106596_1.R1010

5'-most EST jC-atXP20C115G18T7031a1

Method BLASTN
NCBI GI g3241917
BLAST score 46
E value 2.0e-16
Match length 74
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19B1, complete sequence [Arabidopsis thaliana]

Seq. No. 134624

Contig ID 106654 1.R1010

5'-most EST g671782

Method BLASTN

NCBI GI g2570223

BLAST score 237

E value 1.0e-130

Match length 408
% identity 96

NCBI Description Arabidopsis thaliana chromosome 1 BAC F20D22 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 134625

Contig ID 106868_1.R1010 5'-most EST jC-atXP58C192E21T7s3

Method BLASTX

```
NCBI GI
                   q3386603
BLAST score
                   923
E value
                   1.0e-100
                   194
Match length
% identity
                   94
                   (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                   134626
Seq. No.
                   106869 1.R1010
Contig ID
                   q27483\overline{4}7
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4325340
BLAST score
                   312
E value
                   1.0e-175
Match length
                   422
                   93
% identity
NCBI Description Arabidopsis thaliana BAC T1J1
Seq. No.
                   134627
                   106912 1.R1010
Contig ID
                   jC-atX\overline{P}64C205P8T7s1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4678705
BLAST score
                   400
                   0.0e + 00
E value
Match length
                   421
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
                   (ESSA project)
                   134628
Seq. No.
Contig ID
                   106933 1.R1010
5'-most EST
                   g50654\overline{4}
                   134629
Seq. No.
Contig ID
                   106949 1.R1010
5'-most EST
                   g510802
Method
                   BLASTX
NCBI GI
                   g2129655
BLAST score
                   235
                   1.0e-19
E value
Match length
                   46
                   100
% identity
NCBI Description
                   OBP32pep protein - Arabidopsis thaliana (fragment)
                   >gi 1022799 (U37698) OBP32pep [Arabidopsis thaliana]
Seq. No.
                   134630
                   106991 1.R1010
Contig ID
                   jC-atX\overline{2}2012Q1E1C06a1
5'-most EST
Method
                   BLASTN
                   g2924768
NCBI GI
BLAST score
                   231
                   1.0e-127
E value
Match length
                   263
                   97
% identity
                   Arabidopsis thaliana chromosome II BAC F25I18 genomic
NCBI Description
```

15953

sequence, complete sequence [Arabidopsis thaliana]

E value

Match length

% identity

579

99



```
134631
Seq. No.
                  107012 1.R1010
Contig ID
5'-most EST
                  g2749305
Method
                  BLASTX
                  q1707857
NCBI GI
                  50
BLAST score
                  7.0e-31
E value
Match length
                  85
                  80
% identity
                  (Y09291) obtusifoliol 14-alpha-demethylase [Triticum
NCBI Description
                  aestivum]
Seq. No.
                  134632
                  107066 1.R1010
Contig ID
                   jC-atX24109Q1E1B06a1
5'-most EST
                  BLASTX
Method
                   g4510342
NCBI GI
BLAST score
                   409
                   4.0e-40
E value
                   98
Match length
                   83
% identity
                   (AC006921) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   134633
Seq. No.
Contig ID
                   107125 1.R1010
                   jC-atXP123C117C18T7067a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4580471
BLAST score
                   335
E value
                   5.0e-31
Match length
                   65
                   92
% identity
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   134634
                   107125 2.R1010
Contig ID
5'-most EST
                   jC-atXP123C162E13T7073a1
Method
                   BLASTN
NCBI GI
                   q4580454
BLAST score
                   193
E value
                   1.0e-104
                   401
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC T2G17 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   134635
Contig ID
                   107135 1.R1010
5'-most EST
                   jC-atXP112C132G21T7a1
Method
                   BLASTN
NCBI GI
                   q3212846
BLAST score
                   317
                   1.0e-178
```



NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134636

Contig ID 107135 3.R1010

5'-most EST jC-atXP49C178N3T7023a1

Method BLASTN
NCBI GI g3212846
BLAST score 331
E value 0.0e+00
Match length 594
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134637

Contig ID 107146_1.R1010 5'-most EST jC-atX22016Q1E1B07a1

5'-most EST jC-atX22016Q1E1B0 Method BLASTX

NCBI GI g3193301 BLAST score 90 E value 2.0e-37 Match length 89 % identity 99

NCBI Description (AF069298) Arabidopsis putative chloroplast outer envelope

86-like protein T10P11.19 (GB: AC002330) [Arabidopsis

thaliana]

Seq. No. 134638

Contig ID 107217_1.R1010 5'-most EST jC-atXP3C85B2T7093a1

Method BLASTN
NCBI GI g3128143
BLAST score 593
E value 0.0e+00
Match length 635
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTI20, complete sequence [Arabidopsis thaliana]

Seq. No. 134639

Contig ID 107281_1.R1010

5'-most EST g2580671
Method BLASTX
NCBI GI g2492782
BLAST score 249
E value 5.0e-21
Match length 93
% identity 55

NCBI Description ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE)

(ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi_504489 (L27992)

alpha-galactosidase [Coffea arabica]

Seq. No. 134640

Contig ID 107301_1.R1010 5'-most EST jC-atX22021Q1E1D03a1

Method BLASTX

```
NCBI GI
                  q2462836
BLAST score
                  270
                  8.0e-24
E value
Match length
                  60
% identity
                  85
NCBI Description
                  (AF000657) beta-glucanase [Arabidopsis thaliana]
                  134641
Seq. No.
                  107377 1.R1010
Contig ID
5'-most EST
                  q902611
Method
                  BLASTX
NCBI GI
                  q1706739
BLAST score
                  417
                  1.0e-40
E value
Match length
                  146
                  53
% identity
                  FLAVONOL 3-SULFOTRANSFERASE (F3-ST) >gi 285285_pir__B40216
NCBI Description
                  flavonol 3'-sulfotransferase - Flaveria chloraefolia
                  134642
Seq. No.
                  107433_1.R1010
Contig ID
5'-most EST
                  g935698
Method
                  BLASTN
                  g4454022
NCBI GI
                  379
BLAST score
                  0.0e + 00
E value
Match length
                  422
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16
NCBI Description
                   (ESSAII project)
                  134643
Seq. No.
                  107438 1.R1010
Contig ID
5'-most EST
                  jC-atXP52C182L13T7s2
                  BLASTX
Method
NCBI GI
                  q2832632
BLAST score
                   149
                  2.0e-09
E value
```

Match length 54 % identity 54

NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]

134644 Seq. No.

Contig ID 107449 1.R1010 5'-most EST jC-atX25024Q1E1C05a1

Seq. No. 134645

Contig ID 107472 1.R1010

5'-most EST jC-atXP20C114A14T7075a1

Method BLASTX g2245037 NCBI GI BLAST score 400 2.0e-38 E value Match length 214 % identity 40

(Z97342) nuclear antigen homolog [Arabidopsis thaliana] NCBI Description



```
Seq. No.
                   134646
                   107495 1.R1010
Contig ID
5'-most EST
                   jC-atX22029Q1E1A08a1
                   134647
Seq. No.
                   107496 1.R1010
Contig ID
5'-most EST
                   q27491\overline{6}6
Method
                   BLASTX
NCBI GI
                   q3298545
BLAST score
                   241
E value
                   3.0e-20
Match length
                   42
% identity
                   100
NCBI Description
                   (AC004681) unknown protein [Arabidopsis thaliana]
Seq. No.
                   134648
Contig ID
                   107499 1.R1010
                   jC-atX\overline{2}5002Q1E1F10a1
5'-most EST
Seq. No.
                   134649
                   107514 1.R1010
Contig ID
5'-most EST
                   q11033\overline{5}0
Method
                   BLASTX
NCBI GI
                   q3831453
BLAST score
                   475
E value
                   1.0e-47
Match length
                   111
% identity
                   71
NCBI Description
                   (AC005700) unknown protein [Arabidopsis thaliana]
Seq. No.
                   134650
                   107530 1.R1010
Contig ID
5'-most EST
                   jC-atX22031Q1E1A01a1
Method
                   BLASTN
NCBI GI
                   g2435510
BLAST score
                   349
                   0.0e + 00
E value
Match length
                   571
% identity
                   87
NCBI Description Arabidopsis thaliana BAC TM017A05
                   134651
Seq. No.
                   107546 1.R1010
Contig ID
5'-most EST
                   jC-atXP122C117M22T7036a1
Method
                   BLASTN
NCBI GI
                   g3510247
BLAST score
                   541
E value
                   0.0e+00
                   657
Match length
                   95
% identity
                   Arabidopsis thaliana chromosome II BAC F19D11 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```

Seq. No. 134652

Contig ID 107554 1.R1010

5'-most EST g2722604 Method BLASTX



```
NCBI GI
                  q3249084
BLAST score
                  401
E value
                  4.0e-39
Match length
                  87
                  84
% identity
NCBI Description
                  (ACO04473) Similar to red-1 (related to thioredoxin) gene
                  gb X92750 from Mus musculus. ESTs gb AA712687 and
                  gb_Z37223 come from this gene [Arabidopsis thaliana]
                  134653
Seq. No.
Contig ID
                  107566 1.R1010
5'-most EST
                  jC-atX25004Q1E1F05a1
                  134654
Seq. No.
```

Contig ID 107575_1.R1010 5'-most EST jC-atX22033Q1E1F03a1 Seq. No. 134655

Contig ID 107581_1.R1010 5'-most EST jC-atX25012Q1E1F08a1

 Seq. No.
 134656

 Contig ID
 107611_1.R1010

 5'-most EST
 jC-atX22034Q1E2E03a1

 Method
 BLASTN

 NCBI GI
 g3241920

 BLAST score
 198

E value 1.0e-107
Match length 329
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAE1, complete sequence [Arabidopsis thaliana]

 Seq. No.
 134657

 Contig ID
 107808_2.R1010

 5'-most EST
 jC-atX22052Q1E1B08a1

 Method
 BLASTN

 NCBI GI
 g4584531

 BLAST score
 303

BLAST score 303 E value 1.0e-170 Match length 347 % identity 59

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8

(ESSA project)

Seq. No. 134658 Contig ID 107812

Contig ID 107812_1.R1010 5'-most EST g2748926

Seq. No. 134659

Contig ID 107819 1.R1010

5'-most EST jC-atX22052Q1E1C09b1

Seq. No. 134660

Contig ID 107821 1.R1010 5'-most EST 92413479

Seq. No. 134661 107870 1.R1010 Contig ID 5'-most EST $jC-atX\overline{2}2055Q1E1D04a1$ 134662 Seq. No. 107900 1.R1010 Contig ID $jC-atX\overline{2}2056Q1E1F06a1$ 5'-most EST BLASTN Method g2656025 NCBI GI BLAST score 337 0.0e+00E value Match length 353 % identity 94 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MCD7 Seq. No. 134663 107972 1.R1010 Contig ID 5'-most EST $jC-atX\overline{2}2060Q1E1F04a1$ Seq. No. 134664 Contig ID 108048 1.R1010 5'-most EST g2393691 Seq. No. 134665 108058 1.R1010 Contig ID 5'-most EST iC-atX22066Q1E1G02a1 Method BLASTN g3399678 NCBI GI BLAST score 333 0.0e+00E value Match length 333 % identity 100 Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, NCBI Description complete sequence [Arabidopsis thaliana] 134666 Seq. No. 108083 1.R1010 Contig ID jC-atX22068Q1E1B05a1 5'-most EST Method BLASTN NCBI GI g4220644 BLAST score 83 8.0e-39 E value Match length 251 83 % identity NCBI Description

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]

134667 Seq. No. 108086 1.R1010 Contig ID

5'-most EST jC-atX22068Q1E1B12a1

Seq. No. 134668

108093 1.R1010 Contig ID

5'-most EST jC-atXP25C125M21T7024a1

Method BLASTN NCBI GI q2760165



BLAST score 314 E value 1.0e-176 Match length 505 % identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAC9, complete sequence [Arabidopsis thaliana]

Seq. No. 134669

Contig ID 108109_1.R1010

5'-most EST jC-atX\overline{2}2069Q1E1F07a1

Method BLASTN
NCBI GI g3250673
BLAST score 291
E value 1.0e-163
Match length 311
% identity 75

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5

(ESSAII project)

Seq. No. 134670

Contig ID 108161_1.R1010

NCBI Description GLUTATHIONE S-TRANSFERASE PARB (CLASS-PHI)

>gi_285295_pir__A41789 glutathione transferase (EC
2.5.1.18) - common tobacco >gi_218294_dbj_BAA01394_
(D10524) glutathione S-transferase [Nicotiana tabacum]

Seq. No. 134671

Contig ID \ 108181 1.R1010

5'-most EST g2446048
Method BLASTN
NCBI GI g3702731
BLAST score 310
E value 1.0e-174
Match length 388
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MFC19, complete sequence [Arabidopsis thaliana]

Seq. No. 134672

Contig ID 108218_1.R1010

5'-most EST g2062878
Method BLASTN
NCBI GI g3641835
BLAST score 168
E value 1.0e-89
Match length 168
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20

(ESSAII project)



134673

Seq. No.

```
108235 1.R1010
Contig ID
5'-most EST
                  q2048814
Method
                  BLASTX
NCBI GI
                  g4455220
BLAST score
                  1032
E value
                  1.0e-112
                  276
Match length
% identity
NCBI Description
                  (AL035440) putative aconitase [Arabidopsis thaliana]
Seq. No.
                  134674
                  108297 1.R1010
Contig ID
5'-most EST
                  q2048818
                  BLASTN
Method
NCBI GI
                  a2618602
BLAST score
                  336
E value
                  0.0e+00
                  391
Match length
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  134675
                  108332 1.R1010
Contig ID
                  q2062908
5'-most EST
Method
                  BLASTX
                  a2911059
NCBI GI
BLAST score
                  576
                  2.0e-59
E value
                  122
Match length
                  96
% identity
NCBI Description
                  (AL021961) putative protein [Arabidopsis thaliana]
Seq. No.
                  134676
Contig ID
                  108355 1.R1010
5'-most EST
                  g2749201
Method
                  BLASTN
NCBI GI
                  g2924734
BLAST score
                  299
                  1.0e-167
E value
                  447
Match length
% identity
                  95
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXE10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  134677
                  108501 1.R1010
Contiq ID
                  jC-atX\overline{2}2088Q1E1C05a1
5'-most EST
Method
                  BLASTN
                  q3608126
NCBI GI
                  400
BLAST score
                  0.0e+00
E value
                  445
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T32F12 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
```



```
Seq. No.
                  134678
Contig ID
                  108547 1.R1010
5'-most EST
                  jC-atXmonuni27De10b1
Seq. No.
                  134679
Contig ID
                  108647 1.R1010
                  jC-atXmonuni27Bh10a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4587589
BLAST score
                  300
E value
                  3.0e-27
Match length
                  121
                  47
% identity
                  (AC007232) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  134680
Contig ID
                  108675 1.R1010
5'-most EST
                  jC-atXmonuni27Bh08a1
Method
                  BLASTN
NCBI GI
                  g4662609
                  405
BLAST score
E value
                  0.0e+00
Match length
                  437
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F10A5,
NCBI Description
                  complete sequence
Seq. No.
                  134681
Contig ID
                  108720 1.R1010
5'-most EST
                  jC-atX23007Q1E1H05a1
                   134682
Seq. No.
Contig ID
                   108743 1.R1010
5'-most EST
                   jC-atXP3C83G12T7070a1
                  BLASTN
Method
NCBI GI
                  g2462264
BLAST score
                   55
E value
                  8.0e-22
Match length
                   55
% identity
                  100
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                   134683
                   108823 1.R1010
Contig ID
5'-most EST
                   g1033247
Method
                  BLASTX
NCBI GI
                   g2129753
```

5'-most EST g1033247

Method BLASTX

NCBI GI g2129753

BLAST score 846

E value 6.0e-91

Match length 193
% identity 84

NCBI Description threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi_1448917 (L41666) threonine synthase

[Arabidopsis thaliana]

Seq. No. 134684



```
108961 1.R1010
Contig ID
                   jC-atXP94CH5G7T7b1
5'-most EST
Method
                   BLASTN
                   g4454587
NCBI GI
BLAST score
                   234
E value
                   1.0e-129
Match length
                   331
                   97
% identity
                  Arabidopsis thaliana BAC F21A20 from chromosome V near 61
NCBI Description
                   cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134685
                   108984 1.R1010
Contig ID
5'-most EST
                   q3450472
Method
                   BLASTX
NCBI GI
                   q1699024
BLAST score
                   52
E value
                   7.0e-16
Match length
                   85
                   55
% identity
NCBI Description
                   (U78866) gene1000 [Arabidopsis thaliana] >gi 1699057
                   (U78870) unknown [Arabidopsis thaliana]
Seq. No.
                   134686
Contig ID
                   109099 1.R1010
5'-most EST
                   jC-atXP52C181L9T7s2
Method
                   BLASTN
NCBI GI
                   q4589442
BLAST score
                   262
                   1.0e-145
E value
Match length
                   431
                   97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MVP2, complete sequence
                   134687
Seq. No.
Contig ID
                   109110 1.R1010
5'-most EST
                   jC-atX23026Q1E1D07a1
Seq. No.
                   134688
                   109123 1.R1010
Contig ID
5'-most EST
                   jC-atX\overline{2}4001Q1E1B02a1
Method
                   BLASTX
NCBI GI
                   g1731990
BLAST score
                   218
                   4.0e-34
E value
Match length
                   108
                   67
% identity
```

(Y09602) serine carboxypeptidase II, CP-MII [Hordeum NCBI Description

vulgare]

Seq. No. 134689

109127 1.R1010 Contig ID

 $jC-atX\overline{P}26C124P8T7044a1$ 5'-most EST

Method BLASTN g3065834 NCBI GI BLAST score 763



E value 0.0e+00 Match length 836 % identity 98

NCBI Description Arabidopsis thaliana putative methyltransferase gene,

complete cds

Seq. No. 134690

Contig ID 109275_1.R1010

5'-most EST jC-atX24007Q1E1D06a1

Method BLASTX
NCBI GI g3152618
BLAST score 253
E value 1.0e-21
Match length 97
% identity 52

NCBI Description (AC004482) putative pectinesterase [Arabidopsis thaliana]

>gi 3242724 (AC003040) putative pectinesterase [Arabidopsis

thaliana]

Seq. No. 134691

Contig ID 109314 1.R1010

5'-most EST jC-atX24009Q1E1D12a1

Method BLASTN
NCBI GI g3128136
BLAST score 300
E value 1.0e-168
Match length 344
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K1F13, complete sequence [Arabidopsis thaliana]

Seq. No. 134692

Contig ID 109332 1.R1010

5'-most EST $jC-atX\overline{2}4061Q1E1D08a2$

Seq. No. 134693

Contig ID 109466_1.R1010 5'-most EST jC-atX24015Q1E1A01a1

Method BLASTN
NCBI GI g4757409
BLAST score 394
E value 0.0e+00
Match length 394
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MVC8, complete sequence

Seq. No. 134694

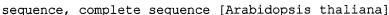
Contig ID 109542_1.R1010 5'-most EST jC-atXP2C76D6T7041a1

Method BLASTN
NCBI GI g3341671
BLAST score 541
E value 0.0e+00
Match length 621
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F16B22 genomic

E value Match length





Seq. No. 134695 109600 1.R1010 Contig ID 5'-most EST g3450410 Method BLASTN g409704 NCBI GI BLAST score 378 E value 0.0e + 00Match length 390 % identity NCBI Description Arabidopsis thaliana ETR1 gene, complete cds. >gi 3011559 gb I75418 I75418 Sequence 1 from patent US 134696 Seq. No. Contig ID 109631 1.R1010 5'-most EST jC-atX24022Q1E1D07a1 134697 Seq. No. Contig ID 109667 1.R1010 jC-atX24023Q1E1F07a1 5'-most EST Method BLASTN NCBI GI g1402915 BLAST score 35 E value 3.0e-10 Match length 51 % identity 92 NCBI Description A.thaliana mRNA for peroxidase, prxr7 Seq. No. 134698 Contig ID 109693 1.R1010 5'-most EST g1103339 Method BLASTN NCBI GI q4587582 BLAST score 152 E value 8.0e-80 Match length 506 % identity 98 NCBI Description Arabidopsis thaliana chromosome II BAC T16B14 genomic sequence, complete sequence 134699 Seq. No. 109788 1.R1010 Contig ID 5'-most EST jC-atXP15C106G5T7021a1 Seq. No. 134700 109839 1.R1010 Contig ID 5'-most EST jC-atX24028Q1E1C08a1 Seq. No. 134701 109844 1.R1010 Contig ID $jC-atX\overline{2}4028Q1E1D01a1$ 5'-most EST Method BLASTN NCBI GI g2351071 BLAST score 292

15965

1.0e-163



% identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MVA3, complete sequence [Arabidopsis thaliana] 134702 Seq. No. Contig ID 109881 1.R1010 5'-most EST $q20627\overline{7}8$ BLASTN Method g3128135 NCBI GI 302 BLAST score E value 1.0e-169 Match length 343 % identity 97 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K19E1, complete sequence [Arabidopsis thaliana] 134703 Seq. No. Contig ID 109918 1.R1010 5'-most EST g2062931 Method BLASTX q2316022 NCBI GI BLAST score 328 E value 2.0e-30 Match length 68 % identity 97 (U96399) MRP-like ABC transporter [Arabidopsis thaliana] NCBI Description 134704 Seq. No. Contig ID 109931 1.R1010 q34501745'-most EST BLASTX Method NCBI GI q4467122 BLAST score 408 E value 8.0e-40 Match length 83 % identity 95 NCBI Description (AL035538) putative protein [Arabidopsis thaliana] Seq. No. 134705 Contig ID 110019 1.R1010 5'-most EST jC-atX24037Q1E2A03a1 Seq. No. 134706 Contig ID 110035 1.R1010 jC-atX24106Q1E1C12b1 5'-most EST Method BLASTN

NCBI GI q3702735 BLAST score 101 2.0e-49 E value Match length 422 % identity 95

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MQL5, complete sequence [Arabidopsis thaliana]

134707 Seq. No.

110098 1.R1010 Contig ID

5'-most EST $jC-atX\overline{2}4040Q1E1F03b1$



Method BLASTX NCBI GI q1361155 BLAST score 146 3.0e-09 E value Match length 84 % identity 44 NCBI Description hypothetical protein o215b - Escherichia coli >gi_537235 (U14003) Kenn Rudd identifies as gpmB [Escherichia coli] >gi 1790856 (AE000509) phosphoglyceromutase 2 [Escherichia coli] Seq. No. 134708 Contig ID 110195 1.R1010 $jC-atX\overline{P}27C133D24T7s2$ 5'-most EST Method BLASTX q2129941 NCBI GI 280 BLAST score 8.0e-25 E value 69

Match length 69
% identity 75
NCBI Description zeaxanthin epoxidase precursor - curled-leaved tobacco
>gi_1370274_emb_CAA65048_ (X95732) zeaxanthin epoxidase
[Nicotiana plumbaginifolia]

Seq. No. 134709 110267 1.R1010 Contig ID 5'-most EST $q27475\overline{3}4$ Method BLASTN NCBI GI q4519195 BLAST score 384 E value 0.0e+00Match length 692

 Seq. No.
 134710

 Contig ID
 110346_1.R1010

 5'-most EST
 jC-atX24051Q1E1C06a1

 Method
 BLASTX

 NCBI GI
 g3033398

 BLAST score
 47

 F malue
 5.00-24

BLAST score 47 E value 5.0e-24 Match length 77 % identity 81

NCBI Description (AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]

Seq. No. 134711

Contig ID 110413_1.R1010

5'-most EST g2393340
Method BLASTN
NCBI GI g4567237
BLAST score 96
E value 2.0e-46
Match length 473
% identity 94



NCBI Description Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

Seq. No. 134712

Contig ID 110418_1.R1010 5'-most EST jC-atXP47C17204T7s2

Method BLASTN
NCBI GI g2337888
BLAST score 225
E value 1.0e-123
Match length 527
% identity 95

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14J16,

complete sequence [Arabidopsis thaliana]

Seq. No. 134713

Contig ID 110423 1.R1010

5'-most EST g1215987

Method BLASTN

NCBI GI g2145357

BLAST score 313

E value 1.0e-176

Match length 394

% identity 97

NCBI Description A.thaliana ATHB-9 gene

Seq. No. 134714

Contig ID 110430_1.R1010 5'-most EST jC-atXP98CH8C11T7b1

Method BLASTN
NCBI GI g3123718
BLAST score 41
E value 1.0e-13
Match length 57
% identity 93

NCBI Description Homo sapiens gene for 24-kDa subunit of complex I, exon

Seq. No. 134715

Contig ID 110454_1.R1010

5'-most EST g2048218
Method BLASTN
NCBI GI g3176693
BLAST score 269
E value 1.0e-150
Match length 372
% identity 93

NCBI Description Arabidopsis thaliana chromosome I BAC T2711 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134716

Contig ID 110468 1.R1010

5'-most EST g2763164
Method BLASTX
NCBI GI g4455359
BLAST score 234
E value 2.0e-19
Match length 50



```
% identity
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   134717
                   110470 1.R1010
Contig ID
5'-most EST
                   g3450356
Method
                   BLASTN
NCBI GI
                   q4159700
BLAST score
                   317
E value
                   1.0e-178
Match length
                   530
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K1L20, complete sequence
Seq. No.
                   134718
Contig ID
                   110525 1.R1010
5'-most EST
                   q27494\overline{5}4
Method
                   BLASTX
                   g3334144
NCBI GI
BLAST score
                   76
E value
                   2.0e-38
Match length
                   132
% identity
                   64
                   G1/S-SPECIFIC CYCLIN C-TYPE >gi 1695698 dbj BAA13181_
NCBI Description
                   (D86925) C-type cyclin [Oryza sativa]
Seq. No.
                   134719
Contig ID
                   110560 1.R1010
                   g507037
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3985958
BLAST score
                   346
E value
                   0.0e+00
Match length
                   540
% identity
                   98
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MZN1, complete sequence [Arabidopsis thaliana]
                   134720
Seq. No.
                   110568 1.R1010
Contig ID
5'-most EST
                   jC-atX\overline{2}4060Q1E1H02a1
Seq. No.
                   134721
                   110675 1.R1010
Contig ID
5'-most EST
                   jC-atX\overline{2}4075Q1E1A09a1
Method
                   BLASTX
NCBI GI
                   q4678230
BLAST score
                   380
                   1.0e-36
E value
Match length
                   74
                   100
% identity
                   (AC007135) putative kinesin related protein [Arabidopsis
NCBI Description
```

Seq. No. 134722 Contig ID 110707

110707 1.R1010

thaliana]



5'-most EST jC-atX24066Q1E1A05a1 Seq. No. 134723 110716 1.R1010 Contig ID jC-atX24066Q1E1B10a1 5'-most EST Seq. No. 134724 110724 1.R1010 Contig ID 5'-most EST $q20484\overline{9}3$ Method BLASTN NCBI GI q3600045 BLAST score 419 E value 0.0e + 00Match length 466 % identity NCBI Description Arabidopsis thaliana BAC F2P3 Seq. No. 134725 110756 1.R1010 Contig ID 5'-most EST g2047950 BLASTX Method NCBI GI q4507075 BLAST score 256 E value 2.0e-28 149 Match length % identity 47 SWI/SNF related, matrix associated, actin dependent NCBI Description regulator of chromatin, subfamily a, member 5 >gi 2967452 dbj BAA25173 (AB010882) hSNF2H [Homo sapiens] Seq. No. 134726 110786 1.R1010 Contig ID 5'-most EST g4714006 Method BLASTN NCBI GI g2191157 BLAST score 302 E value 1.0e-169 445 Match length % identity 99 NCBI Description Arabidopsis thaliana BAC IG002P16 Seq. No. 134727 Contig ID 110790 1.R1010 5'-most EST $g12158\overline{4}4$ Seq. No. 134728 110856 1.R1010 Contig ID

 $jC-atX\overline{2}4075Q1E1G12a1$ 5'-most EST

Method BLASTX NCBI GI g4314359 BLAST score 125 5.0e-45 E value Match length 110 % identity 84

(AC006340) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 134729



```
Contig ID
                   110922 1.R1010
5'-most EST
                   jC-atX24082Q1E1C11a1
                   134730
Seq. No.
                   110929 1.R1010
Contig ID
5'-most EST
                   jC-atX\overline{2}4082Q1E1G04a1
Method
                   BLASTX
                   q3688528
NCBI GI
BLAST score
                   333
                   4.0e-31
E value
Match length
                   86
% identity
                   70
NCBI Description
                   (AJ004958) pre-pro-TPE4A protein [Pisum sativum]
                   134731
Seq. No.
Contig ID
                   111043 1.R1010
5'-most EST
                   jC-atX24103Q1E2G11a1
Method
                   BLASTX
NCBI GI
                   q4325368
BLAST score
                   254
                   1.0e-39
E value
Match length
                   79
                   94
% identity
NCBI Description
                   (AF128396) Arabidopsis thaliana flavin-type blue-light
                   photoreceptor (SW:Q43125) (Pfam: PF00875, Score=765.2,
                   E=2.6e-226, N=1) [Arabidopsis thaliana]
                   134732
Seq. No.
                   111053_1.R1010
Contig ID
                   q50945\overline{4}
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2264309
BLAST score
                   422
E value
                   0.0e+00
                   426
Match length
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MJJ3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134733
                   111056 1.R1010
Contig ID
5'-most EST
                   g2062862
Method
                   BLASTN
NCBI GI
                   g4756963
BLAST score
                   411
E value
                   0.0e+00
Match length
                   444
% identity
                   100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
NCBI Description
                   (ESSA project)
Seq. No.
                   134734
```

111066 1.R1010 Contig ID 5'-most EST

g2048246

Seq. No. 134735

111073 1.R1010 Contig ID

% identity

NCBI Description

53

thaliana]



```
5'-most EST
                  q17155
Method
                  BLASTN
NCBI GI
                  q4538895
BLAST score
                  108
E value
                  1.0e-53
Match length
                  263
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8
NCBI Description
                  (ESSA project)
Seq. No.
                  134736
Contig ID
                  111077_1.R1010
                  jC-atX24106Q1E1B06a2
5'-most EST
Method
                  BLASTX
                  q2275202
NCBI GI
                  368
BLAST score
                  3.0e-35
E value
Match length
                  75
% identity
                  99
                  (AC002337) acyl-CoA synthetase isolog [Arabidopsis
NCBI Description
                  thaliana]
                  134737
Seq. No.
Contig ID
                  111122 1.R1010
5'-most EST
                  g398623
Method
                  BLASTX
                  q2569938
NCBI GI
                  365
BLAST score
                  1.0e-34
E value
Match length
                  93
                  73
% identity
NCBI Description (Y15193) GAI [Arabidopsis thaliana]
Seq. No.
                  134738
Contig ID
                  111145 1.R1010
5'-most EST
                  jC-atXP90C246H11T7s2
Method
                  BLASTX
NCBI GI
                  q3281849
BLAST score
                   632
E value
                   6.0e-66
Match length
                  120
% identity
                  100
                   (AL031004) methyltransferase - like protein [Arabidopsis
NCBI Description
                  thaliana]
                  134739
Seq. No.
Contig ID
                   111159 1.R1010
5'-most EST
                   jC-atX24109Q1E1B06a2
Method
                  BLASTX
NCBI GI
                   g2191165
BLAST score
                   51
                   1.0e-21
E value
Match length
                   113
```

15972

(AF007270) A IG002P16.14 gene product [Arabidopsis



Seq. No. 134740

Contig ID 111191_1.R1010

5'-most EST $g25806\overline{2}9$

Seq. No. 134741

Contig ID 111205_1.R1010

5'-most EST g2749355

Seq. No. 134742

Contig ID 111222 1.R1010

5'-most EST jC-atX24111Q1E1B12a1

Method BLASTN
NCBI GI g3128143
BLAST score 256
E value 1.0e-142
Match length 263
% identity 60

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTI20, complete sequence [Arabidopsis thaliana]

Seq. No. 134743

Contig ID 111228 1.R1010 5'-most FST iC-atyP117C141N5

5'-most EST jC-atXP117C141N5T7a1

Method BLASTN
NCBI GI g2462264
BLAST score 54
E value 3.0e-21
Match length 54
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 134744

Contig ID 111246_1.R1010

5'-most EST jC-atXP22C122D21T7008a1

Method BLASTX
NCBI GI g3236240
BLAST score 381
E value 2.0e-36
Match length 100
% identity 70

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 134745

Contig ID 111246 2.R1010

5'-most EST g315765
Method BLASTX
NCBI GI g3236240
BLAST score 211
E value 2.0e-16
Match length 128
% identity 43

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 134746

Contig ID 111252_1.R1010

5'-most EST g2748810 Method BLASTN



NCBI GI g4760411
BLAST score 241
E value 1.0e-133
Match length 340
% identity 98
NCBI Description Arabidops

NCBI Description Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,

complete sequence

Seq. No. 134747

Contig ID 111331_1.R1010

5'-most EST g1053286
Method BLASTX
NCBI GI g4455293
BLAST score 520
E value 2.0e-64
Match length 162
% identity 90

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 134748

Contig ID 111331_2.R1010

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5

(ESSAII project)

Seq. No. 134749

Contig ID 111531_1.R1010

5'-most EST jC-atX\(\overline{2}\)5053Q1E1H11a1

Method BLASTN
NCBI GI g4115930
BLAST score 360
E value 0.0e+00
Match length 397
% identity 97

NCBI Description Arabidopsis thaliana BAC T4B21

Seq. No. 134750

Contig ID 111544 1.R1010

5'-most EST g2413369
Method BLASTN
NCBI GI g4646215
BLAST score 382
E value 0.0e+00
Match length 457
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC T22013 genomic

sequence, complete sequence

Seq. No. 134751

Contig ID 111568 1.R1010

5'-most EST $g49332\overline{6}$



134752 Seq. No. 111806 1.R1010 Contig ID 5'-most EST g2763318 Method BLASTN NCBI GI q4589434 BLAST score 369 E value 0.0e+00Match length 476 78 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MNJ7, complete sequence Seq. No. 134753 111970 1.R1010 Contig ID q1932875 5'-most EST Method BLASTN NCBI GI q2827513 BLAST score 210 E_value 1.0e-114 Match length 273 95 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16 (ESSAII project) Seq. No. 134754 Contig ID 112083 1.R1010 5'-most EST g17632 Seq. No. 134755 112109 1.R1010 Contig ID 5'-most EST g1215841 Seq. No. 134756 112294 1.R1010 Contig ID $jC-atX\overline{2}5027Q1E1B01a1$ 5'-most EST Method BLASTN NCBI GI g3176695 BLAST score 470 0.0e+00E value Match length 538 97 % identity Arabidopsis thaliana chromosome I BAC F14J9 genomic NCBI Description sequence contains phyA marker, complete sequence [Arabidopsis thaliana] 134757 Seq. No. 112307 1.R1010 Contig ID 5'-most EST jC-atX25027Q1E1F03a1 134758 Seq. No. Contig ID 112331 1.R1010

5'-most EST jC-atX\(\overline{2}\)5029\(\overline{2}\)1E1B12a1

Method BLASTX
NCBI GI g4680318
BLAST score 134
E value 5.0e-69



Match length 151 % identity 95

NCBI Description (AF124376) 30S ribosomal protein S7 [Brassica napus]

Seq. No. 134759

Contig ID 112346 1.R1010

5'-most EST jC-atX\(\overline{2}\)5031Q1E1A09a1

Method BLASTN
NCBI GI g4538990
BLAST score 185
E value 1.0e-99
Match length 350
% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19

(ESSA project)

Seq. No. 134760

Contig ID 112362 1.R1010

5'-most EST $g27638\overline{8}1$

Seq. No. 134761

Contig ID 112384 1.R1010

5'-most EST jC-atXP110C119G10T7058a1

Method BLASTN
NCBI GI g2760168
BLAST score 242
E value 1.0e-133
Match length 500
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MEE6, complete sequence [Arabidopsis thaliana]

Seq. No. 134762

Contig ID 112384_2.R1010 5'-most EST jC-atXP13C104A8T7d2

Method BLASTN
NCBI GI g2760168
BLAST score 271
E value 1.0e-151
Match length 472
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MEE6, complete sequence [Arabidopsis thaliana]

Seq. No. 134763

Contig ID 112424_1.R1010

5'-most EST jC-atX\(\frac{7}{2}\)5034Q1E1B02a1

Method BLASTN

NCBI GI g1707006

BLAST score 345

E value 0.0e+00

Match length 417

% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC T1B8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134764



```
112520 1.R1010
Contig ID
5'-most EST
                   jC-atX25038Q1E1E11a1
Seq. No.
                   134765
                   112604 1.R1010
Contig ID
5'-most EST
                   jC-atX\overline{2}5041Q1E1F12a2
Method
                   BLASTX
                   g1769891
NCBI GI
BLAST score
                   209
E value
                   1.0e-16
Match length
                   40
% identity
                   97
                   (X99747) bZIP transcription factor [Arabidopsis thaliana]
NCBI Description
                   >gi 1865679 emb CAB04795 (Z82043) ATB2 [Arabidopsis
                   thaliana]
Seq. No.
                   134766
                   112703 1.R1010
Contig ID
5'-most EST
                   jC-atXmonuni26Ca01a1
Method
                   BLASTN
NCBI GI
                   q4589437
BLAST score
                   252
E value
                   1.0e-140
Match length
                   308
% identity
                   95
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MPN9, complete sequence
Seq. No.
                   134767
                   112708 1.R1010
Contig ID
5'-most EST
                   jC-atXmonuni26Ca06a1
                   BLASTX
Method
NCBI GI
                   g3128188
BLAST score
                   274
                   3.0e-25
E value
Match length
                   97
                   59
% identity
                  (AC004521) putative beta-glucosidase [Arabidopsis thaliana]
NCBI Description
                   134768
Seq. No.
                   112776 1.R1010
Contig ID
5'-most EST
                   jC-atX25057Q1E1B05b1
Method
                   BLASTN
                   g3859658
NCBI GI
BLAST score
                   183
                   1.0e-98
E value
Match length
                   215
                   98
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1
                   (ESSAII project)
Seq. No.
                   134769
```

112852 1.R1010 Contig ID

jC-atX25060Q1E1H09a1 5'-most EST

Seq. No. 134770

Contig ID 112897 1.R1010

Match length

% identity

620 98

complete sequence



```
jC-atXP14C105N12T7s1
5'-most EST
Method
                  BLASTN
                  g2262135
NCBI GI
BLAST score
                  240
E value
                  1.0e-132
Match length
                  499
% identity
                  100
                  Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
NCBI Description
                  cM, complete sequence
Seq. No.
                  134771
Contia ID
                  113035 1.R1010
5'-most EST
                  jC-atXL1031Q1E1E04a1
                  BLASTN
Method
NCBI GI
                  q4519195
BLAST score
                  118
E value
                  1.0e-59
Match length
                  281
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MQC12, complete sequence
                  134772
Seq. No.
Contig ID
                  113100 1.R1010
                  jC-atX25071Q1E1E03a1
5'-most EST
                  BLASTN
Method
NCBI GI
                  a4589419
BLAST score
                  502
E value
                  0.0e + 00
Match length
                  582
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K2I5, complete sequence
                  134773
Seq. No.
                  113119 1.R1010
Contig ID
                  jC-atX25073Q1E1B033a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4455366
BLAST score
                  189
                  3.0e-14
E value
Match length
                  50
% identity
                  72
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]
                  134774
Seq. No.
                  113137 1.R1010
Contig ID
                  jC-atXP122C118G17T7074a1
5'-most EST
Method
                  BLASTN
                  q4580745
NCBI GI
                  583
BLAST score
                  0.0e+00
E value
```

15978

NCBI Description Arabidopsis thaliana chromosome 1 BAC F1003 sequence,

NCBI Description

Seq. No.

134781



```
Seq. No.
                   134775
                   113172 1.R1010
Contig ID
                   jC-atX25074Q1E1F06a1
5'-most EST
                   134776
Seq. No.
                   113238 1.R1010
Contig ID
5'-most EST
                   jC-atXP123C159016T7065a1
Method
                   BLASTN
                   g4589445
NCBI GI
BLAST score
                   215
                   1.0e-117
E value
Match length
                   462
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MWL2, complete sequence
Seq. No.
                   134777
                   113538 1.R1010
Contig ID
                   jC-atXP5C90D4T7085a1
5'-most EST
Method
                   BLASTX
                   q4056505
NCBI GI
BLAST score
                   1088
E value
                   1.0e-119
Match length
                   237
% identity
                   91
                  (AC005896) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   134778
                   113709 1.R1010
Contig ID
                   jC-atX25102Q1E1E06a1
5'-most EST
Seq. No.
                   134779
                   113757 1.R1010
Contig ID
5'-most EST
                   jC-atX25103Q1E1E11a1
Method
                   BLASTX
                   g114339
NCBI GI
BLAST score
                   413
                   2.0e-40
E value
Match length
                   81
                   100
% identity
                   PLASMA MEMBRANE ATPASE 3 (PROTON PUMP)
NCBI Description
                   >gi 67974 pir PXMUP3 H+-transporting ATPase (EC 3.6.1.35)
                   type 3, plasma membrane - Arabidopsis thaliana >gi_166625
                   (J04737) ATPase [Arabidopsis thaliana]
                   134780
Seq. No.
                   113971 1.R1010
Contig ID
5'-most EST
                   jC-atX\overline{2}5114Q1E1E02a1
                   BLASTX
Method
NCBI GI
                   g2467274
                   228
BLAST score
                   2.0e-18
E value
                   99
Match length
                   56
% identity
```

15979

(Z99759) rna binding protein [Schizosaccharomyces pombe]



```
114018 1.R1010
Contig ID
5'-most EST
                  jC-atX25116Q1E1C05a1
                  BLASTN
Method
                  q3869075
NCBI GI
                  450
BLAST score
                  0.0e + 00
E value
Match length
                  454
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXK3, complete sequence [Arabidopsis thaliana]
                  134782
Seq. No.
Contig ID
                  114068 1.R1010
                   jC-atXmonuni26Cc06a1
5'-most EST
Method
                  BLASTN
                  q2244829
NCBI GI
BLAST score
                   293
E value
                  1.0e-164
Match length
                   436
                   97
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   134783
Seq. No.
Contig ID
                   114074 1.R1010
                   jC-atXmonuni26Cb11a1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g3738313
BLAST score
                   292
E value
                   1.0e-163
Match length
                   453
% identity
                   97
                  Arabidopsis thaliana chromosome II BAC T29E15 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134784
Contig ID
                   114093 1.R1010
5'-most EST
                   q2412884
Method
                   BLASTX
NCBI GI
                   q3377673
BLAST score
                   233
E value
                   3.0e-19
Match length
                   86
                   57
% identity
                   (AF078079) UDP-glucose:flavonoid 3-O-glucosyltransferase
NCBI Description
                   [Forsythia x intermedia]
Seq. No.
                   134785
                   114098 1.R1010
Contig ID
5'-most EST
                   jC-atXmonuni26Ce01a1
Seq. No.
                   134786
```

114101 1.R1010 Contig ID $jC-atX\overline{3}5005Q1E1G04a1$ 5'-most EST

Method BLASTX g3242721 NCBI GI BLAST score 450



E value 6.0e-45
Match length 90
% identity 94

NCBI Description (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis

thaliana]

Seq. No. 134787

Contig ID 114130 1.R1010

5'-most EST jC-atXmonuni26Cf03a1

Method BLASTN
NCBI GI g4490324
BLAST score 166
E value 3.0e-88
Match length 387
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14

(ESSA project)

Seq. No. 134788

Contig ID 114188 1.R1010

5'-most EST jC-atXmonuni27Bb05a1

Method BLASTN
NCBI GI g2656031
BLAST score 301
E value 1.0e-169
Match length 384
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXC20

Seq. No. 134789

Contig ID 114208_1.R1010

5'-most EST jC-atXmonuni26Ch02a1

Method BLASTX
NCBI GI g3249077
BLAST score 217
E value 3.0e-49
Match length 117
% identity 83

NCBI Description (AC004473) Similar to prunasin hydrolase precursor

gb_U50201 from Prunus serotina. ESTs gb_T21225 and gb_AA586305 come from this gene. [Arabidopsis thaliana]

Seq. No. 134790

Contig ID 114234_1.R1010

5'-most EST jC-atXmonuni27Aa06a1

Method BLASTX
NCBI GI g132942
BLAST score 139
E value 1.0e-08
Match length 40
% identity 60

NCBI Description 60S RIBOSOMAL PROTEIN L35A (L32) >gi_71348_pir__R5XL32

ribosomal protein L35a - African clawed frog

>gi 65064 emb CAA38849 (X55030) ribosomal protein L32

[Xenopus Taevis]



```
Seq. No.
                   134791
                   114255 1.R1010
Contig ID
5 most EST
                   iC-atXmonuni27Bb10a1
Method
                   BLASTN
NCBI GI
                   q2924728
BLAST score
                   278
E value
                   1.0e-155
Match length
                   419
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXH1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134792
Contig ID
                   114326 1.R1010
5'-most EST
                   jC-atXmonuni27Bd09a1
                   134793
Seq. No.
Contig ID
                   114427 1.R1010
5'-most EST
                   jC-atX35033Q1E1H05a1
                   BLASTN
Method
NCBI GI
                   q4512656
                   135
BLAST score
E value
                   5.0e-70
Match length
                   213
% identity
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   134794
                   114429 1.R1010
Contig ID
                   jC-atXP80C240F24T7s1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4713943
BLAST score
                   93
                   1.0e-44
E value
Match length
                   185
% identity
                   90
                   Arabidopsis thaliana chromosome 1 BAC T8K14 sequence,
NCBI Description
                   complete sequence
                   134795
Seq. No.
                   114619 1.R1010
Contig ID
                   g2763413
5'-most EST
Method
                   BLASTN
                   g3355463
NCBI GI
                   182
BLAST score
E value
                   1.0e-97
Match length
                   404
```

97 % identity

Arabidopsis thaliana chromosome II BAC F12L6 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

134796 Seq. No.

114631 1.R1010 Contig ID

5'-most EST g3449804 Method BLASTN NCBI GI q4589415



BLAST score 250 E value 1.0e-138 Match length 496 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K14A3, complete sequence

Seq. No. 134797

Contig ID 114637_1.R1010

5'-most EST jC-atX35053Q1E1B10a2

Method BLASTN
NCBI GI g3241923
BLAST score 440
E value 0.0e+00
Match length 464
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MMN10, complete sequence [Arabidopsis thaliana]

Seq. No. 134798

Contig ID 114648_1.R1010 5'-most EST jC-atX35054Q1E1F12a1

Method BLASTX
NCBI GI g3763918
BLAST score 203
E value 5.0e-50
Match length 123
% identity 79

NCBI Description (AC004450) putative isopropylmalate dehydratase

[Arabidopsis thaliana]

Seq. No. 134799

Contig ID 114720_1.R1010

5'-most EST jC-atXL1024Q1B1D01b1

Method BLASTX
NCBI GI g2462827
BLAST score 395
E value 2.0e-38
Match length 100
% identity 82

NCBI Description (AF000657) probable thiamin biosynthetic enzyme

[Arabidopsis thaliana]

Seq. No. 134800

Contig ID 114722_1.R1010

5'-most EST g2048827
Method BLASTN
NCBI GI g452815
BLAST score 356
E value 0.0e+00
Match length 444
% identity 96

NCBI Description A.thaliana phyE gene

Seq. No. 134801

Contig ID 114739 1.R1010

5'-most EST g2047808



```
BLASTX
Method
NCBI GI
                  q4510348
BLAST score
                   247
                  7.0e-21
E value
                  94
Match length
                  48
% identity
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
                  134802
Seq. No.
                  114749 1.R1010
Contig ID
                   jC-atXP107C40F2T7s1
5'-most EST
                  BLASTX
Method
                  g2281086
NCBI GI
BLAST score
                   349
                   6.0e-33
E value
                   114
Match length
                   59
% identity
                  (AC002333) indole-3-acetate beta-glucosyltransferase isolog
NCBI Description
                   [Arabidopsis thaliana]
                   134803
Seq. No.
                   114753 1.R1010
Contig ID
5'-most EST
                   g1033249
Method
                   BLASTN
NCBI GI
                   q4512656
BLAST score
                   340
                   0.0e + 00
E value
                   407
Match length
                   96
% identity
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                   sequence, complete sequence
                   134804
Seq. No.
Contig ID
                   114763 1.R1010
5'-most EST
                   g2393247
                   134805
Seq. No.
                   114798 1.R1010
Contig ID
                   jC-atXP29C135I12T7001d1
5'-most EST
Method
                   BLASTX
                   a2245144
NCBI GI
                   502
BLAST score
                   2.0e-50
E value
                   177
Match length
% identity
                   (Y10846) O-acetylserine(thiol) lyase [Brassica juncea]
NCBI Description
Seq. No.
                   134806
                   114798 2.R1010
Contig ID
5'-most EST
                   iC-atXL1030Q1B1D05b1
Method
                   BLASTX
NCBI GI
                   q2245144
BLAST score
                   252
                   1.0e-21
E value
```

% identity 67
NCBI Description (Y10846) O-acetylserine(thiol) lyase [Brassica juncea]

81

Match length



Seq. No. 134807

Contig ID 114928_1.R1010 5'-most EST jC-atXL1040Q1E1C07a1

Method BLASTN
NCBI GI g2459406
BLAST score 363
E value 0.0e+00
Match length 470
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134808

Contig ID 115337 1.R1010

5'-most EST jC-atXP100C251I2T7d1

Seq. No. 134809

Contig ID 115339_1.R1010 5'-most EST jC-atXP100C251P4T7b1

Method BLASTX
NCBI GI g2244797
BLAST score 431
E value 5.0e-45
Match length 128
% identity 82

NCBI Description (297336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 134810

Contig ID 115339_2.R1010 5'-most EST jC-atXP100C251J8T7d1

Method BLASTN
NCBI GI g4589414
BLAST score 164
E value 6.0e-87
Match length 596
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K14B15, complete sequence

Seq. No. 134811

Contig ID 115340_1.R1010

5'-most EST jC-atXP100C268B11T7b1

Method BLASTX
NCBI GI g4455319
BLAST score 111
E value 8.0e-05
Match length 187
% identity 10

NCBI Description (AL035528) putative disease resistance protein [Arabidopsis

thaliana]

Seq. No. 134812

Contig ID 115341_1.R1010 5'-most EST jC-atXP100CE3D5T7b1

Method BLASTX NCBI GI g1705678



```
BLAST score
                   276
                   3.0e-24
E value
                   178
Match length
                   21
% identity
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
NCBI Description
                   PROTEIN HOMOLOG) (VCP) >gi 862480 (U20213)
                   valosin-containing protein [Glycine max]
Seq. No.
                   134813
                   115385 1.R1010
Contig ID
                   jC-atX\overline{P}107C107F5T7s1
5'-most EST
                   BLASTN
Method
                   g4115370
NCBI GI
BLAST score
                   273
E value
                   1.0e-152
                   366
Match length
% identity
                   92
                  Arabidopsis thaliana chromosome II BAC F27D4 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   134814
Seq. No.
                   115399_1.R1010
Contig ID
                   jC-atXP107C113K21T7s1
5'-most EST
                   BLASTX
Method
                   g2213595
NCBI GI
                   503
BLAST score
                   6.0e-51
E value
                   101
Match length
% identity
                   98
                   (AC000348) T7N9.15 [Arabidopsis thaliana]
NCBI Description
                   134815
Seq. No.
                   115409 1.R1010
Contig ID
                   g2048684
5'-most EST
Method
                   BLASTX
                   g3880353
NCBI GI
BLAST score
                   241
E value
                   6.0e-20
                   153
Match length
                   39
% identity
                   (Z82285) predicted using Genefinder [Caenorhabditis
NCBI Description
                   elegans]
                   134816
Seq. No.
                   115444_1.R1010
Contig ID
                   jC-atX\overline{P}107C123C17T7d1
5'-most EST
                   BLASTX
Method
                   q3874563
NCBI GI
BLAST score
                   293
                   6.0e-30
E value
```

Match length 128 % identity NCBI Description

(Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ... >gi 3924825 emb CAB05549 (Z83113) similar to Yeast



hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA

Seq. No. 134817

Contig ID 115473_1.R1010

Method BLASTX
NCBI GI g584741
BLAST score 214
E value 9.0e-17
Match length 104
% identity 20

NCBI Description ANKYRIN REPEAT PROTEIN (AKRP) >gi_322461_pir__JQ1729

ankyrin-repeat protein - Arabidopsis thaliana >gi_166744 (M82883) ankyrin repeat-containing protein [Arabidopsis

thaliana]

Seq. No. 134818

Contig ID 115476_1.R1010

5'-most EST jC-at \overline{XP} 108C150L7T7s1

Method BLASTX
NCBI GI g4115916
BLAST score 270
E value 1.0e-23
Match length 93
% identity 59

NCBI Description (AF118222) F3H7.9 gene product [Arabidopsis thaliana]

>gi 4539441 emb_CAB40029.1_ (AL049523) putative protein

[Arabidopsis thaliana]

Seq. No. 134819

Contig ID 115479 1.R1010

5'-most EST jC-atXP108C157G23T7035d1

Method BLASTX
NCBI GI g4510371
BLAST score 531
E value 5.0e-54
Match length 179
% identity 62

NCBI Description (AC007017) putative harpin-induced protein [Arabidopsis

thaliana]

Seq. No. 134820

Contig ID 115481 1.R1010

5'-most EST jC-atXP108C161K24T7s1

Seq. No. 134821

Contig ID 115497 1.R1010 5'-most EST jC-atXP109C91B11T7s1

Method BLASTN
NCBI GI g2828186
BLAST score 473
E value 0.0e+00
Match length 505
% identity 99



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18I23, complete sequence [Arabidopsis thaliana]

Seq. No. 134822
Contig ID 115501_1.R1010
5'-most EST jC-atXP108C184024T7s1

Method BLASTX
NCBI GI g4835232
BLAST score 368
E value 2.0e-41
Match length 140
% identity 75

NCBI Description (AL049862) putative protein [Arabidopsis thaliana]

Seq. No. 134823

Contig ID 115535_1.R1010 5'-most EST g1053980

Seq. No. 134824

Contig ID 115545_1.R1010 5'-most EST jC-atXP109C204J8T7d1

Method BLASTX
NCBI GI g3608154
BLAST score 691
E value 5.0e-73
Match length 166
% identity 89

NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 134825

Contig ID 115546_1.R1010

5'-most EST g2445957
Method BLASTX
NCBI GI g3608154
BLAST score 114
E value 2.0e-36
Match length 94
% identity 88

NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 134826

Contig ID 115549_1.R1010

5'-most EST g3719140
Method BLASTN
NCBI GI g2264316
BLAST score 420
E value 0.0e+00
Match length 740
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRO11, complete sequence [Arabidopsis thaliana]

Seq. No. 134827

Contig ID 115555_1.R1010

5'-most EST g936979
Method BLASTX
NCBI GI g4218987



BLAST score 446 4.0e - 44E value Match length 111 89 % identity (AF098630) putative cell wall-plasma membrane disconnecting NCBI Description CLCT protein [Arabidopsis thaliana] >gi_4725954_emb_CAB41725.1_ (AL049730) putative cell wall-plasma membrane disconnecting CLCT protein (AIR1A) [Arabidopsis thaliana] 134828 Seq. No. 115560 1.R1010 Contig ID 5'-most EST jC-atXP109C205P11T7s1 BLASTN g3510346

Method BLASTN
NCBI GI g3510346
BLAST score 120
E value 8.0e-61
Match length 456
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNL12, complete sequence [Arabidopsis thaliana]

Seq. No. 134829

Contig ID 115561_1.R1010

5'-most EST g936229

Method BLASTN

NCBI GI g4581138

BLAST score 319

E value 1.0e-179

Match length 458

% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F1011 genomic

sequence, complete sequence

Seq. No. 134830

Contig ID 115562_1.R1010

5'-most EST jC-atXP109C206E11T7s1

Method BLASTN
NCBI GI 94581138
BLAST score 405
E value 0.0e+00
Match length 484
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC F1011 genomic

sequence, complete sequence

Seq. No. 134831

Contig ID 115580 1.R1010

5'-most EST g2763397
Method BLASTN
NCBI GI g2264302
BLAST score 328
E value 0.0e+00
Match length 623
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAC12, complete sequence [Arabidopsis thaliana]



134832 Seq. No. 115596 1.R1010 Contig ID $jC-atX\overline{P}109C215B3T7d1$ 5'-most EST BLASTN Method g2924653 NCBI GI 124 BLAST score 4.0e-63 E value 527 Match length 99 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana] 134833 Seq. No. Contig ID 115646 1.R1010 jC-atXP109C91C14T7d1 5'-most EST BLASTX Method q4585901 NCBI GI 309 BLAST score 1.0e-37 E value Match length 156 52 % identity (AC007133) hypothetical protein [Arabidopsis thaliana] NCBI Description 134834 Seq. No. 115674 1.R1010 Contig ID jC-atXP109C95E3T7d15'-most EST BLASTX Method g2565009 NCBI GI 331 BLAST score 8.0e-31 E value 68 Match length 81 % identity (AC002983) putative zinc finger protein [Arabidopsis NCBI Description thaliana] 134835 Seq. No. 115705 1.R1010 Contig ID jC-atXP10C94M1T7d2 5'-most EST BLASTX Method g3269291 NCBI GI 591 BLAST score 7.0e-99 E value 183 Match length 100 % identity (AL030978) putative receptor protein kinase [Arabidopsis NCBI Description thaliana] 134836 Seq. No. 115721 1.R1010 Contig ID 5'-most EST g2757102 BLASTX Method g3885334 NCBI GI 708 BLAST score 5.0e-75 E value Match length 147 % identity 94

Seq. No.

Contig ID 5'-most EST



```
(AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
                  134837
Seq. No.
                  115723 1.R1010
Contig ID
                  jC-atXP10C95A9T7s2
5'-most EST
Method
                  BLASTN
                  q3885325
NCBI GI
                  370
BLAST score
                  0.0e + 00
E value
Match length
                  417
% identity
                  98
                  Arabidopsis thaliana chromosome II BAC T20P8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  134838
Seq. No.
                  115728 1.R1010
Contig ID
                  jC-atXP10C95K14T7s1
5'-most EST
                  BLASTX
Method
                  q4678221
NCBI GI
                  191
BLAST score
                  3.0e-14
E value
Match length
                   129
% identity
                  (AC007135) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   134839
                   115728 2.R1010
Contig ID
5'-most EST
                   q2048855
                   134840
Seq. No.
Contig ID
                   115761 1.R1010
5'-most EST
                   jC-atXP10C95M15T7d1
Method
                   BLASTX
NCBI GI
                   q4099076
BLAST score
                   149
                   2.0e-09
E value
Match length
                   65
% identity
                   (U82510) IAP [Choristoneura fumiferana
NCBI Description
                   nucleopolyhedrovirus]
                   134841
Seq. No.
                   115765 1.R1010
Contig ID
                   jC-atX\overline{P}10C95M21T7d2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4580522
                   278
BLAST score
                   1.0e-155
E value
                   310
Match length
% identity
                  Arabidopsis thaliana scarecrow-like 8 (SCL8) mRNA, partial
NCBI Description
                   cds
                   134842
```

15991

115767 1.R1010

g2581747

Contig ID



```
BLASTX
Method
                   g4580523
NCBI GI
                   54
BLAST score
                   8.0e-41
E value
                   95
Match length
                   92
% identity
NCBI Description (AF036305) scarecrow-like 8 [Arabidopsis thaliana]
                   134843
Seq. No.
                   115767 2.R1010
Contig ID
                   jC-atXP61C201A2T7d1
5'-most EST
                   BLASTX
Method
                   g4580523
NCBI GI
                   277
BLAST score
                   2.0e-52
E value
                   160
Match length
                   83
% identity
                   (AF036305) scarecrow-like 8 [Arabidopsis thaliana]
NCBI Description
                   134844
Seq. No.
                   115771 1.R1010
Contig ID
                   g2048794
5'-most EST
                   BLASTX
Method
                   g2160185
NCBI GI
                   644
BLAST score
                   3.0e-67
E value
                   247
Match length
% identity
                   54
                   (AC000132) Similar to S. pombe ISP4 (gb_D83992).
NCBI Description
                   [Arabidopsis thaliana]
                   134845
Seq. No.
                   115773 1.R1010
Contig ID
                   g2048870
5'-most EST
Method
                   BLASTX
                   g2160185
NCBI GI
                   351
BLAST score
                   4.0e-33
E value
                   90
Match length
                   70
% identity
                    (ACO00132) Similar to S. pombe ISP4 (gb_D83992).
NCBI Description
                    [Arabidopsis thaliana]
                   134846
Seq. No.
                    115792 1.R1010
Contig ID
                    q50232\overline{4}
5'-most EST
                    BLASTX
Method
                    g3928100
NCBI GI
BLAST score
                    324
                    3.0e - 30
E value
Match length
                    62
                    100
% identity
                    (AC005770) putative protease inhibitor [Arabidopsis
NCBI Description
                    thaliana]
                    134847
Seq. No.
                    115793 1.R1010
```

NCBI Description



```
jC-atXP10C96B2T7d1
5'-most EST
                  BLASTN
Method
                  q3080352
NCBI GI
                   201
BLAST score
                  1.0e-109
E value
                   371
Match length
                   99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18
NCBI Description
                   (ESSAII project)
                   134848
Seq. No.
                   115795 1.R1010
Contig ID
                   q2048873
5'-most EST
                   BLASTN
Method
                   g3080352
NCBI GI
                   291
BLAST score
                   1.0e-162
E value
                   454
Match length
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18
NCBI Description
                   (ESSAII project)
                   134849
Seq. No.
                   115807 1.R1010
Contig ID
5'-most EST
                   g2048875
                   BLASTN
Method
                   g2264318
NCBI GI
                   335
BLAST score
                   0.0e + 00
E value
                   384
Match length
                   98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUP24, complete sequence [Arabidopsis thaliana]
                   134850
Seq. No.
                   115817 1.R1010
Contig ID
                   jC-atX\overline{P}10C96I11T7d1
5'-most EST
Method
                   BLASTN
                   g3046853
NCBI GI
BLAST score
                   170
E value
                   2.0e-90
Match length
                   574
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MRA19, complete sequence [Arabidopsis thaliana]
                   134851
Seq. No.
                   115819 1.R1010
Contig ID
                   jC-atXP10C96I11T7s2
5'-most EST
                   BLASTN
Method
                   g3046853
NCBI GI
                   217
BLAST score
                   1.0e-118
E value
Match length
                   463
 % identity
                   94
```

MRA19, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



```
134852
Seq. No.
                   115833 1.R1010
Contig ID
                   jC-atX\overline{P}10C96L18T7d2
5'-most EST
                   BLASTN
Method
                   g4732168
NCBI GI
BLAST score
                   299
E value
                   1.0e-167
                   323
Match length
                   98
% identity
NCBI Description Arabidopsis thaliana BAC T1J24
                   134853
Seq. No.
Contig ID
                   115843 1.R1010
                   jC-atXP10C96P17T7d2
5'-most EST
                   134854
Seq. No.
                   115848 1.R1010
Contig ID
5'-most EST
                   jC-atXP33C151A11T7s2
                   134855
Seq. No.
                   115854 1.R1010
Contig ID
5'-most EST
                   jC-atXP10C97A3T7d1
                   BLASTN
Method
NCBI GI
                   g2760169
                   304
BLAST score
                   1.0e-170
E value
                   550
Match length
                   95
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MFB13, complete sequence [Arabidopsis thaliana]
                   134856
Seq. No.
Contig ID
                   115905_1.R1010
                   jC-atX\overline{P}10C97C23T7d2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2760170
                   423
BLAST score
                   0.0e + 00
E value
Match length
                   945
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MIO24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134857
Contig ID
                   115937 1.R1010
5'-most EST
                   jC-atXP10C97D3T7s2
```

Seq. No. 134858

Contig ID 115941_1.R1010 5'-most EST jC-atXP110C119E4T7d1

Seq. No. 134859

Contig ID 115942 1.R1010

5'-most EST g2759874
Method BLASTN
NCBI GI g2351069



```
BLAST score
E value
                  0.0e + 00
                  850
Match length
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSH12, complete sequence [Arabidopsis thaliana]
                  134860
Seq. No.
                  115946 1.R1010
Contig ID
                  jC-atXP110C105L21T7d1
5'-most EST
                  BLASTX
Method
                  g4678950
NCBI GI
BLAST score
                  504
E value
                  4.0e-51
                  163
Match length
                  67
% identity
                  (AL049711) putative protein [Arabidopsis thaliana]
NCBI Description
                  134861
Seq. No.
                  115950 1.R1010
Contig ID
                  g2757018
5'-most EST
                  BLASTN
Method
                  g3236234
NCBI GI
BLAST score
                  441
                  0.0e + 00
E value
Match length
                   482
% identity
                  Arabidopsis thaliana chromosome II BAC F13M22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   134862
Seq. No.
                   115951 1.R1010
Contig ID
5'-most EST
                   jC-atXP110C119D20T7025a1
Method
                   BLASTX
                   q4262185
NCBI GI
BLAST score
                   641
E value
                   6.0e-67
Match length
                   123
% identity
                   (AC005508) 64038 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   134863
                   115952 1.R1010
Contig ID
5'-most EST
                   g933511
Method
                   BLASTX
NCBI GI
                   g1617270
BLAST score
                   520
E value
                   6.0e-53
Match length
                   154
% identity
                   64
                  (X94624) acyl-CoA synthetase [Brassica napus]
NCBI Description
```

Seq. No. 134864

Contig ID 115967_1.R1010

5'-most EST jC-atXP110C119G23T7d1

Seq. No. 134865



```
115979 1.R1010
Contig ID
                   jC-atXP98CH8A11T7b1
5'-most EST
                   BLASTX
Method
                   g3341680
NCBI GI
                   71
BLAST score
                   2.0e-28
E value
                   185
Match length
                   50
% identity
NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]
                   134866
Seq. No.
                   115981 1.R1010
Contig ID
                    jC-atXP121C96C18T7092d1
5'-most EST
                   BLASTN
Method
                    g3702735
NCBI GI
                    238
BLAST score
                    1.0e-131
E value
                    357
Match length
                    98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MQL5, complete sequence [Arabidopsis thaliana]
                    134867
Seq. No.
                    115983 1.R1010
Contig ID
5'-most EST
                    jC-atXP121C96L4T7029d1
                    BLASTX
Method
                    g1703153
NCBI GI
                    281
BLAST score
                    1.0e-24
E value
Match length
                    226
% identity
                    38
                   ACTIN >gi_2147076_pir__S65079 actin - Cyanidioschyzon merolae >gi_1167501_dbj_BAA06866_ (D32140) actin
NCBI Description
                    [Cyanidioschyzon merolae]
                    134868
Seq. No.
Contig ID
                    115988 1.R1010
                    jC-atX\overline{P}111C105M8T7s1
5'-most EST
Method
                    BLASTX
NCBI GI
                    a4417298
                    798
BLAST score
                    3.0e-85
E value
                    184
Match length
                    92
% identity
                    (AC007019) putative RAS-related protein RAB7 [Arabidopsis
NCBI Description
                    thaliana]
                    134869
Seq. No.
                    115994 1.R1010
Contig ID
                    jC-atXP111C106L5T7s1
5'-most EST
```

Method BLASTX
NCBI GI g3894171
BLAST score 512
E value 5.0e-52
Match length 106
% identity 92

NCBI Description (AC005312) putative glutathione s-transferase [Arabidopsis



thaliana]

```
134870
Seq. No.
                  115997 1.R1010
Contig ID
                  q2597278
5'-most EST
                  BLASTX
Method
                  g1621461
NCBI GI
BLAST score
                   183
                   2.0e-13
E value
                   117
Match length
                   34
% identity
NCBI Description (U73103) laccase [Liriodendron tulipifera]
                   134871
Seq. No.
                   116010 1.R1010
Contig ID
                   g2393229
5'-most EST
                   BLASTX
Method
                   q1621465
NCBI GI
BLAST score
                   352
                   3.0e-33
E value
                   98
Match length
                   61
% identity
NCBI Description (U73105) laccase [Liriodendron tulipifera]
Seq. No.
                   134872
                   116011 1.R1010
Contig ID
                   jC-atX\overline{P}111C119L1T7d1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q3985949
BLAST score
                   229
                   1.0e-126
E value
                   272
Match length
                   100
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MOB24, complete sequence [Arabidopsis thaliana]
                   134873
Seq. No.
                   116013 1.R1010
Contig ID
                   jC-atXP111C116J23T7d1
5'-most EST
Method
                   BLASTX
                   q3046815
NCBI GI
BLAST score
                   335
E value
                   1.0e-65
Match length
                   128
% identity
                   (AL021687) cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   134874
Seq. No.
                   116016 1.R1010
Contig ID
                   jC-atXP111C116L23T7s1
5'-most EST
                   BLASTN
Method
                   q2335089
NCBI GI
                   346
BLAST score
                   0.0e+00
E value
                   433
Match length
                   96
 % identity
 NCBI Description Arabidopsis thaliana chromosome II BAC T11A7 genomic
```



sequence, complete sequence [Arabidopsis thaliana]

 Seq. No.
 134875

 Contig ID
 116017_1.R1010

 5'-most EST
 g2048060

 Method
 BLASTN

 NCBI GI
 g4376087

 BLAST score
 245

BLAST score 245 E value 1.0e-135 Match length 715 % identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 134876

Contig ID 116018_1.R1010

5'-most EST g2048483

Seq. No. 134877

Contig ID 116026_1.R1010

5'-most EST jC-atXP111C116P22T7d1

Method BLASTX
NCBI GI g3152613
BLAST score 299
E value 5.0e-27
Match length 162
% identity 42

NCBI Description (AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 134878

Contig ID 116035_1.R1010

5'-most EST g2048476

Seq. No. 134879

Contig ID 116037_1.R1010

5'-most EST jC-atXP111C119I23T7d1

Method BLASTX
NCBI GI g3786011
BLAST score 611
E value 1.0e-63
Match length 118
% identity 100

NCBI Description (AC005499) putative elongation factor [Arabidopsis

thaliana]

Seq. No. 134880

Contig ID 116039_1.R1010

5'-most EST $g94780\overline{2}$ Method BLASTX NCBI GI g4584110 BLAST score 209 E value 2.0e-16 Match length 100 % identity 46

NCBI Description (AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No. 134881

Match length

% identity



```
116042 1.R1010
Contig ID
5'-most EST
                  q2758268
                  134882
Seq. No.
                  116046 1.R1010
Contig ID
                  g2048473
5'-most EST
                   BLASTN
Method
                  q3785992
NCBI GI
                   284
BLAST score
                   1.0e-158
E value
                   356
Match length
                   98
% identity
                  Arabidopsis thaliana chromosome II BAC T6A23 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   134883
Seq. No.
                   116048 1.R1010
Contig ID
                   jC-atX\overline{P}111C119K22T7s1
5'-most EST
                   134884
Seq. No.
                   116052 1.R1010
Contig ID
                   jC-atXP111C119L1T7s1
5'-most EST
Seq. No.
                   134885
                   116057 1.R1010
Contig ID
                   jC-atX\overline{P}111C122I17T7d1
5'-most EST
                   BLASTX
Method
                   g3334133
NCBI GI
                   562
BLAST score
                   5.0e-58
E value
                   196
Match length
                   59
% identity
                   CYTOCHROME P450 89A2 (CYPLXXXIX) (ATH 6-1) >gi_1432145
NCBI Description
                   (U61231) cytochrome P450 [Arabidopsis thaliana]
                   134886
Seq. No.
                   116063 1.R1010
Contig ID
                   jC-atXP111C122M18T7d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3881820
                   131
BLAST score
E value
                   3.0e-09
                   93
Match length
                    43
% identity
                    (Z73898) similar to dehydrogenase [Caenorhabditis elegans]
NCBI Description
                   >gi_3881832_emb_CAA98083_ (Z73899) similar to dehydrogenase
                    [Caenorhabditis elegans]
                    134887
Seq. No.
                    116067 1.R1010
 Contig ID
                    jC-atXP111C122M20T7d1
 5'-most EST
                    BLASTN
Method
                    g4220635
 NCBI GI
 BLAST score
                    653
                    0.0e+00
 E value
                    653
```

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MDB19, complete sequence [Arabidopsis thaliana]
                   134888
Seq. No.
                   116071 1.R1010
Contig ID
                   jC-atX\overline{P}111C122021T7d1
5'-most EST
                   134889
Seq. No.
                    116073 1.R1010
Contig ID
                   g20486<del>2</del>2
5'-most EST
                    134890
Seq. No.
                    116084 1.R1010
Contig ID
5'-most EST
                    jC-atXP111C124D7T7d1
                    134891
Seq. No.
                    116091 1.R1010
Contig ID
                    jC-atX\overline{P}111C124H12T7d1
5'-most EST
                    BLASTX
Method
                    g3258569
NCBI GI
                    615
BLAST score
                    4.0e-64
E value
                    157
Match length
                    80
% identity
                   (U89959) Similar to yeast general negative regulator of
NCBI Description
                    transcription subunit 1 [Arabidopsis thaliana]
                    134892
Seq. No.
                    116103 1.R1010
Contig ID
                    jC-atX\overline{P}111C124K5T7d1
5'-most EST
                    134893
Seq. No.
                    116106 1.R1010
Contig ID
                    g957822
5'-most EST
                    BLASTX
Method
```

g2447107 NCBI GI 196 BLAST score

7.0e-15 E value 98 Match length 44 % identity

(U42580) A638R [Paramecium bursaria Chlorella virus 1] NCBI Description

134894 Seq. No. 116106 2.R1010 Contig ID 5'-most EST g2393231

134895 Seq. No.

116109 1.R1010 Contig ID jC-atXP111C124L22T7d1 5'-most EST

BLASTN Method NCBI GI q3461885 41 BLAST score 1.0e-13 E value 53 Match length 94 % identity

Arabidopsis thaliana gene for phosphoribosyl-ATP NCBI Description

pyrophosphohydrolase, complete cds



```
Seq. No.
                  134896
Contia ID
                   116112 1.R1010
5'-most EST
                   jC-atXP25C125K19T7063a1
                  BLASTX
Method
NCBI GI
                  g2618699
BLAST score
                   760
E value
                   6.0e-81
Match length
                  149
                   97
% identity
NCBI Description
                  (AC002510) unknown protein [Arabidopsis thaliana]
Seq. No.
                  134897
Contia ID
                   116125 1.R1010
5'-most EST
                  g1216040
Seq. No.
                  134898
                  116132 1.R1010
Contig ID
5'-most EST
                   jC-atXP111C125J19T7d1
                   BLASTN
Method
NCBI GI
                  q2335089
BLAST score
                  277
E value
                  1.0e-154
Match length
                   493
% identity
                   92
                  Arabidopsis thaliana chromosome II BAC T11A7 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  134899
Contig ID
                   116134 1.R1010
5'-most EST
                   jC-atXP111C125J6T7d1
Method
                  BLASTX
NCBI GI
                  q3935176
BLAST score
                   599
E value
                   3.0e-62
Match length
                  151
% identity
NCBI Description (AC004557) F17L21.19 [Arabidopsis thaliana]
Seq. No.
                  134900
                  116136 1.R1010
Contig ID
5'-most EST
                   jC-atX\overline{P}111C125L15T7d1
Method
                  BLASTX
NCBI GI
                  g4314366
BLAST score
                  226
E value
                  2.0e-18
Match length
                  91
% identity
                   65
NCBI Description
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
                  134901
Seq. No.
```

Contig ID 116137_1.R1010

5'-most EST jC-atXP111C125L24T7d1

Method BLASTN
NCBI GI g2618600
BLAST score 126
E value 2.0e-64



Match length 407 % identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDC12, complete sequence [Arabidopsis thaliana]

Seq. No. 134902

Contig ID 116144 1.R1010

5'-most EST g2048673

Method BLASTX

NCBI GI g4417286

BLAST score 357

E value 8.0e-34

Match length 99 % identity 76

NCBI Description (AC007019) putative shikimate kinase [Arabidopsis thaliana]

Seq. No. 134903

Contig ID 116148 1.R1010

5'-most EST jC-atXP111C126H21T7d1

Method BLASTX
NCBI GI g2190558
BLAST score 385
E value 2.0e-67
Match length 136
% identity 96

NCBI Description (AC001229) F5I14.14 [Arabidopsis thaliana]

Seq. No. 134904

Contig ID 116152 1.R1010

5'-most EST jC-atXP111C126K2T7d1

Method BLASTX
NCBI GI g2864613
BLAST score 598
E value 4.0e-62
Match length 157
% identity 76

NCBI Description (AL021811) S-receptor kinase -like protein [Arabidopsis

thaliana] >gi 4049333 emb CAA22558 (AL034567) S-receptor

kinase-like protein [Arabidopsis thaliana]

Seq. No. 134905

Contig ID 116155 1.R1010

5'-most EST g2048681
Method BLASTN
NCBI GI g4159700
BLAST score 299
E value 1.0e-167
Match length 382
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K1L20, complete sequence

Seq. No. 134906

Contig ID 116157_1.R1010 5'-most EST jC-atXP111C126M5T7s1

Seq. No. 134907



```
Contig ID
                   116158 1.R1010
5'-most EST
                   jC-atXP111C126M8T7d1
Method
                   BLASTX
NCBI GI
                   q119745
BLAST score
                   73
E value
                   3.0e-12
Match length
                   139
% identity
                   44
NCBI Description
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                   (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                   >gi_67242_pir__PAWTF fructose-bisphosphatase (EC 3.1.3.11)
                   precursor, chloroplast - wheat >gi_21737 emb CAA30612
                   (X07780) pre-FBPase [Triticum aestivum]
                   >gi_21741_emb_CAA37908 (X53957) fructose-bisphosphatase
                   [Triticum aestivum]
Seq. No.
                   134908
Contig ID
                  116163 1.R1010
5'-most EST
                   jC-atXP113C125C9T7d1
Method
                  BLASTX
NCBI GI
                  g4115383
BLAST score
                   470
E value
                  2.0e-47
Match length
                  95
% identity
                   95
                  (AC005967) receptor-like protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  134909
                  116164 1.R1010
Contig ID
5'-most EST
                  jC-atXP98CH8A4T7b1
Method
                  BLASTX
NCBI GI
                  g3643604
BLAST score
                  106
E value
                  4.0e-04
Match length
                  101
% identity
NCBI Description
                  (AC005395) receptor-like protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  134910
Contig ID
                  116167 1.R1010
5'-most EST
                  g934161
Method
                  BLASTN
NCBI GI
                  g4589440
BLAST score
                  107
E value
                  5.0e-53
Match length
                  428
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSD21, complete sequence
```

Seq. No. 134911

116172 1.R1010 Contig ID

5'-most EST g2762283 Method BLASTN NCBI GI g3510347



```
BLAST score
E value
                   5.0e-40
                   305
Match length
                   92
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134912
Contig ID
                   116174_1.R1010
5'-most EST
                   jC-atXP113C134I5T7d1
Method
                   BLASTN
NCBI GI
                   q4589437
BLAST score
                   279
E value
                   1.0e-155
Match length
                   401
% identity
                   96
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MPN9, complete sequence
Seq. No.
                   134913
Contig ID
                   116186 1.R1010
5'-most EST
                   jC-atXP113C221P16T7d1
Method
                   BLASTN
NCBI GI
                   g3337347
BLAST score
                   266
E value
                   1.0e-148
Match length
                   289
% identity
                   98
                  Arabidopsis thaliana chromosome II BAC F13P17 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134914
Contig ID
                  116193 1.R1010
5'-most EST
                  g1216849
Method
                  BLASTX
NCBI GI
                  g3236253
BLAST score
                  294
E value
                  1.0e-26
Match length
                  104
% identity
                  58
NCBI Description
                   (AC004684) receptor-like protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  134915
Contig ID
                  116201 1.R1010
5'-most EST
                  jC-atXP113C230D16T7d1
                  134916
Seq. No.
Contig ID
                  116217 1.R1010
5'-most EST
                  q957536
                  BLASTX
Method
```

NCBI GI g2281109 BLAST score 835 E value 8.0e-90 Match length 151 % identity 100

(AC002333) endochitinase isolog [Arabidopsis thaliana] NCBI Description



```
Seq. No.
                   134917
Contig ID
                   116217 2.R1010
5'-most EST
                   jC-atXP14C105010T7s1
                   BLASTX
Method
NCBI GI
                   g2281109
BLAST score
                   526
E value
                   1.0e-53
Match length
                   111
                   89
% identity
                   (AC002333) endochitinase isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   134918
Contig ID
                   116222 1.R1010
5'-most EST
                   q2723003
Method
                   BLASTX
NCBI GI
                   g2864613
BLAST score
                   165
E value
                   3.0e-11
Match length
                   72
% identity
                   46
NCBI Description
                   (AL021811) S-receptor kinase -like protein [Arabidopsis
                   thaliana] >gi_4049333_emb_CAA22558_ (AL034567) S-receptor
                   kinase-like protein [Arabidopsis thaliana]
Seq. No.
                   134919
Contig ID
                   116231 1.R1010
5'-most EST
                   g934740
Method
                   BLASTX
NCBI GI
                   g3420054
BLAST score
                   258
E value
                   5.0e-22
Match length
                   112
% identity
                   50
                  (AC004680) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   134920
Contig ID
                   116235 1.R1010
5'-most EST
                   q12171\overline{2}9
Method
                   BLASTX
NCBI GI
                   g3212867
BLAST score
                   496
E value
                   5.0e-50
Match length
                   150
% identity
                   65
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
                   134921
Seq. No.
Contig ID
                   116238 1.R1010
                   g12693\overline{4}7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3982576
BLAST score
                   195
```

E value 7.0e-15 Match length 39

100

% identity

NCBI Description (AF023140) imidazoleglycerol phosphate dehydratase [Thlaspi



goesingense]

134922 Seq. No. Contig ID 116239 1.R1010 5'-most EST g906702 Method BLASTN NCBI GI g4589425 BLAST score 36 E value 2.0e-10 Match length 68 % identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBA10, complete sequence

Seq. No. 134923

Contig ID 116245 1.R1010

5'-most EST jC-atXP114C231C23T7d1

Method BLASTN
NCBI GI g2264367
BLAST score 600
E value 0.0e+00
Match length 658
% identity 98

NCBI Description Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm,

complete sequence [Arabidopsis thaliana]

Seq. No. 134924

Contig ID 116246_1.R1010

5'-most EST g2749394
Method BLASTN
NCBI GI g2264367
BLAST score 226
E value 1.0e-124
Match length 399
% identity 98

NCBI Description Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm,

complete sequence [Arabidopsis thaliana]

Seq. No. 134925

Contig ID 116257 1.R1010

5'-most EST g1217170
Method BLASTX
NCBI GI g4753650
BLAST score 554
E value 6.0e-57
Match length 106
% identity 100

NCBI Description (AL049751) putative protein [Arabidopsis thaliana]

Seq. No. 134926

Contig ID 116259_1.R1010

5'-most EST jC-atXP114C231J12T7d1

Method BLASTN
NCBI GI g2494106
BLAST score 517
E value 0.0e+00
Match length 521



% identity

NCBI Description Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 134927

Contig ID 116267 1.R1010

5'-most EST g2580666

Seq. No. 134928

Contig ID 116277 1.R1010

5'-most EST jC-atXP114C231L24T7d1

Method BLASTN NCBI GI q2760170 BLAST score 524 E value 0.0e+00 593 Match length 98 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MIO24, complete sequence [Arabidopsis thaliana]

Seq. No. 134929

116289 1.R1010 Contig ID

5'-most EST q1217183 Method BLASTX NCBI GI q4558678 BLAST score 160 E value 1.0e-10 Match length 60 47 % identity

NCBI Description

(AC006586) unknown protein [Arabidopsis thaliana]

Seq. No. 134930

Contig ID 116291 1.R1010

5'-most EST $q12174\overline{0}7$ BLASTX Method NCBI GI g3193318 BLAST score 341 E value 6.0e-32 Match length 111 % identity 62

NCBI Description (AF069299) No definition line found [Arabidopsis thaliana]

Seq. No. 134931

Contig ID 116297 1.R1010

5'-most EST g1217413

Seq. No. 134932

Contig ID 116299 1.R1010

5'-most EST $jC-atX\overline{P}114C232F4T7d1$

Method BLASTX NCBI GI g1903367 BLAST score 596 E value 5.0e-74 Match length 177 % identity

NCBI Description (AC000104) ESTs gb_N65789, gb_T04628 come from this gene.

[Arabidopsis thaliana]



Seq. No. 134933

Contig ID 116300 1.R1010

5'-most EST g2596171
Method BLASTN
NCBI GI g2341023
BLAST score 249

E value 1.0e-138
Match length 336
% identity 99

NCBI Description Sequence of BAC F19P19 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 134934

Contig ID 116315 1.R1010

5'-most EST jC-atXP19C111K12T7d2

Method BLASTX
NCBI GI g4006827
BLAST score 959
E value 1.0e-104
Match length 193
% identity 98

NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 134935

Contig ID 116323_1.R1010

5'-most EST g936304
Method BLASTX
NCBI GI g4220454
BLAST score 590
E value 1.0e-76
Match length 157
% identity 62

NCBI Description (AC006216) Similar to gi 3413714 T19L18.21 putative

myrosinase-binding protein from Arabidopsis thaliana BAC gb_AC004747. ESTs gb_65870 and gb_T20812 come from this

gene. [Arabidopsis thaliana]

Seq. No. 134936

Contig ID 116323 2.R1010

5'-most EST jC-atXP114C240G22T7d1

Method BLASTX
NCBI GI g4220454
BLAST score 362
E value 2.0e-34
Match length 70
% identity 56

NCBI Description (AC006216) Similar to gi 3413714 T19L18.21 putative

myrosinase-binding protein from Arabidopsis thaliana BAC gb AC004747. ESTs gb 65870 and gb T20812 come from this

gene. [Arabidopsis thaliana]

Seq. No. 134937

Contig ID 116335 1.R1010

5'-most EST g1217274 Method BLASTN NCBI GI g3928074



```
BLAST score
E value
                   1.0e-110
                   407
Match length
                   98
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T7F6 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134938
Contig ID
                   116337 1.R1010
5'-most EST
                   g1217276
Seq. No.
                   134939
Contig ID
                   116358 1.R1010
5'-most EST
                   g2762981
Method
                   BLASTN
NCBI GI
                   q4757402
BLAST score
                   46
E value
                   2.0e-16
                   298
Match length
% identity
                   85
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MIG5, complete sequence
Seq. No.
                   134940
                   116365 1.R1010
Contig ID
5'-most EST
                   jC-atXP115C244E9T7d1
Method
                  BLASTN
NCBI GI
                   g2098816
BLAST score
                   411
E value
                   0.0e+00
                   500
Match length
% identity
                   97
NCBI Description Arabidopsis thaliana BAC F19G10, complete sequence
Seq. No.
                   134941
                  116376 1.R1010
Contig ID
5'-most EST
                   jC-atXP115C248F7T7d1
Method
                  BLASTX
NCBI GI
                  q3080418
BLAST score
                  641
                  7.0e-67
E value
Match length
                  143
% identity
                  87
NCBI Description
                  (AL022604) putative protein [Arabidopsis thaliana]
Seq. No.
                  134942
                  116380 1.R1010
Contig ID
5'-most EST
                  g2762308
Method
                  BLASTN
```

q2570223 NCBI GI BLAST score 621 E value 0.0e+00Match length 625 % identity 100

NCBI Description Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana]



Seq. No. 134943

Contig ID 116381_1.R1010

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:

MMJ24, complete sequence

Seq. No. 134944

Contig ID 116394 1.R1010

5'-most EST g2762872

Method BLASTX

NCBI GI g2924517

BLAST score 498

E value 2.0e-53

Match length 124

% identity 90

NCBI Description (AL022023) putative protein [Arabidopsis thaliana]

Seq. No. 134945

Contig ID 116399 1.R1010

5'-most EST g2762782

Method BLASTX

NCBI GI g4587540

BLAST score 177

E value 1.0e-18

Match length 136
% identity 45

NCBI Description (AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase

with GDSL-motif family. [Arabidopsis thaliana]

Seq. No. 134946

Contig ID 116418 1.R1010

5'-most EST g506907
Method BLASTX
NCBI GI g2347188
BLAST score 313
E value 1.0e-28
Match length 57
% identity 96

NCBI Description (AC002338) laccase isolog [Arabidopsis thaliana]

>gi 3150401 (AC004165) putative laccase [Arabidopsis

thaliana]

Seq. No. 134947

Contig ID 116420_1.R1010

5'-most EST jC-atXP115C24908T7s1

Method BLASTN
NCBI GI g2244788
BLAST score 204
E value 1.0e-111
Match length 375
% identity 90





```
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  134948
Contig ID
                  116424 1.R1010
5'-most EST
                  jC-atXP115C250G24T7s1
Seq. No.
                  134949
                  116426 1.R1010
Contig ID
5'-most EST
                  g2762878
Method
                  BLASTN
NCBI GI
                  g2252848
BLAST score
                  178
E value
                  2.0e-95
Match length
                  407
% identity
                  97
NCBI Description Arabidopsis thaliana BAC TM018A10
Seq. No.
                  134950
Contig ID
                  116427 1.R1010
5'-most EST
                  g2062769
Method
                  BLASTN
NCBI GI
                  g2252848
BLAST score
                  311
E value
                  1.0e-174
Match length
                  439
% identity
                  98
NCBI Description Arabidopsis thaliana BAC TM018A10
Seq. No.
                  134951
                  116429 1.R1010
Contig ID
5'-most EST
                  jC-atXP115C251B22T7d1
Seq. No.
                  134952
                  116431 1.R1010
Contig ID
5'-most EST
                  jC-atXP115C251D4T7d1
Method
                  BLASTN
NCBI GI
                  g3985931
BLAST score
                  366
E value
                  0.0e+00
Match length
                  410
% identity
                  93
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K21H1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  134953
```

116442 1.R1010 Contig ID 5'-most EST g1269420 Method BLASTX NCBI GI q2494144

BLAST score 134 E value 1.0e-07 Match length 116 % identity 5

NCBI Description (AC002329) predicted leucine-rich protein [Arabidopsis

thaliana



Seq. No. 134954 Contig ID 116464 1.R1010

5'-most EST jC-atXP94CG11D3T7b1

Seq. No. 134955

Contig ID 116470_1.R1010

5'-most EST jC-atXP115C248O19T7029d1

Method BLASTX
NCBI GI g2739010
BLAST score 62
E value 1.0e-75
Match length 185

Match length 185 % identity 73

NCBI Description (AF022464) CYP77A3p [Glycine max]

Seq. No. 134956

Contig ID 116472 1.R1010

5'-most EST jC-atXP115C248O20T7037d1

Method BLASTX
NCBI GI g2632254
BLAST score 303
E value 3.0e-27
Match length 166
% identity 39

NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No. 134957

Contig ID 116475_1.R1010

5'-most EST g1217236
Method BLASTN
NCBI GI g3869069
BLAST score 145
E value 1.0e-75
Match length 417
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 134958

Contig ID 116495 1.R1010

5'-most EST jC-atXP116C136F20T7d1

Method BLASTN
NCBI GI g3355463
BLAST score 343
E value 0.0e+00
Match length 347
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F12L6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134959

Contig ID 116496 1.R1010

5'-most EST jC-atXP115C248G24T7012d1

Method BLASTX
NCBI GI g4587529
BLAST score 445
E value 7.0e-44

16012

, =· ~



Match length 188 % identity 46

NCBI Description (AC007060) Strong similarity to F19I3.2 gi 3033375 putative

berberine bridge enzyme from Arabidopsis thaliana BAC

gb AC004238. EST gb H76902 comes from this gene

Seq. No. 134960

Contig ID 116503 1.R1010

5'-most EST jC-atXP115C248I24T7036d1

Method BLASTX
NCBI GI 94454019
BLAST score 969
E value 1.0e-105
Match length 189
% identity 100

NCBI Description (AL035396) SRG1-like protein [Arabidopsis thaliana]

Seq. No. 134961

Contig ID 116528 1.R1010

5'-most EST g2445860

Seq. No. 134962

Contig ID 116537 1.R1010

5'-most EST jC-atXP115C249L1T7006d1

Method BLASTN
NCBI GI g17818
BLAST score 57
E value 6.0e-23
Match length 216
% identity 88

NCBI Description B.napus BnGRP10 gene encoding glycine-rich RNA-binding

protein

Seq. No. 134963

Contig ID 116537 2.R1010

5'-most EST g2412827
Method BLASTN
NCBI GI g17818
BLAST score 57
E value 3.0e-23
Match length 149
% identity 89

NCBI Description B.napus BnGRP10 gene encoding glycine-rich RNA-binding

protein

Seq. No. 134964

Contig ID 116545 1.R1010

5'-most EST jC-atXP115C24908T7046d1

Method BLASTX
NCBI GI g4056421
BLAST score 1252
E value 1.0e-138
Match length 249
% identity 93

NCBI Description (AC005322) Similar to gb_Z30094 basic transcripion factor

2, 44 kD subunit from Homo sapiens. EST gb_W43325 comes

from this gene. [Arabidopsis thaliana]



```
134965
Seq. No.
Contig ID
                   116563 1.R1010
5'-most EST
                  g511214
Method
                  BLASTX
NCBI GI
                   g3033375
BLAST score
                   723
E value
                   2.0e-76
Match length
                   240
% identity
                   57
NCBI Description
                   (AC004238) putative berberine bridge enzyme [Arabidopsis
                   134966
Seq. No.
                   116563 7.R1010
Contig ID
5'-most EST
                   jC-atXP48C178D14T7s2
Method
                  BLASTX
NCBI GI
                   q4587526
BLAST score
                   251
E value
                   1.0e-21
Match length
                   75
% identity
                   60
NCBI Description
                  (AC007060) Strong similarity to F19I3.2 gi_3033375 putative
                  berberine bridge enzyme from Arabidopsis thaliana BAC
                   gb_AC004238. ESTs gb F19886, gb Z30784 and gb Z30785 come
                   from this gene
Seq. No.
                  134967
Contig ID
                   116580 1.R1010
5'-most EST
                  jC-atXP117C140F7T7a1
Seq. No.
                  134968
Contig ID
                  116581 1.R1010
5'-most EST
                  jC-atXP117C140J18T7a1
Method
                  BLASTN
NCBI GI
                  g2351064
BLAST score
                  62
E value
                  8.0e-26
Match length
                  1008
                  83
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDJ22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  134969
                  116583 1.R1010
Contig ID
5'-most EST
                  jC-atXP117C140K16T7d1
Seq. No.
                  134970
                  116584 1.R1010
Contig ID
5'-most EST
                  jC-atXP117C140L2T7a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
```

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

5.0e-20

52

56

98

E value

Match length

% identity



Seq. No. 134971

Contig ID 116595_1.R1010 5'-most EST jC-atXP117C141J1T7a1

Method BLASTX
NCBI GI g3242705

BLAST score 481
E value 4.0e-48
Match length 100
% identity 89

NCBI Description (AC003040) putative nicotinate phosphoribosyltransferase

[Arabidopsis thaliana]

Seq. No. 134972

Contig ID 116596_1.R1010

5'-most EST jC-atXP117C141K23T7a1

Method BLASTX
NCBI GI g4587527
BLAST score 325
E value 7.0e-30
Match length 130
% identity 50

NCBI Description (AC007060) Strong similarity to F19I3.2 gi 3033375 putative

berberine bridge enzyme from Arabidopsis thaliana BAC

gb_AC004238

Seq. No. 134973

Contig ID 116600_1.R1010

5'-most EST jC-atXP117C141M18T7a1

Method BLASTX
NCBI GI g231660
BLAST score 465
E value 3.0e-46
Match length 153
% identity 61

NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No. 134974

Contig ID 116605 1.R1010

5'-most EST jC-atXP117C143A20T7a1

Method BLASTN
NCBI GI g3885325
BLAST score 403
E value 0.0e+00
Match length 507
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC T20P8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134975

Contig ID 116609_1.R1010

 5'-most EST
 g936843

 Method
 BLASTN

 NCBI GI
 g2351062

 BLAST score
 331

 E value
 0.0e+00

 Match length
 429



% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAH20, complete sequence [Arabidopsis thaliana]

Seq. No. 134976

Contig ID 116612 1.R1010

5'-most EST jC-atXP119C166H13T7024a1

Method BLASTN
NCBI GI g2582640
BLAST score 34
E value 3.0e-09
Match length 73
% identity 89

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 134977

Contig ID 116621_1.R1010 5'-most EST jC-atXP11C97F18T7s1

Method BLASTN
NCBI GI g3702728
BLAST score 375
E value 0.0e+00
Match length 475
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19M13, complete sequence [Arabidopsis thaliana]

Seq. No. 134978

Contig ID 116622 1.R1010

5'-most EST g2048894
Method BLASTX
NCBI GI g4581111
BLAST score 217
E value 9.0e-18
Match length 81
% identity 55

NCBI Description (AC005825) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 134979

Contig ID 116627_1.R1010 5'-most EST jC-atXP11C97011T7s1

Method BLASTX
NCBI GI g4678356
BLAST score 189
E value 4.0e-23
Match length 76
% identity 71

NCBI Description (AL049659) cytochrome P450-like protein [Arabidopsis

thaliana]

Seq. No. 134980

Contig ID 116631_1.R1010 5'-most EST jC-atXP16C109D21T7s1

Method BLASTN NCBI GI g2564051



```
BLAST score
E value
                   0.0e + 00
Match length
                   419
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MWD9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  134981
Contig ID
                  116636 1.R1010
5'-most EST
                  jC-atXP11C98C15T7s1
                  134982
Seq. No.
                  116639 1.R1010
Contig ID
5'-most EST
                  q2048905
Method
                  BLASTN
NCBI GI
                  g3395421
BLAST score
                  194
E value
                  1.0e-105
Match length
                  374
                  99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T19C21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  134983
                  116648 1.R1010
Contig ID
5'-most EST
                  q936220
Method
                  BLASTX
NCBI GI
                  g1279598
BLAST score
                  391
                  9.0e-38
E value
Match length
                  108
% identity
                  64
NCBI Description
                  (Z71752) pectin methylesterase [Nicotiana plumbaginifolia]
                  134984
Seq. No.
Contig ID
                  116653 1.R1010
5'-most EST
                  jC-atXP122C158F2T7079a1
Method
                  BLASTX
NCBI GI
                  g2244893
BLAST score
                  665
                  1.0e-102
E value
Match length
                  375
% identity
                  56
NCBI Description
                  (Z97338) similarity to cytochrome P450 [Arabidopsis
                  thaliana]
Seq. No.
                  134985
                  116655 1.R1010
Contig ID
5'-most EST
                  q2757310
Method
                  BLASTN
NCBI GI
                  g2262155
BLAST score
                  189
```

E value 1.0e-102 Match length 421

96 % identity

NCBI Description DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]



```
134986
Seq. No.
                   116668 1.R1010
Contig ID
                   jC-atX\overline{P}11C98N10T7s1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2623294
BLAST score
                   213
E value
                   1.0e-116
Match length
                   321
                   93
% identity
                   Arabidopsis thaliana chromosome II BAC T20B5 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   134987
                   116672 1.R1010
Contig ID
5'-most EST
                   jC-atX\overline{P}11C99A10T7s1
Method
                   BLASTN
NCBI GI
                   q3805839
                   238
BLAST score
E value
                   1.0e-131
Match length
                   506
                   95
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14
                   (ESSAII project)
                   134988
Seq. No.
Contig ID
                   116680 1.R1010
5'-most EST
                   q2758176
Method
                   BLASTX
                   q3482925
NCBI GI
BLAST score
                   223
                   1.0e-31
E value
Match length
                   151
% identity
                   48
                  (AC003970) Highly similar to cinnamyl alcohol
NCBI Description
                   dehydrogenase, gi_1143445 [Arabidopsis thaliana]
Seq. No.
                   134989
Contia ID
                   116681 1.R1010
5'-most EST
                   g2758196
Seq. No.
                   134990
Contig ID
                   116688 1.R1010
5'-most EST
                   jC-atXP122C117J22T7d1
                   134991
Seq. No.
Contig ID
                   116690 1.R1010
5'-most EST
                   jC-atXP122C117J5T7d1
```

Method BLASTN
NCBI GI g1946354
BLAST score 329
E value 0.0e+00
Match length 429
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T06B20 genomic

sequence, complete sequence

BLAST score

Match length % identity

E value

242 1.0e-133

336

99



```
Seq. No.
                  116692 1.R1010
Contig ID
                  iC-atXP122C117K20T7d1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2245073
BLAST score
                  302
E value
                  1.0e-169
Match length
                  451
                  97
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  134993
Contig ID
                  116693 1.R1010
5'-most EST
                  q2758219
Method
                  BLASTN
NCBI GI
                  g3510346
BLAST score
                  258
E value
                  1.0e-143
Match length
                  278
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNL12, complete sequence [Arabidopsis thaliana]
                  134994
Seq. No.
Contig ID
                  116697 1.R1010
5'-most EST
                  jC-atXP122C118F20T7034a1
Method
                  BLASTN
NCBI GI
                  q2264312
BLAST score
                  411
E value
                  0.0e + 00
Match length
                  504
% identity
                  95
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOK16, complete sequence [Arabidopsis thaliana]
                  134995
Seq. No.
                  116700 1.R1010
Contig ID -
5'-most EST
                  g2758256
Method
                  BLASTX
                  g3776576
NCBI GI
BLAST score
                  283
E value
                  9.0e-25
Match length
                  94
% identity
                  56
                  (AC005388) ESTs gb Z25669 and gb Z33817 come from this
NCBI Description
                  gene. [Arabidopsis thaliana]
                  134996
Seq. No.
                  116703 1.R1010
Contig ID
5'-most EST
                  jC-atXP122C118H3T7d1
                  BLASTN
Method
NCBI GI
                  g3335356
```



NCBI Description Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134997

Contig ID 116704 1.R1010

5'-most EST jC-atXP122C118I13T7d1

Seq. No. 134998

Contig ID 116706 1.R1010

5'-most EST g2722487

Method BLASTN

NCBI GI g2264318

BLAST score 328

E value 0.0e+00

Match length 356
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUP24, complete sequence [Arabidopsis thaliana]

Seq. No. 134999

Contig ID 116707 1.R1010

5'-most EST $g27474\overline{3}1$

Seq. No. 135000

Contig ID 116708 1.R1010

5'-most EST jC-atXP122C152H15T7094a1

Method BLASTN
NCBI GI g3399678
BLAST score 406
E value 0.0e+00
Match length 458
% identity 98

NCBI Description Arabidopsis thaliana chromosome 1 BAC F13M7 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 135001

Contig ID 116708_2.R1010

5'-most EST jC-atXP122C152H15T7d1

Method BLASTN
NCBI GI g3399678
BLAST score 433
E value 0.0e+00
Match length 577
% identity 96

NCBI Description Arabidopsis thaliana chromosome 1 BAC F13M7 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 135002

Contig ID 116712 1.R1010

5'-most EST $q93600\overline{1}$

Seq. No. 135003

Contig ID 116713_1.R1010 5'-most EST jC-atXP122C158F2T7d1

Method BLASTX
NCBI GI g2244893
BLAST score 155



E value 5.0e-18
Match length 68
% identity 71

NCBI Description (Z97338) similarity to cytochrome P450 [Arabidopsis

thaliana]

Seq. No. 135004

Contig ID 116716 2.R1010

5'-most EST jC-atXP122C159H19T7d1

Method BLASTN
NCBI GI g3540210
BLAST score 399
E value 0.0e+00
Match length 441
% identity 98

NCBI Description Arabidopsis thaliana chromosome I BAC F5A8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135005

Contig ID 116717 1.R1010

5'-most EST jC-atXP122C159H23T7d1

Method BLASTX
NCBI GI g2499812
BLAST score 588
E value 2.0e-60
Match length 135
% identity 83

NCBI Description PROFILIN 3 > gi 1353765 (U43323) profilin 3 [Arabidopsis

thaliana]

Seq. No. 135006

Contig ID 116722 1.R1010

5'-most EST g2763951
Method BLASTX
NCBI GI g3912922
BLAST score 311
E value 5.0e-28
Match length 88
% identity 65

NCBI Description (AF001308) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135007

Contig ID 116723_1.R1010

5'-most EST g2759562
Method BLASTX
NCBI GI g4263787
BLAST score 693
E value 4.0e-83
Match length 166
% identity 96

NCBI Description (AC006068) unknown protein [Arabidopsis thaliana]

Seq. No. 135008

Contig ID 116724 1.R1010

5'-most EST jC-atXP124C118M17T7d1

Method BLASTN NCBI GI g2160132



BLAST score 199
E value 1.0e-108
Match length 369
% identity 100

NCBI Description Sequence of BAC F19K23 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 135009

Contig ID 116731_1.R1010

5'-most EST jC-atXP124C118N2T7d1

Method BLASTX
NCBI GI g1172019
BLAST score 222
E value 5.0e-18
Match length 95
% identity 45

NCBI Description PEROXISOME BIOSYNTHESIS PROTEIN PAS1 (PEROXIN-1)

>gi_1076972_pir__A55152 PAS1 protein - yeast (Pichia
pastoris) >gi 537420 emb CAA85450 (Z36987) PAS1 [Pichia

pastoris]

Seq. No. 135010

Contig ID 116739 1.R1010

5'-most EST g2758688
Method BLASTN
NCBI GI g4159701
BLAST score 115
E value 9.0e-58
Match length 516
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K22G18, complete sequence

Seq. No. 135011

Contig ID 116748 1.R1010

5'-most EST g2758702

Seq. No. 135012

Contig ID 116754 1.R1010

5'-most EST g938006
Method BLASTX
NCBI GI g3695383
BLAST score 379
E value 2.0e-36
Match length 73
% identity 97

NCBI Description (AF096370) similar to inorganic pyrophosphatase (Pfam:

PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis

thaliana]

Seq. No. 135013

Contig ID 116756 1.R1010

5'-most EST jC-atXP124C121B23T7d1

Method BLASTN
NCBI GI g4467094
BLAST score 311
E value 1.0e-174



Match length 984 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10

(ESSA project)

Seq. No. 135014

Contig ID 116757 1.R1010

5'-most EST jC-atXP124C121B9T7d1

Method BLASTX
NCBI GI g4760370
BLAST score 369
E value 4.0e-35
Match length 187
% identity 36

NCBI Description (AF082565) ATP dependent copper transporter [Arabidopsis

thaliana] >gi_4760380_gb_AAD29115.1_ (AF091112) ATP dependent copper transporter [Arabidopsis thaliana]

Seq. No. 135015

Contig ID 116776 1.R1010

NCBI Description (AC004557) F17L21.23 [Arabidopsis thaliana]

Seq. No. 135016

Contig ID 116780_1.R1010

5'-most EST g2758441
Method BLASTX
NCBI GI g1208497
BLAST score 335
E value 7.0e-31
Match length 192
% identity 41

NCBI Description (D38125) EREBP-4 [Nicotiana tabacum]

Seq. No. 135017

Contig ID 116780 2.R1010

5'-most EST g936643
Method BLASTX
NCBI GI g1208497
BLAST score 150
E value 4.0e-12
Match length 119
% identity 44

NCBI Description (D38125) EREBP-4 [Nicotiana tabacum]

Seq. No. 135018

Contig ID 116784 2.R1010

 5'-most EST
 g2758455

 Method
 BLASTX

 NCBI GI
 g2997593

BLAST score 276



E value 3.0e-24 Match length 124 % identity 51

NCBI Description (AF020816) glucose-6-phosphate/phosphate-translocator

precursor [Solanum tuberosum]

Seq. No. 135019

Contig ID 116797_1.R1010

5'-most EST jC-atXP124C122B2T7d1

Method BLASTX
NCBI GI g2506277
BLAST score 241
E value 2.0e-31
Match length 130
% identity 58

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60

KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >qi 806808

(U21139) chaperonin precursor [Pisum sativum]

Seq. No. 135020

Contig ID 116807 1.R1010

5'-most EST jC-atXP125C125N19T7d2

Method BLASTX
NCBI GI g3913435
BLAST score 279
E value 1.0e-24
Match length 97
% identity 49

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE F56D2.6 >gi_532106 (U13644) similar to S.

cerevisiae pre-mRNA splicing factor RNA helicase PRP22 and

other DEAD box family helicases (DEAH subfamily)

[Caenorhabditis elegans]

Seq. No. 135021

Contig ID 116810_1.R1010

5'-most EST g2413992
Method BLASTX
NCBI GI g4490733
BLAST score 731
E value 1.0e-77
Match length 139
% identity 99

NCBI Description (AL035709) putative protein [Arabidopsis thaliana]

Seq. No. 135022

Contig ID 116811 1.R1010

5'-most EST g2762251
Method BLASTX
NCBI GI g731456
BLAST score 175
E value 2.0e-12
Match length 75
% identity 41

NCBI Description HYPOTHETICAL 27.7 KD PROTEIN IN PIP1-GLN3 INTERGENIC REGION

>gi_1077649_pir__S50542 hypothetical protein YER039c yeast (Saccharomyces cerevisiae) >gi 603272 (U18796)



Yer039cp [Saccharomyces cerevisiae]

Seq. No. 135023 Contig ID 116813 1.R1010 5'-most EST jC-atXP125C133H7T7d1 Seq. No. 135024

Contig ID 116814_1.R1010

5'-most EST jC-atXP125C133H9T7d1

Seq. No. 135025

Contig ID 116819 1.R1010

5'-most EST g2763262
Method BLASTX
NCBI GI g1001355
BLAST score 146
E value 3.0e-09
Match length 81
% identity 40

NCBI Description (D64006) auxin-induced protein [Synechocystis sp.]

Seq. No. 135026

Contig ID 116836_1.R1010 5'-most EST jC-atXP125C193P6T7d1

Method BLASTX
NCBI GI g2494143
BLAST score 628
E value 4.0e-73
Match length 149
% identity 97

NCBI Description (AC002329) Mlo-like protein [Arabidopsis thaliana]

Seq. No. 135027

Contig ID 116840 1.R1010

5'-most EST g1216605
Method BLASTX
NCBI GI g4581123
BLAST score 270
E value 5.0e-44
Match length 113
% identity 84

NCBI Description (AC005825) unknown protein [Arabidopsis thaliana]

Seq. No. 135028

Contig ID 116855 1.R1010

5'-most EST jC-atXP12C103G5T7069a1

Method BLASTX
NCBI GI g1709925
BLAST score 359
E value 5.0e-35
Match length 97
% identity 71

NCBI Description PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE PRECURSOR (AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR

SYNTHASE) >gi_945060 (U30895) aminoimidazole ribonucleotide

(AIRS) synthetase [Vigna unguiculata]



```
Seq. No.
                   116861 1.R1010
Contig ID
                   jC-atXP12C103D21T7d2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2982283
BLAST score
                   483
E value
                   2.0e-48
Match length
                   191
% identity
                   55
NCBI Description
                  (AF051226) PREG-like protein [Picea mariana]
Seq. No.
                   135030
Contig ID
                   116861 2.R1010
5'-most EST
                   g2048149
                   BLASTX
Method
NCBI GI
                   a2982283
BLAST score
                   327
                   3.0e-30
E value
Match length
                   114
% identity
                   54
                  (AF051226) PREG-like protein [Picea mariana]
NCBI Description
Seq. No.
                   135031
Contig ID
                   116866 1.R1010
5'-most EST
                   jC-atXP12C103M24T7094a1
Method
                   BLASTN
NCBI GI
                   a1865682
BLAST score
                   310
E value
                   1.0e-174
Match length
                   503
% identity
                   99
NCBI Description A.thaliana 16 kb chromosome 1 DNA fragment
                   135032
Seq. No.
Contig ID
                   116870 1.R1010
5'-most EST
                   q2596534
Method
                   BLASTN
                   q2264312
NCBI GI
BLAST score
                   408
                   0.0e+00
E value
Match length
                   514
% identity
                   96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MOK16, complete sequence [Arabidopsis thaliana]
Seq. No.
                   135033
                   116873 1.R1010
Contig ID
5'-most EST
                   q2596541
Method
                   BLASTN
NCBI GI
                   q3193311
BLAST score
                   302
```

E value 1.0e-169 Match length 430 97 % identity

NCBI Description Arabidopsis thaliana BAC F6N15

Seq. No. 135034



Contig ID 116874 1.R1010

5'-most EST jC-at \overline{XP} 12C103K22T7d2

Method BLASTN
NCBI GI g2979540
BLAST score 403
E value 0.0e+00
Match length 563
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135035

Contig ID 116875 1.R1010

5'-most EST g2596544
Method BLASTX
NCBI GI g4726110
BLAST score 274
E value 9.0e-24
Match length 181
% identity 26

NCBI Description (AC006436) unknown protein [Arabidopsis thaliana]

Seq. No. 135036

Contig ID 116879 1.R1010

5'-most EST g2596549
Method BLASTX
NCBI GI g2541876
BLAST score 264
E value 3.0e-24
Match length 142
% identity 46

NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein

[Nicotiana tabacum]

Seq. No. 135037

Contig ID 116880_1.R1010

5'-most EST g576968
Method BLASTX
NCBI GI g3874433
BLAST score 231
E value 7.0e-19
Match length 152
% identity 36

NCBI Description (Z81038) predicted using Genefinder; Similarity to Yeast

ABD1 protein (SW:P32783); cDNA EST EMBL:T01105 comes from

this gene [Caenorhabditis elegans]

Seq. No. 135038

Contig ID 116895 1.R1010

5'-most EST g2596863
Method BLASTX
NCBI GI g2832642
BLAST score 461
E value 7.0e-78
Match length 178
% identity 82

NCBI Description (AL021710) putative protein [Arabidopsis thaliana]



Seq. No. 135039

Contig ID 116898_1.R1010 5'-most EST jC-atXP12C99M14T7d2

Method BLASTX
NCBI GI 94689473
BLAST score 157
E value 2.0e-10
Match length 40
% identity 68

NCBI Description (AC007213) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 135040

Contig ID 116900_1.R1010 5'-most EST jC-atXP12C99M18T7d2

Seq. No. 135041

Contig ID 116901_1.R1010 5'-most EST jC-atXP12C99M20T7d2

Method BLASTX
NCBI GI g2281103
BLAST score 599
E value 4.0e-62
Match length 111
% identity 99

NCBI Description (AC002333) Glucan endo-1,3-beta glucosidase isolog

[Arabidopsis thaliana]

Seq. No. 135042

Contig ID 116903 1.R1010 5'-most EST jC-atXP12C99M23T7d2

Method BLASTX
NCBI GI g3377517
BLAST score 213
E value 4.0e-17
Match length 100
% identity 41

NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No. 135043

Contig ID 116921_1.R1010

5'-most EST g2596947

Seq. No. 135044

Contig ID 116933 1.R1010

5'-most EST g25965\(\overline{83}\)
Method BLASTX
NCBI GI g2911067
BLAST score 400
E value 6.0e-39
Match length 114
% identity 71

NCBI Description (AL021960) UV-damaged DNA-binding protein-like [Arabidopsis

thaliana]

Seq. No. 135045



```
116942 1.R1010
Contig ID
                  jC-atXP13C104E2T7d2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3702314
BLAST score
                  378
                  2.0e-36
E value
Match length
                  144
                  62
% identity
NCBI Description
                  (AC002535) similar to SWI/SNF complex subunit BAF170
                   [Arabidopsis thaliana]
                  135046
Seq. No.
                  116945 1.R1010
Contig ID
                  jC-atXP13C104G18T7d2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1653395
BLAST score
                  386
E value
                  3.0e-37
Match length
                  170
                  49
% identity
                  (D90913) PET112 [Synechocystis sp.]
NCBI Description
Seq. No.
                  135047
                  116947 1.R1010
Contig ID
5'-most EST
                  jC-atXP13C104G23T7d2
Method
                  BLASTX
NCBI GI
                  q3341695
BLAST score
                  562
E value
                  1.0e-105
                  221
Match length
% identity
NCBI Description
                  (AC003672) putative thiamin pyrophosphokinase [Arabidopsis
                  thaliana]
                  135048
Seq. No.
Contig ID
                  116951 1.R1010
5'-most EST
                  q2596602
Method
                  BLASTX
NCBI GI
                  g4468984
BLAST score
                  345
E value
                  2.0e-32
Match length
                  90
% identity
                  74
NCBI Description (AL035605) putative protein [Arabidopsis thaliana]
Seq. No.
                  135049
Contig ID
                  116960 1.R1010
5'-most EST
                  jC-atXP13C104K22T7d2
Method
                  BLASTN
```

NCBI GI q4580454 BLAST score 342 E value 0.0e + 00Match length 470 % identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T2G17 genomic

sequence, complete sequence



```
Seq. No.
                   135050
                   116961 1.R1010
Contig ID
                   jC-atXP13C104L10T7d2
5'-most EST
                   BLASTX
Method
                   g4097547
NCBI GI
BLAST score
                   369
E value
                   3.0e-35
Match length
                   113
% identity
                   38
NCBI Description
                  (U64906) ATFP3 [Arabidopsis thaliana]
Seq. No.
                   135051
Contig ID
                   116971 1.R1010
                   jC-atXP13C104N12T7d2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2262116
BLAST score
                   627
E value
                   2.0e-65
Match length
                   124
% identity
                   99
NCBI Description
                  (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
Seq. No.
                   135052
                   116977 1.R1010
Contig ID
                   jC-atXP13C104014T7d2
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4713943
BLAST score
                   181
E value
                   4.0e-97
Match length
                   332
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T8K14 sequence,
                   complete sequence
Seq. No.
                   135053
                   116978 1.R1010
Contig ID
5'-most EST
                   jC-atXP13C104O15T7d2
Method
                   BLASTX
NCBI GI
                   q4586045
BLAST score
                   55
                   1.0e-52
E value
Match length
                   169
% identity
                   67
NCBI Description
                   (AC007020) putative ankyrin protein [Arabidopsis thaliana]
Seq. No.
                   135054
Contig ID
                   116979 1.R1010
                   g12694\overline{4}7
5'-most EST
```

Method BLASTX NCBI GI g2244859 BLAST score 556 7.0e-57 E value Match length 143 80 % identity

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135055



Contig ID 116980 1.R1010

NCBI Description - Arabidopsis thaliana chromosome II BAC F3K12 genomic

sequence, complete sequence

Seq. No. 135056

% identity

Contig ID 116984_1.R1010 5'-most EST jC-atXP14C104P22T7d1

94

Method BLASTX
NCBI GI g4455206
BLAST score 58
E value 4.0e-35
Match length 148
% identity 53

NCBI Description (AL035440) putative beta-1, 3-glucanase [Arabidopsis

thaliana]

Seq. No. 135057

Contig ID 116988_1.R1010 5'-most EST jC-atXP14C104P2T7d1

Method BLASTX
NCBI GI g3021506
BLAST score 820
E value 7.0e-88
Match length 207
% identity 77

NCBI Description (X96727) isocitrate dehydrogenase (NAD+) [Nicotiana

tabacum]

Seq. No. 135058

Contig ID 116992_1.R1010 5'-most EST jC-atXP14C105A3T7d1

Method BLASTN
NCBI GI g2245031
BLAST score 477
E value 0.0e+00
Match length 517
% identity 38

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 135059

Contig ID 116994_1.R1010

5'-most EST g2597025
Method BLASTX
NCBI GI g2342687
BLAST score 230
E value 1.0e-32
Match length 147
% identity 52

NCBI Description (AC000106) Similar to Beta integral membrane protein





(gb_U43629). EST gb_W43122 comes from this gene. [Arabidopsis thaliana]

Seq. No. 135060

Contig ID 116997_1.R1010

5'-most EST g2597035
Method BLASTX
NCBI GI g1495804
BLAST score 429
E value 2.0e-42
Match length 113
% identity 73

NCBI Description (X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No. 135061

Contig ID 116999 1.R1010

5'-most EST jC-atXP14C105C12T7d1

Method BLASTX
NCBI GI g4115381
BLAST score 191
E value 8.0e-15
Match length 45
% identity 78

NCBI Description (AC005967) putative limonene cyclase [Arabidopsis thaliana]

Seq. No. 135062

Contig ID 117008_1.R1010

5'-most EST g3450085

Seq. No. 135063

Contig ID 117013_1.R1010 5'-most EST jC-atXP14C105E9T7d1

Method BLASTN
NCBI GI g4159703
BLAST score 289
E value 1.0e-161
Match length 417
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K5F14, complete sequence

Seq. No. 135064

Contig ID 117017_1.R1010

5'-most EST jC-at $X\overline{P}$ 14C105H16T7d1

Seq. No. 135065

Contig ID 117027_1.R1010

5'-most EST jC-atXP14C105K12T7d1

Seq. No. 135066

Contig ID 117031_1.R1010

5'-most EST jC-atXP14C105K19T7s1

Method BLASTN
NCBI GI g3522932
BLAST score 271
E value 1.0e-151

Match length 398



% identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135067

Contig ID 117042 1.R1010

5'-most EST g2597223

Method BLASTN

NCBI GI g2262135

BLAST score 316

E value 1.0e-178

Match length 328

% identity 99

NCBI Description Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15

cM, complete sequence

Seq. No. 135068

Contig ID 117048 1.R1010

5'-most EST jC-atXP14C105N24T7d1

Seq. No. 135069

Contig ID 117050_1.R1010 5'-most EST jC-atXP14C105N3T7d1

Method BLASTX
NCBI GI g4835225
BLAST score 493
E value 7.0e-50
Match length 121
% identity 84

NCBI Description (ALO49862) UTP-glucose glucosyltransferase like protein

[Arabidopsis thaliana]

Seq. No. 135070

Contig ID 117051 1.R1010

5'-most EST g3450100

Method BLASTN

NCBI GI g4835223

BLAST score 441

E value 0.0e+00

Match length 498

% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3

(ESSA project)

Seq. No. 135071

Contig ID 117052_1.R1010 5'-most EST jC-atXP14C105O10T7d1

Method BLASTX
NCBI GI g2281109
BLAST score 556
E value 4.0e-57
Match length 159
% identity 69

NCBI Description (AC002333) endochitinase isolog [Arabidopsis thaliana]

Seq. No. 135072

Contig ID 117062_1.R1010



```
5'-most EST
                  jC-atXP14C105P24T7d1
Method
                  BLASTX
NCBI GI
                  q1351203
BLAST score
                  502
E value
                  1.0e-73
Match length
                  187
% identity
                  80
NCBI Description
                  TUBULIN BETA CHAIN
Seq. No.
                  135073
Contig ID
                  117064 1.R1010
5'-most EST
                  g2597241
Method
                  BLASTX
NCBI GI
                  q4455276
BLAST score
                  321
E value
                  2.0e-30
Match length
                  137
% identity
                  52
                  (AL035527) peptide transporter-like protein [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                  135074
Contig ID
                  117068 1.R1010
                  q3450107
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4262221
BLAST score
                  262
E value
                  1.0e-145
Match length
                  438
% identity
                  93
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F10A8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  135075
Contig ID
                  117076 1.R1010
5'-most EST
                  jC-atXP14C106C5T7s1
Method
                  BLASTN
NCBI GI
                  g3046856
BLAST score
                  289
E value
                  1.0e-161
Match length
                  508
% identity
                  96
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXI22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  135076
                  117079 1.R1010
Contig ID
5'-most EST
                  q2596732
Method
                  BLASTX
```

NCBI GI q4646203 BLAST score **2**56 5.0e-22 E value Match length 143 37 % identity

(AC007230) Belongs to PF 00026 Eukaryotic aspartyl protease NCBI Description

family. [Arabidopsis thaliana]



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135077
Seq. No.
                   117081 1.R1010
Contig ID
5'-most EST
                   g2597490
Method
                  BLASTN
NCBI GI
                   g3080352
BLAST score
                   313
E value
                   1.0e-176
Match length
                   465
% identity
                   93
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18
                   (ESSAII project)
                   135078
Seq. No.
Contig ID
                   117085 1.R1010
5'-most EST
                  g2597246
```

Seq. No. 135079

117090 1.R1010 Contig ID

5'-most EST g2596753 Method BLASTX NCBI GI g3152563 BLAST score 691 E value 4.0e-94 Match length 213 % identity

NCBI Description (AC002986) Similar to myb-related transcription factors

e.g., gb X98308. EST gb T22093 and gb T22697 come from

this gene. [Arabidopsis thaliana]

Seq. No. 135080

117109 1.R1010 Contig ID

5'-most EST jC-atXP15C108A20T7d1

Method BLASTX NCBI GI g3128185 BLAST score 226 E value 4.0e-18 Match length 164 % identity 41

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

135081 Seq. No.

Contig ID 117114 1.R1010

5'-most EST $g25974\overline{2}2$

Seq. No. 135082

Contig ID 117129 1.R1010

5'-most EST g2048194 Method BLASTN NCBI GI q4220632 BLAST score 249 E value 1.0e-137 Match length 460 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K6M13, complete sequence [Arabidopsis thaliana]

Seq. No. 135083



Contig ID 117129_2.R1010 5'-most EST jC-atXP80C240G12T7d1

Method BLASTN
NCBI GI g4220632
BLAST score 471
E value 0.0e+00
Match length 637
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K6M13, complete sequence [Arabidopsis thaliana]

Seq. No. 135084

Contig ID 117136 1.R1010

5'-most EST g3450153
Method BLASTN
NCBI GI g2244901
BLAST score 297
E value 1.0e-166
Match length 553
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 135085

Contig ID 117137 1.R1010

5'-most EST jC-atXP16C108K11T7d1

Method BLASTX
NCBI GI g3129952
BLAST score 368
E value 6.0e-35
Match length 125
% identity 45

NCBI Description (AJ006052) copper amine oxidase [Cicer arietinum]

Seq. No. 135086

Contig ID 117163_1.R1010

5'-most EST $q63448\overline{8}$

Seq. No. 135087

Contig ID 117172_1.R1010

5'-most EST g3450198
Method BLASTX
NCBI GI g3763919
BLAST score 479
E value 4.0e-48
Match length 96
% identity 98

NCBI Description (AC004450) putative isopropylmalate dehydratase

[Arabidopsis thaliana] >gi 4531436 gb AAD22121.1 AC006224 3

(AC006224) putative isopropylmalate dehydratase

[Arabidopsis thaliana]

Seq. No. 135088

Contig ID 117174 1.R1010

5'-most EST $g20482\overline{4}0$

Seq. No. 135089

E value

Match length

% identity

8.0e-49

152

72



```
Contig ID
                   117177 1.R1010
5'-most EST
                   g2393261
                   135090
Seq. No.
Contig ID
                   117180 1.R1010
5'-most EST
                   g634615
Method
                   BLASTX
NCBI GI
                   q4406759
BLAST score
                   395
E value
                   3.0e-38
Match length
                   134
% identity
                   60
NCBI Description
                  (AC006836) hypothetical protein [Arabidopsis thaliana]
                   135091
Seq. No.
                   117201 1.R1010
Contig ID
5'-most EST
                   q2393267
Method
                   BLASTX
NCBI GI
                   q3334162
BLAST score
                   223
E value
                   6.0e-18
Match length
                   102
% identity
                   43
NCBI Description
                  DOWN SYNDROME CRITICAL REGION PROTEIN A
                   >gi 2588993 dbj BAA23270 (AB001990) Dcra [Mus musculus]
                   135092
Seq. No.
Contig ID
                   117205 1.R1010
5'-most EST
                   g1268399
Method
                   BLASTX
                   g3540181
NCBI GI
BLAST score
                   203
E value
                   1.0e-15
Match length
                   130
% identity
                   42
                  (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   135093
                   117215 1.R1010
Contig ID
                   jC-atX\overline{P}17C110F15T7s3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2911073
BLAST score
                   226
E value
                   6.0e-28
Match length
                   123
% identity
                   51
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                   135094
Seq. No.
Contig ID
                   117218 1.R1010
5'-most EST
                   jC-atXP17C110F21T7d3
Method
                   BLASTX
NCBI GI
                   g4567283
BLAST score
                   486
```

(AC006841) unknown protein [Arabidopsis thaliana] NCBI Description 135095 Seq. No. 117230 1.R1010 Contiq ID 5'-most EST jC-atXP17C110G3T7d3 Method BLASTX NCBI GI q2827665 BLAST score 653 2.0e-68 E value 183 Match length % identity 53 NCBI Description (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana] Seq. No. 135096 117232 1.R1010 Contig ID 5'-most EST jC-atXP17C110G6T7d3 Method BLASTN g4589430 NCBI GI BLAST score 470 0.0e + 00E value 514 Match length % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence

135097 Seq. No. Contig ID 117233 1.R1010 5'-most EST jC-atXP17C110G6T7s3 Method BLASTX NCBI GI g3046694 BLAST score 346 E value 2.0e-32 Match length 112

Match length 112
% identity 62
NCRI Description (ALO22

NCBI Description (AL022224) vacuolar sorting receptor-like protein

[Arabidopsis thaliana]

Seq. No. 135098

Contig ID 117235_1.R1010 5'-most EST jC-atXP17C110G7T7s3

Method BLASTX
NCBI GI g2827699
BLAST score 146
E value 4.0e-09
Match length 46
% identity 63

NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

Seq. No. 135099

Contig ID 117236_1.R1010

5'-most EST jC-atXP17C110H10T7d3

Method BLASTN
NCBI GI g4159707
BLAST score 212
E value 1.0e-115
Match length 368



```
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MJK13, complete sequence
                   135100
Seq. No.
Contig ID
                   117237 1.R1010
                   jC-atX\overline{P}17C110H10T7s3
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2244796
BLAST score
                   466
E value
                   1.0e-46
Match length
                   130
% identity
                   75
NCBI Description
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
                   135101
Seq. No.
                   117240 1.R1010
Contig ID
5'-most EST
                   q27575\overline{0}2
                   BLASTN
Method
NCBI GI
                   q4406776
BLAST score
                   295
                   1.0e-165
E value
Match length
                   398
% identity
                   95
                   Arabidopsis thaliana chromosome II BAC F14H20 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   135102
Contig ID
                   117241 1.R1010
5'-most EST
                   q24461\overline{0}3
Method
                   BLASTX
                   g2129661
NCBI GI
BLAST score
                   349
                   7.0e-33
E value
Match length
                   67
% identity
                   97
                   OR23 protein - Arabidopsis thaliana (fragment) >gi 1022809
NCBI Description
                   (U37704) OR23peptide [Arabidopsis thaliana]
Seq. No.
                   135103
                   117274 1.R1010
Contig ID
                   jC-atXP17C110L6T7d3
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4519192
BLAST score
                   211
E value
                   1.0e-115
Match length
                   447
% identity
                   98
```

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MBK21, complete sequence

135104 Seq. No.

117283 1.R1010 Contig ID

5'-most EST $g24460\overline{4}4$ Method BLASTX NCBI GI g3426039 BLAST score 153



E value 7.0e-10
Match length 109
% identity 37

NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 135105

Contig ID 117286_1.R1010

5'-most EST jC-atXP17C110N24T7d3

Method BLASTX
NCBI GI g3024893
BLAST score 151
E value 1.0e-09
Match length 160
% identity 13

NCBI Description HYPOTHETICAL WD-REPEAT PROTEIN SLR0143

>gi 1653631 dbj BAA18543 (D90915) beta transducin-like

protein [Synechocystis sp.]

Seq. No. 135106

Contig ID 117297 1.R1010

5'-most EST g634772
Method BLASTX
NCBI GI g2570515
BLAST score 250
E value 3.0e-21
Match length 120
% identity 47

NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

Seq. No. 135107

Contig ID 117311_1.R1010 5'-most EST jC-atXP17C110P5T7s3

Seq. No. 135108

Contig ID 117318_2.R1010 5'-most EST jC-atXP17C113F6T7s3

Method BLASTN
NCBI GI g2656026
BLAST score 244
E value 1.0e-135
Match length 462
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDF20

Seq. No. 135109

Contig ID 117328_1.R1010

5'-most EST g2048270
Method BLASTN
NCBI GI g2828186
BLAST score 288
E value 1.0e-161
Match length 440
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18I23, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                   117341 1.R1010
Contig ID
                   jC-atXP18C108N14T7d2
5'-most EST
                   BLASTX
Method
                   q2130473
NCBI GI
BLAST score
                   153
E value
                   5.0e-10
Match length
                   78
                   44
% identity
                  RAD8 protein - fission yeast (Schizosaccharomyces pombe)
NCBI Description
                   (fragment) >gi_1008986_emb_CAA91094_ (Z54308) DNA helicase
                   [Schizosaccharomyces pombe]
                   135111
Seq. No.
                   117342 1.R1010
Contig ID
                   a20482\overline{0}1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3420051
BLAST score
                   126
                   2.0e-41
E value
                   92
Match length
                   90
% identity
NCBI Description
                  (AC004680) unknown protein [Arabidopsis thaliana]
                   135112
Seq. No.
                   117342 2.R1010
Contig ID
5'-most EST
                   jC-atXP18C108N16T7d2
Method
                   BLASTX
NCBI GI
                   g3420051
BLAST score
                   367
                   2.0e-38
E value
Match length
                   113
% identity
                   76
                  (AC004680) unknown protein [Arabidopsis thaliana]
NCBI Description
                   135113
Seq. No.
                   117345 1.R1010
Contig ID
5'-most EST
                   jC-atXP18C108N4T7d2
Seq. No.
                   135114
                   117347 1.R1010
Contig ID
                   jC-atXP18C108P20T7d2
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2696018
BLAST score
                   243
                   1.0e-134
E value
                   459
Match length
% identity
                   98
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXC9, complete sequence [Arabidopsis thaliana]
```

135115

Seq. No.

Contig ID 117353 1.R1010

5'-most EST jC-atXP18C111B23T7d2

BLASTX Method NCBI GI g2660668 223 BLAST score



```
E value
                    2.0e-32
Match length
% identity
                    85
NCBI Description
                    (AC002342) unknown protein [Arabidopsis thaliana]
                   135116
Seq. No.
Contig ID
                   117359_1.R1010
5'-most EST
                   q23932\overline{9}7
```

Seq. No. 135117 Contig ID 117359_2.R1010

5'-most EST g634809

Seq. No. 135118

Contig ID 117363 1.R1010 $jC-atX\overline{P}18C111E17T7d2$ 5'-most EST

Method BLASTX NCBI GI g3915866 BLAST score 762 5.0e-81 E value

Match length 190 % identity 75

NCBI Description GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)

>gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine

synthetase [Lupinus luteus]

Seq. No. 135119

117366 1.R1010 Contig ID jC-atXP18C111F3T7d2 5'-most EST

BLASTX Method g3228664 NCBI GI BLAST score 221 E value 2.0e-27 Match length 113 % identity 58

(AF069986) nitrilase and fragile histidine triad fusion NCBI Description

protein NitFhit [Caenorhabditis elegans]

Seq. No. 135120

Contig ID 117369 1.R1010

5'-most EST q2757778 Method BLASTN g2760165 NCBI GI BLAST score 39 1.0e-12 E value Match length 123 % identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAC9, complete sequence [Arabidopsis thaliana]

135121 Seq. No.

117371 1.R1010 Contia ID

5'-most EST jC-atXP40C162L8T7046a1

Method BLASTN NCBI GI g4371278 BLAST score 230 E value 1.0e-126



Match length 607 % identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135122

Contig ID 117371 2.R1010

5'-most EST g2749233

Method BLASTN

NCBI GI g4371278

BLAST score 189

E value 1.0e-102

Match length 352

% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135123

Contig ID 117374 1.R1010

5'-most EST g635077

Seq. No. 135124

Contig ID 117383_1.R1010

5'-most EST jC-atXP18C113N14T7d2

Method BLASTX
NCBI GI g3746060
BLAST score 298
E value 5.0e-27
Match length 67
% identity 78

NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 135125

Contig ID 117390 1.R1010

5'-most EST g2597071
Method BLASTX
NCBI GI g1806140
BLAST score 503
E value 1.0e-58
Match length 132
% identity 82

NCBI Description (X97314) cdc2MsC [Medicago sativa]

Seq. No. 135126

Contig ID 117393_1.R1010

5'-most EST jC-atXP18C113P14T7d2

Method BLASTN
NCBI GI g2583106
BLAST score 475
E value 0.0e+00
Match length 495
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F4L23 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135127

Contig ID 117403_1.R1010

BLAST score

E value Match length 524 3.0e-53

104



```
5'-most EST
                  jC-atXP18C115B8T7d2
                  135128
Seq. No.
                  117409 1.R1010
Contig ID
                  jC-atXP19C111014T7d2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3033374
                  1074
BLAST score
                  1.0e-118
E value
                  213
Match length
% identity
                  100
                  (AC004238) unknown protein [Arabidopsis thaliana]
NCBI Description
                  135129
Seq. No.
                  117424 1.R1010
Contig ID
                  jC-atXP19C113C5T7096a1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4455262
                  197
BLAST score
                  1.0e-106
E value
Match length
                  365
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
                  (ESSAII project)
Seq. No.
                  135130
Contig ID
                  117424 2.R1010
                  jC-atXP19C111H14T7d2
5'-most EST
Method
                  BLASTN
                  q4455262
NCBI GI
BLAST score
                  172
                  1.0e-91
E value
Match length
                  513
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
                   (ESSAII project)
Seq. No.
                  135131
Contig ID
                  117448 1.R1010
5'-most EST
                  jC-atXP19C111N8T7d2
Method
                  BLASTX
NCBI GI
                  g2245137
BLAST score
                  239
E value
                  2.0e-94
Match length
                  202
% identity
                  91
NCBI Description
                  (Z97344) MYB transcription factor homolog [Arabidopsis
                  thaliana]
                  135132
Seq. No.
                  117457 1.R1010
Contig ID
                  q931295
5'-most EST
                  BLASTX
Method
NCBI GI
                  g132714
```



```
% identity
                  CHLOROPLAST 50S RIBOSOMAL PROTEIN L16 (RIBOSOMAL PROTEIN
NCBI Description
                  CS-L24) >gi_71248_pir__R5SP16 ribosomal protein L16 -
                  spinach chloroplast >gi 12311 emb CAA31716 (X13336)
                  ribosomal protein L16 [Spinacia oleracea]
Seq. No.
                  135133
Contig ID
                  117462 1.R1010
5'-most EST
                  q576983
                  BLASTX
Method
NCBI GI
                  q2245048
BLAST score
                  245
E value
                  1.0e-20
                  67
Match length
                  78
% identity
NCBI Description
                  (Z97342) resistance gene homolog [Arabidopsis thaliana]
Seq. No.
                  135134
                  117470 1.R1010
Contig ID
                  g2393490
5'-most EST
                  135135
Seq. No.
Contig ID
                  117473_1.R1010
5'-most EST
                  q931315
Method
                  BLASTN
                  q4733953
NCBI GI
                  287
BLAST score
                  1.0e-160
E value
Match length
                  392
                  99
% identity
                  Arabidopsis thaliana chromosome I BAC F13011 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  135136
                  117474 1.R1010
Contig ID
                  jC-atXP1C63C2T7s2
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4733953
BLAST score
                  259
                  1.0e-144
E value
Match length
                  419
                  93
% identity
                  Arabidopsis thaliana chromosome I BAC F13011 genomic
NCBI Description
                  sequence, complete sequence
                  135137
Seq. No.
                  117478 1.R1010
Contig ID
```

5'-most EST g2393493 BLASTN Method

q4589412 NCBI GI 143 BLAST score 2.0e-74E value 285 Match length 97 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description F6N7, complete sequence



```
Seq. No.
                  117488 1.R1010
Contig ID
5'-most EST
                  q931326
                  135139
Seq. No.
Contig ID
                  117498 1.R1010
5'-most EST
                  q931334
                  BLASTX
Method
NCBI GI
                  q1931641
BLAST score
                   147
E value
                   3.0e-09
Match length
                   98
% identity
                   72
NCBI Description
                  (U95973) unknown protein [Arabidopsis thaliana]
                   135140
Seq. No.
                   117499 1.R1010
Contig ID
5'-most EST
                   g2393496
Seq. No.
                   135141
                   117502 1.R1010
Contig ID
5'-most EST
                   jC-atXP1C64C8T7d1
Method
                   BLASTN
NCBI GI
                   q3241916
BLAST score
                   347
E value
                   0.0e + 00
Match length
                   502
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K15N18, complete sequence [Arabidopsis thaliana]
Seq. No.
                   135142
Contig ID
                   117516 1.R1010
5'-most EST
                   jC-atXP1C65F10T7d1
Seq. No.
                   135143
                   117517 1.R1010
Contig ID
5'-most EST
                   jC-atXP1C64F1T7s2
                   135144
Seq. No.
                   117518 1.R1010
Contig ID
                   jC-atXP1C64F9T7d1
5'-most EST
                   BLASTX
Method
                   g3056583
NCBI GI
BLAST score
                   161
                   3.0e-12
E value
                   86
Match length
% identity
                   51
                  (AC004255) T1F9.4 [Arabidopsis thaliana]
NCBI Description
                   135145
Seq. No.
```

117533 1.R1010 Contig ID

5'-most EST g2722976

135146 Seq. No.

Contig ID 117538 1.R1010 5'-most EST jC-atXP1C66E6T7d1



```
Method
NCBI GI
                  q2833499
BLAST score
                  63
E value
                  2.0e-15
Match length
                  109
                  45
% identity
                  HYPOTHETICAL PROTEIN MJ0326 >gi 2128002 pir F64340
NCBI Description
                  hypothetical protein homolog MJ0326 - Methanococcus
                  jannaschii >gi_1591045 (U67487) conserved hypothetical
                  protein [Methanococcus jannaschii]
Seq. No.
                  135147
Contig ID
                  117543 1.R1010
5'-most EST
                  jC-atXP1C66F2T7s2
                  BLASTN
Method
NCBI GI
                  q4531433
```

BLAST score 294 E value 1.0e-164 Match length 492 92 % identity

Arabidopsis thaliana chromosome II P1 MFL8 genomic NCBI Description

sequence, complete sequence

117552 1.R1010 Contig ID jC-atXP1C67A8T7d1 5'-most EST Method BLASTX NCBI GI a2842484 BLAST score 358 E value 2.0e-37

Match length 135 % identity 51

Seq. No.

NCBI Description (AL021749) tyrosine transaminase-like protein [Arabidopsis

135148

135149 Seq. No.

117559 1.R1010 Contig ID 5'-most EST jC-atXP1C67F2T7d1

Method BLASTN g3075383 NCBI GI BLAST score 392 0.0e+00E value Match length 456 % identity 98

Arabidopsis thaliana chromosome II BAC T1D16 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135150

117572 1.R1010 Contig ID

5'-most EST q906622 Method BLASTX NCBI GI g585165 BLAST score 722 1.0e-76 E value Match length 163 % identity 85

NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM



(G6PD) >gi_2129985_pir__S60287 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - potato >gi_471345_emb_CAA52442_ (X74421) glucose-6-phosphate 1-dehydrogenase [Solanum tuberosum]

Seq. No. 135151

Contig ID 117572_2.R1010 5'-most EST jC-atXP1C70E9T7s2

Method BLASTX
NCBI GI g3023815
BLAST score 170
E value 3.0e-12
Match length 35
% identity 83

NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM

(G6PD) >gi 1362053_pir__S57785 glucose-6-phosphate

1-dehydrogenase (EC 1.1.1.49) - alfalfa >gi_603219 (U18238) glucose-6-phosphate dehydrogenase [Medicago sativa subsp.

sativa]

Seq. No. 135152

Contig ID 117580_1.R1010 5'-most EST jC-atXP1C70G8T7d1

Seq. No. 135153

Contig ID 117581_1.R1010 5'-most EST jC-atXP1C70G8T7s2

Seq. No. 135154

Contig ID 117594_1.R1010

 5'-most EST
 g949384

 Method
 BLASTX

 NCBI GI
 g3426037

 BLAST score
 360

 E value
 4.0e-34

 Match length
 143

 % identity
 43

NCBI Description (AC005168) putative ABC transporter protein [Arabidopsis

thaliana]

Seq. No. 135155

Contig ID 117595_1.R1010

5'-most EST g2748322
Method BLASTN
NCBI GI g3426033
BLAST score 464
E value 0.0e+00
Match length 500
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F12C20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135156

Contig ID 117595 2.R1010

 5'-most EST
 g2749544

 Method
 BLASTX

 NCBI GI
 g3426037



BLAST score 592 E value 6.0e-71 Match length 134 % identity 62

NCBI Description (AC005168) putative ABC transporter protein [Arabidopsis

thaliana]

Seq. No. 135157

Contig ID 117600_1.R1010

5'-most EST g2733553

Seq. No. 135158

Contig ID 117601_1.R1010

5'-most EST g2393515

Seq. No. 135159

Contig ID 117610_1.R1010 5'-most EST jC-atXP1C72D2T7d1

Method BLASTX
NCBI GI g3128201
BLAST score 471
E value 3.0e-47
Match length 115
% identity 76

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 135160

Contig ID 117621_1.R1010

5'-most EST g2733572

Method BLASTN

NCBI GI g4159703

BLAST score 74

E value 3.0e-33

Match length 378

% identity 45

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K5F14, complete sequence

Seq. No. 135161

Contig ID 117628 1.R1010

5'-most EST jC-atXP20C113D19T7d2

Method BLASTX
NCBI GI g3176675
BLAST score 566
E value 4.0e-58
Match length 175
% identity 65

NCBI Description (AC003671) F1707.4 [Arabidopsis thaliana]

Seq. No. 135162

Contig ID 117630_1.R1010

5'-most EST jC-atXP34C150N13T7d1

Method BLASTN
NCBI GI g3449330
BLAST score 880
E value 0.0e+00
Match length 1307



Seq. No. 135163

Contig ID 117632 1.R1010

5'-most EST jC-atXP20C113G16T7d2

Method BLASTN
NCBI GI g2749918
BLAST score 178
E value 2.0e-95
Match length 375
% identity 99

NCBI Description Arabidopsis thaliana chromosome I BAC F316 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135164

Contig ID 117635 1.R1010

Method BLASTN
NCBI GI g2462264
BLAST score 43
E value 1.0e-14
Match length 51
% identity 96

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 135165

Contig ID 117635_2.R1010

5'-most EST g2048264

Seq. No. 135166

Contig ID 117642_1.R1010

5'-most EST jC-at \overline{P} 20C114A24T7004a1

Method BLASTN
NCBI GI g3063690
BLAST score 285
E value 1.0e-159
Match length 611
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11

(ESSAII project)

Seq. No. 135167

Contig ID 117646_1.R1010

5'-most EST g2757829

Seq. No. 135168

Contig ID 117658 1.R1010

5'-most EST g2597580

Seq. No. 135169

Contig ID 117665 1.R1010

5'-most EST g2581686 Method BLASTN NCBI GI g3985949

BLAST score 495



```
0.0e + 00
E value
                   889
Match length
% identity
                   98
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MOB24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   135170
                   117674 1.R1010
Contig ID
5'-most EST
                   jC-atXP20C115H3T7d2
Method
                   BLASTX
NCBI GI
                   q4006872
BLAST score
                   149
                   2.0e-09
E value
Match length
                   84
                   50
% identity
                   (Z99707) methionyl aminopeptidase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   135171
Seq. No.
                   117675 1.R1010
Contig ID
5'-most EST
                   g2597671
Method
                  BLASTX
NCBI GI
                   q4204315
BLAST score
                   237
E value
                   1.0e-52
Match length
                   174
                   62
% identity
NCBI Description
                  (AC003027) Unknown protein [Arabidopsis thaliana]
                   135172
Seq. No.
                   117676 1.R1010
Contig ID
5'-most EST
                   g2597672
Method
                   BLASTN
                   g4757678
NCBI GI
BLAST score
                   291
                   1.0e-163
E value
                   345
Match length
                   98
% identity
                  Arabidopsis thaliana chromosome I BAC F9H16 genomic
NCBI Description
                   sequence, complete sequence
                   135173
Seq. No.
                   117679 1.R1010
Contig ID
5'-most EST
                   jC-atXP20C116A10T7d2
Method
                   BLASTN
NCBI GI
                   g4467131
```

BLAST score 338 0.0e + 00E value Match length 387

97

Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 NCBI Description

(ESSA project)

Seq. No. 135174

% identity

117683_1.R1010 Contig ID

5'-most EST g2759073 Seq. No.

```
Seq. No.
                   117686 1.R1010
Contig ID
5'-most EST
                   g2757923
                   135176
Seq. No.
Contig ID
                   117687 1.R1010
5'-most EST
                   g2576763
                   135177
Seq. No.
Contig ID
                   117693 1.R1010
5'-most EST
                   q2048306
Method
                   BLASTX
NCBI GI
                   q4507703
BLAST score
                   146
                   5.0e-09
E value
                   62
Match length
% identity
                   45
NCBI Description
```

NCBI Description tumor suppressing subtransferable candidate 1
>gi_2655037_gb_AAC51911_ (AF019952) tumor suppressing STF
cDNA 1 [Homo sapiens]

Contig ID 117694_1.R1010
5'-most EST jC-atXP21C114I24T7d2
Method BLASTN
NCBI GI g3249094
BLAST score 294
E value 1.0e-164
Match length 468
% identity 94

135178

NCBI Description Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135179 117695 1.R1010 Contig ID 5'-most EST q2048307 Method BLASTN NCBI GI q3249094 BLAST score 351 E value 0.0e + 00Match length 402 98 % identity

NCBI Description Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, complete sequence [Arabidopsis thaliana]

 Seq. No.
 135180

 Contig ID
 117697_1.R1010

 5'-most EST
 jC-atXP21C114I3T7d2

 Method
 BLASTX

 NCBI GI
 g2459410

NCBI GI g2459410
BLAST score 358
E value 8.0e-34
Match length 115
% identity 50

NCBI Description (AC002332) putative thioredoxin [Arabidopsis thaliana]

Seq. No. 135181

```
117715 1.R1010
Contig ID
                   jC-atXP21C114K11T7d2
5'-most EST
Method
                   BLASTN
                   g4220631
NCBI GI
BLAST score
                   349
E value
                   0.0e + 00
Match length
                   384
                   99
% identity
```

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K5J14, complete sequence [Arabidopsis thaliana]

Seq. No. 135182 117716 1.R1010 Contig ID q3449413 5'-most EST BLASTN Method g4220631 NCBI GI BLAST score 237 E value 1.0e-130 385 Match length

98

% identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K5J14, complete sequence [Arabidopsis thaliana]

Seq. No. 135183 117724 1.R1010 Contig ID g3450311 5'-most EST BLASTN Method q4415905 NCBI GI BLAST score 42 2.0e-14 E value 179 Match length 86 % identity

Arabidopsis thaliana chromosome II BAC F13K3 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135184 117726 1.R1010 Contig ID 5'-most EST g3450323 Method BLASTX NCBI GI q4467147 59 BLAST score 1.0e-08 E value Match length 43

81

(AL035540) putative protein [Arabidopsis thaliana] NCBI Description

135185 Seq. No. 117736 1.R1010 Contig ID

% identity

5'-most EST q3450327 Method BLASTN q4544381 NCBI GI BLAST score 298 1.0e-167 E value 323 Match length 98 % identity

Arabidopsis thaliana chromosome II BAC F16F14 genomic NCBI Description sequence, complete sequence



```
Seq. No.
                  135186
                  117739 1.R1010
Contig ID
                  jC-atXP21C115L21T7d2
5'-most EST
                  BLASTX
Method
                  q3377800
NCBI GI
BLAST score
                  47
                  1.0e-34
E value
                  109
Match length
                  73
% identity
                  (AF075597) similar to glycosyl hydrolases family 9
NCBI Description
                  (PFam:glycosyl hydro5.hmm, score: 100.70) [Arabidopsis
                  thaliana]
                  135187
Seq. No.
Contig ID
                  117744 1.R1010
                  q2757955
5'-most EST
Method
                  BLASTN
                  g4415928
NCBI GI
                  202
BLAST score
                  1.0e-110
E value
Match length
                  266
% identity
                  Arabidopsis thaliana chromosome II BAC F13A10 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  135188
Seq. No.
                  117791 1.R1010
Contig ID
                  g2597643
5'-most EST
                  BLASTX
Method
                   q4758340
NCBI GI
                   330
BLAST score
                   2.0e-36
E value
Match length
                   143
% identity
                  phenylalanine-tRNA synthetase-like >gi_2102679 (U07424)
NCBI Description
                   putative tRNA synthetase-like protein [Homo sapiens]
                   >gi_4104935_gb_AAD02221_ (AF042347) putative
                   phenylalanyl-tRNA synthetase alpha-subunit; PheHA [Homo
                   sapiens]
                   135189
Seq. No.
                   117793 1.R1010
Contig ID
5'-most EST
                   jC-atXP21C116H15T7d2
Method
                   BLASTX
                   g4741188
NCBI GI
BLAST score
                   157
E value
                   2.0e-10
Match length
                   43
                   67
% identity
                  (AL049746) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. * 135190

Contig ID 117795_1.R1010

5'-most EST g933370

Seq. No. 135191

NCBI GI BLAST score



```
117796 1.R1010
Contig ID
                   jC-atX\overline{P}22C114M6T7018a1
5'-most EST
                   BLASTX
Method
                   g1653333
NCBI GI
                   294
BLAST score
E value
                   4.0e-26
                   92
Match length
% identity
                   60
                   (D90912) ferredoxin [Synechocystis sp.]
NCBI Description
                   135192
Seq. No.
                   117796 2.R1010
Contig ID
5'-most EST
                   g933372
Seq. No.
                   135193
                   117801 1.R1010
Contig ID
5'-most EST
                   g25974\overline{9}2
Method
                   BLASTX
NCBI GI
                   q3540219
BLAST score
                   155
                   4.0e-10
E value
                   104
Match length
% identity
                   37
                   (D87686) KIAA0017 protein [Homo sapiens]
NCBI Description
                   135194
Seq. No.
                   117804 1.R1010
Contig ID
                   q2597497
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3335349
BLAST score
                   466
E value
                   1.0e-46
Match length
                   166
% identity
                   71
                   (ACO04512) Similar to gb U46691 putative chromatin
NCBI Description
                   structure regulator (SUPT6H) from Homo sapiens. ESTs
                   gb T42908, gb AA586170 and gb AA395125 come from this gene.
                   [Arabidopsis thaliana]
                   135195
Seq. No.
                   117808 1.R1010
Contig ID
                   g2597507
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2244950
BLAST score
                   151
                   3.0e-79
E value
Match length
                   483
% identity
                   95
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   135196
Seq. No.
                   117811 1.R1010
Contig ID
                   g25977\overline{2}3
5'-most EST
                   BLASTN
Method
```

16055

g3510336



E value 2.0e-98
Match length 436
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18J17, complete sequence [Arabidopsis thaliana]

Seq. No. 135197

Contig ID 117814 1.R1010

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135198

Contig ID 117821 1.R1010

5'-most EST g2597738
Method BLASTX
NCBI GI g2443887
BLAST score 128
E value 2.0e-09
Match length 102
% identity 45

NCBI Description (AC002294) Similar to transcription factor

gb Z46606 1658307 and others [Arabidopsis thaliana]

Seq. No. 135199

Contig ID 117828 1.R1010

5'-most EST g2758054
Method BLASTN
NCBI GI g4756963
BLAST score 122
E value 4.0e-62
Match length 296
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23

(ESSA project)

Seq. No. 135200

Contig ID 117831_1.R1010

5'-most EST $g27590\overline{9}0$

Seq. No. 135201

Contig ID 117832_1.R1010

5'-most EST jC-atXP22C119C5T7046a1

Seq. No. 135202

Contig ID 117836_1.R1010

5'-most EST jC-atXP22C119D12T7d2

Seq. No. 135203

Contig ID 117837_1.R1010

5'-most EST g933507 Method BLASTN



NCBI GI g2244950 BLAST score 269 E value 1.0e-149 Match length 403 % identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 135204

Contig ID 117838 1.R1010

5'-most EST g2597779
Method BLASTN
NCBI GI g4165340
BLAST score 292
E value 1.0e-163
Match length 353
% identity 96

NCBI Description Arabidopsis thaliana chromosome I BAC F11M15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135205

Contig ID 117840 1.R1010

5'-most EST g2597554

Seq. No. 135206

Contig ID 117853 1.R1010

5'-most EST jC-atXP22C122E6T7016a1

Method BLASTX
NCBI GI g629669
BLAST score 142
E value 6.0e-17
Match length 102

% identity 45

NCBI Description hypothetical protein - tomato

Seq. No. 135207

Contig ID 117856 1.R1010

5'-most EST jC-atXP22C114P21T7083a1

Method BLASTN
NCBI GI g4388714
BLAST score 381
E value 0.0e+00
Match length 541
% identity 89

NCBI Description Arabidopsis thaliana chromosome II BAC F5K7 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135208

Contig ID 117863 1.R1010

5'-most EST jC-atXP23C120K21T7d2

Method BLASTN
NCBI GI g4753195
BLAST score 380
E value 0.0e+00
Match length 452
% identity 96

NCBI Description Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5



cM, complete sequence

```
135209
Seq. No.
                  117865 1.R1010
Contig ID
                  jC-atXP23C121N4T7s2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2661422
BLAST score
                  432
E value
                  1.0e-42
Match length
                  93
% identity
                  91
NCBI Description
                  (AJ001342) Putative S-phase-specific ribosomal protein
                   [Arabidopsis thaliana] >gi 3096936 emb CAA18846.1
                   (AL023094) Putative S-phase-specific ribosomal protein
                   [Arabidopsis thaliana]
                  135210
Seq. No.
Contig ID
                  117869 1.R1010
5'-most EST
                  g2758765
                  BLASTX
Method
                  g2961373
NCBI GI
BLAST score
                  331
E value
                  8.0e-31
Match length
                  103
% identity
                   (AL022141) putative disease resistance protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   135211
Contig ID
                   117877 1.R1010
5'-most EST
                   g2048555
Method
                  BLASTX
NCBI GI
                   g3269297
BLAST score
                   171
E value
                   3.0e-12
Match length
                   58
% identity
                   57
                   (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   135212
Seq. No.
                   117878 1.R1010
Contig ID
                   g2048508
5'-most EST
                   BLASTN
Method
                   g3869069
NCBI GI
BLAST score
                   288
                   1.0e-161
E value
Match length
                   403
% identity
                   94
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MEB5, complete sequence [Arabidopsis thaliana]
                   135213
Seq. No.
                   117884 1.R1010
Contig ID
5'-most EST
                   g2758771
```

135214 Seq. No.

Contig ID 117886 1.R1010



```
5'-most EST
                  q2758773
                  BLASTX
Method
                  g3241944
NCBI GI
                  307
BLAST score
                  5.0e-28
E value
                  111
Match length
                  59
% identity
                   (AC004625) DNA-(apurinic or apyrimidinic site) lyase, ARP
NCBI Description
                   [Arabidopsis thaliana]
                  135215
Seq. No.
                  117890 1.R1010
Contig ID
                  g2758778
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4678322
BLAST score
                   395
                  2.0e-38
E value
                  154
Match length
                   76
% identity
                  (AL049658) putative protein [Arabidopsis thaliana]
NCBI Description
                   135216
Seq. No.
                   117900 1.R1010
Contig ID
                   g2758382
5'-most EST
                  BLASTN
Method
NCBI GI
                   g1871173
BLAST score
                   149
                   5.0e-78
E value
                   456
Match length
                   91
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T06D20 genomic
                   sequence, complete sequence
                   135217
Seq. No.
                   117902 1.R1010
Contig ID
5'-most EST
                   g2758793
                   BLASTX
Method
                   q3193298
NCBI GI
                   792
BLAST score
E value
                   1.0e-84
                   150
Match length
                   100
% identity
NCBI Description (AF069298) T14P8.17 gene product [Arabidopsis thaliana]
Seq. No.
                   135218
                   117905 1.R1010
Contig ID
5'-most EST
                   q2576784
                   BLASTN
Method
NCBI GI
                   q4235150
BLAST score
                   115
E value
                   8.0e-58
Match length
                   446
% identity
                   98
                   Arabidopsis thaliana chromosome I BAC T25B24 genomic
NCBI Description
                   sequence, complete sequence
```

16059

135219

Seq. No.

NCBI Description



```
117908 1.R1010
Contig ID
5'-most EST
                   q27587\overline{9}9
Method
                   BLASTN
                   g4455321
NCBI GI
BLAST score
                   763
                   0.0e+00
E value
Match length
                   903
% identity
                   97
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10
NCBI Description
                   (ESSAII project)
                   135220
Seq. No.
                   117911 1.R1010
Contig ID
5'-most EST
                   g2758472
Method
                   BLASTX
                   g7758
NCBI GI
                   131
BLAST score
                   2.0e-07
E value
                   103
Match length
% identity
                   6
                   (X58374) crn [Drosophila melanogaster]
NCBI Description
                   135221
Seq. No.
                   117913 1.R1010
Contig ID
5'-most EST
                   g558156
                   BLASTX
Method
                   g3377509
NCBI GI
BLAST score
                   685
                   6.0e-72
E value
Match length
                   161
                   83
% identity
                   (AF056027) auxin transport protein REH1 [Oryza sativa]
NCBI Description
                   135222
Seq. No.
                   117915 1.R1010
Contig ID
5'-most EST
                   q572535
Method
                   BLASTN
                   q3785968
NCBI GI
                   278
BLAST score
E value
                   1.0e-155
                   376
Match length
                   97
% identity
                   Arabidopsis thaliana chromosome II BAC F2I9 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   135223
Seq. No.
                   117918 1.R1010
Contig ID
                   q94803\overline{4}
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3021265
BLAST score
                   294
E value
                   6.0e-42
Match length
                   153
% identity
                   66
```

16060

kinase - like protein [Arabidopsis thaliana]

(AL022347) protein kinase - like protein [Arabidopsis

thaliana] >gi_3292839_emb_CAA19829_ (AL031018) protein



```
Seq. No.
                   135224
                   117920 1.R1010
Contig ID
5'-most EST
                   g2758482
                   BLASTX
Method
                   q4585873
NCBI GI
BLAST score
                   377
                   5.0e-50
E value
Match length
                   129
                   87
% identity
                  (AC005850) Putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   135225
Contig ID
                   117923_1.R1010
                   g3449476
5'-most EST
                   BLASTN
Method
                   g3449312
NCBI GI
BLAST score
                   179
                   5.0e-96
E value
Match length
                   318
                   95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K16L22, complete sequence [Arabidopsis thaliana]
                   135226
Seq. No.
                   117929 1.R1010
Contig ID
                   a2048580
5'-most EST
                   BLASTN
Method
NCBI GI
                   q2351068
                   429
BLAST score
                   0.0e + 00
E value
                   512
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MRH10, complete sequence [Arabidopsis thaliana]
Seq. No.
                   135227
                   117936 1.R1010
Contig ID
5'-most EST
                   g2758505
Method
                   BLASTN
                   q4580522
NCBI GI
BLAST score
                   422
                   0.0e + 00
E value
Match length
                   504
% identity
                   96
                   Arabidopsis thaliana scarecrow-like 8 (SCL8) mRNA, partial
NCBI Description
                   cds
                   135228
Seq. No.
                   117938 1.R1010
Contig ID
                   g20485\overline{1}2
5'-most EST
                   BLASTX
Method
                   g3241944
NCBI GI
BLAST score
                   142
                   1.0e-49
E value
```

16061

118

82

Match length % identity

```
(AC004625) DNA-(apurinic or apyrimidinic site) lyase, ARP
NCBI Description
                   [Arabidopsis thaliana]
                   135229
Seq. No.
                   117944 1.R1010
Contig ID
                   jC-atXP23C122F9T7s2
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2245126
BLAST score
                   313
E value
                   1.0e-176
Match length
                   394
                   95
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
                   135230
Seq. No.
Contig ID
                   117945 1.R1010
5'-most EST
                   q27585\overline{2}0
                   135231
Seq. No.
Contig ID
                   117963 1.R1010
                   jC-atX\overline{P}23C122H7T7s2
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2351069
BLAST score
                   513
E value ·
                   0.0e + 00
Match length
                   517
                   100
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSH12, complete sequence [Arabidopsis thaliana]
                   135232
Seq. No.
                   117967 1.R1010
Contig ID
5'-most EST
                   g2758977
                   135233
Seq. No.
Contig ID
                   117978 1.R1010
5'-most EST
                   q2758559
Method
                   BLASTX
NCBI GI
                   q3540181
BLAST score
                   189
E value
                   4.0e-14
Match length
                   158
                   32
% identity
                   (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 135234

Contig ID 117982_1.R1010 5'-most EST g2758982

Seq. No. 135235

Contig ID 117984 1.R1010

 5'-most EST
 g576979

 Method
 BLASTN

 NCBI GI
 g2264310

 BLAST score
 522

 E value
 0.0e+00



Match length 522 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MKP11, complete sequence [Arabidopsis thaliana]

Seq. No. 135236

Contig ID 117985_1.R1010

5'-most EST $g20485\overline{83}$

Seq. No. 135237

Contig ID 117991_1.R1010

NCBI Description (Z97335) transport protein [Arabidopsis thaliana]

Seq. No. 135238

Contig ID 117995_1.R1010 5'-most EST jC-atXP24C122J8T7s1

Method BLASTX
NCBI GI g2739373
BLAST score 148
E value 2.0e-12
Match length 175
% identity 31

NCBI Description (AC002505) putative flavonol 3-o-glucosyltransferase

[Arabidopsis thaliana]

Seq. No. 135239

Contig ID 118002_1.R1010 5'-most EST jC-atXP25C122N16T7d1

Method BLASTX
NCBI GI g4263522
BLAST score 375
E value 9.0e-36
Match length 145
% identity 48

NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135240

Contig ID 118012_1.R1010 5'-most EST jC-atXP25C123O17T7d1 Method BLASTN

Method BLASTN
NCBI GI g3738275
BLAST score 403
E value 0.0e+00
Match length 466
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F17A22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135241

Contig ID 118013_1.R1010

NCBI GI

E value

BLAST score



```
5'-most EST
                  q2759108
Method
                  BLASTN
NCBI GI
                  q2264311
                  469
BLAST score
                  0.0e + 00
E value
                  512
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLN1, complete sequence [Arabidopsis thaliana]
                  135242
Seq. No.
                  118016_1.R1010
Contig ID
5'-most EST
                  g2759536
                  BLASTX
Method
                  q2827715
NCBI GI
                  459
BLAST score
                  2.0e-45
E value
Match length
                  213
% identity
                  48
                   (ALO21684) receptor protein kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                  135243
Seq. No.
Contig ID
                  118032 1.R1010
                  q507088
5'-most EST
Method
                  BLASTX
                  q3912917
NCBI GI
                   561
BLAST score
E value
                   1.0e-57
                   169
Match length
                   73
% identity
                   (AF001308) putative NAK-like ser/thr protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   135244
Seq. No.
Contig ID
                   118038 1.R1010
5'-most EST
                   q2759224
                   BLASTN
Method
                   q2832667
NCBI GI
BLAST score
                   179
E value
                   6.0e-96
Match length
                   378
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14
NCBI Description
                   (ESSAII project)
Seq. No.
                   135245
                   118039 1.R1010
Contig ID
                   jC-atXP25C125E3T7d1
5'-most EST
                   135246
Seq. No.
                   118046 1.R1010
Contig ID
                   jC-atXP69C217G1T7065d1
5'-most EST
                   BLASTX
Method
```

16064

g4039155

2.0e-29



Match length 164 % identity 47

NCBI Description (AF104258) putative copper-inducible 35.6 kDa protein

[Festuca rubra]

Seq. No. 135247

Contig ID 118048_1.R1010

5'-most EST jC-atXP25C125I16T7d1

Method BLASTX
NCBI GI g2760839
BLAST score 390
E value 2.0e-37
Match length 108
% identity 69

NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 135248

Contig ID 118057_1.R1010 5'-most EST jC-atXP32C147H21T7d2

Method BLASTX
NCBI GI g3695379
BLAST score 1265
E value 1.0e-140
Match length 307
% identity 66

NCBI Description (AF096370) contains similarity to a C. elegans hypothetical

protein F44G4.1 (GB:Z49910) and several yeast hypothetical proteins such as 35.1 KD protein in NAM8-GAR1 intergenic

region (SP:P38805) [Arabidopsis thaliana]

Seq. No. 135249

Contig ID 118058_1.R1010 5'-most EST jC-atXP25C125N11T7d1

Seq. No. 135250

Contig ID 118059_1.R1010 5'-most EST jC-atXP25C125N5T7d1

Method BLASTX
NCBI GI g2492813
BLAST score 275
E value 4.0e-24
Match length 145
% identity 39

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE >gi_2313265_gb_AAD07246.1_

(AE000538) fructose-bisphosphate aldolase (tsr)

[Helicobacter pylori 26695]

Seq. No. 135251

Contig ID 118061_1.R1010 5'-most EST jC-atXP25C125O4T7d1

Method BLASTX
NCBI GI g3047116
BLAST score 1082
E value 1.0e-142
Match length 288
% identity 94

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.



```
135252
Seq. No.
                   118072 1.R1010
Contig ID
5'-most EST
                   q2759695
                   135253
Seq. No.
                   118089 1.R1010
Contig ID
                   jC-atX\overline{P}26C128L1T7d1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g3241925
BLAST score
                   364
E value
                   0.0e + 00
Match length
                   412
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MOK9, complete sequence [Arabidopsis thaliana]
                   135254
Seq. No.
                   118105 1.R1010
Contig ID
5'-most EST
                   jC-atXP27C128O19T7d2
                   BLASTX
Method
NCBI GI
                   g4371280
BLAST score
                   367
E value
                   8.0e-35
Match length
                   83
                   87
% identity
                  (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   135255
Seq. No.
                   118121 1.R1010
Contia ID
5'-most EST
                   jC-atXP27C132A15T7s2
                   135256
Seq. No.
Contig ID
                   118123 1.R1010
                   jC-atX\overline{P}27C129023T7d2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3461838
BLAST score
                   408
E value
                   9.0e-40
Match length
                   82
                   96
% identity
                   (AC005315) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   135257
                   118150 1.R1010
Contig ID
5'-most EST
                   jC-atXP27C131E22T7d2
Method
                   BLASTX
                   q2244888
NCBI GI
                   388
BLAST score
                   3.0e-37
E value
Match length
                   166
                   48
% identity
                   (Z97338) similarity to cytochrome P450 [Arabidopsis
NCBI Description
```

16066

thaliana]



```
118159 1.R1010
Contig ID
5'-most EST
                  q2762500
                  BLASTN
Method
                  g3242700
NCBI GI
                  543
BLAST score
                  0.0e+00
E value
Match length
                  685
% identity
                  Arabidopsis thaliana chromosome II BAC F26B6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  135259
Seq. No.
Contig ID
                  118163 1.R1010
                  g2762215
5'-most EST
                  BLASTX
Method
                  g4322940
NCBI GI
BLAST score
                  164
                   4.0e-11
E value
Match length
                  90
                  26
% identity
                  (AF096299) DNA-binding protein 2 [Nicotiana tabacum]
NCBI Description
                  135260
Seq. No.
Contig ID
                  118167 1.R1010
5'-most EST
                  g2762474
Method
                  BLASTN
                   g4159705
NCBI GI
BLAST score
                   113
E value
                   1.0e-56
Match length
                   328
% identity
                   100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGD8, complete sequence
                   135261
Seq. No.
Contig ID
                   118175 1.R1010
5'-most EST
                   jC-atXP27C131M21T7s2
                   135262
Seq. No.
                   118196 1.R1010
Contig ID
5'-most EST
                   jC-atXP27C132E19T7s2
                   135263
Seq. No.
Contig ID
                   118201 1.R1010
5'-most EST
                   g933999
Method
                   BLASTX
NCBI GI
                   g4220477
BLAST score
                   113
                   1.0e-16
E value
Match length
                   72
                   47
% identity
```

(AC006069) unknown protein [Arabidopsis thaliana] NCBI Description

135264 Seq. No.

118254 1.R1010 Contig ID 5'-most EST jC-atXP28C134M20T7d1

BLASTX Method



```
NCBI GI
                   q2809262
BLAST score
                   539
E value
                   3.0e-55
Match length
                   126
                   87
% identity
NCBI Description
                   (AC002560) F21B7.31 [Arabidopsis thaliana]
                   135265
Seq. No.
                   118257 1.R1010
Contig ID
5'-most EST
                   g27632\overline{3}9
Seq. No.
                   135266
Contig ID
                   118258 1.R1010
                   jC-atXP28C135E23T7s1
5'-most EST
                   135267
Seq. No.
                   118261 1.R1010
Contig ID
5'-most EST
                   jC-atXP44C170I9T7005a1
Method
                   BLASTN
                   g4490324
NCBI GI
BLAST score
                   368
                   0.0e + 00
E value
Match length
                   653
% identity
                   95
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14
NCBI Description
                   (ESSA project)
                   135268
Seq. No.
Contig ID
                   118273_1.R1010
                   q2047768
5'-most EST
                   BLASTN
Method
                   g3080430
NCBI GI
BLAST score
                   205
E value
                   1.0e-111
Match length
                   288
% identity
                   98
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19
NCBI Description
                   (ESSAII project)
                   135269
Seq. No.
                   118281 1.R1010
Contig ID
5'-most EST
                   g473349
Seq. No.
                   135270
                   118282_1.R1010
Contig ID
                   g27623\overline{2}8
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4337186
BLAST score
                   128
                   1.0e-65
E value
                   344
Match length
                   97
```

% identity

Arabidopsis thaliana chromosome II BAC T28I24 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

135271 Seq. No.

118284 1.R1010 Contig ID

Method

NCBI GI BLAST score

E value



```
5'-most EST
                   q2762684
Method
                  BLASTN
                  a3367500
NCBI GI
                  97
BLAST score
                   4.0e-47
E value
                  297
Match length
                  83
% identity
                  REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1
NCBI Description
                  TO: 93489, complete sequence [Arabidopsis thaliana]
                  135272
Seq. No.
Contig ID
                  118312 1.R1010
5'-most EST
                   g2062776
Method
                  BLASTN
                   q4056429
NCBI GI
                   529
BLAST score
                   0.0e + 00
E value
Match length
                   577
                   99
% identity
                  Arabidopsis thaliana chromosome 1 BAC F508 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                   135273
Seq. No.
Contig ID
                   118314_1.R1010
                   g2062799
5'-most EST
Method
                   BLASTX
                   g2262165
NCBI GI
BLAST score
                   84
                   3.0e-31
E value
Match length
                   81
% identity
                   93
                   (AC002329) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   135274
Seq. No.
                   118315 1.R1010
Contig ID
5'-most EST
                   g2445895
Method
                   BLASTN
NCBI GI
                   q3128166
BLAST score
                   346
E value
                   0.0e + 00
Match length
                   358
                   99
% identity
                   Arabidopsis thaliana chromosome II BAC F4I1 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   135275
Contig ID
                   118324 1.R1010
                   jC-atXP2C74B2T7d1
5'-most EST
Seq. No.
                   135276
                   118325 1.R1010
Contig ID
                   g2756992
5'-most EST
```

16069

BLASTX

145 6.0e-09

g3894385



Match length 113 % identity 4

NCBI Description (AF053994) Hcr2-OA [Lycopersicon esculentum]

Seq. No. 135277

Contig ID 118330_1.R1010 5'-most EST jC-atXP2C75F5T7d1

Seq. No. 135278

Contig ID 118331_1.R1010 5'-most EST jC-atXP2C75H9T7d1

Method BLASTX
NCBI GI 94581143
BLAST score 243
E value 2.0e-20
Match length 154
% identity 35

NCBI Description (AC006919) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135279

Contig ID 118334_1.R1010

5'-most EST g933548

Seq. No. 135280

Contig ID 118343_1.R1010 5'-most EST jC-atXP2C78C9T7d1

Method BLASTN
NCBI GI 94753195
BLAST score 49
E value 2.0e-18
Match length 96
% identity 95

NCBI Description Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5

cM, complete sequence

Seq. No. 135281

Contig ID 118347 1.R1010

5'-most EST g2047524

Method BLASTN

NCBI GI g2351070

BLAST score 78

E value 1.0e-35

Match length 147 % identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTH12, complete sequence [Arabidopsis thaliana]

Seq. No. 135282

Contig ID 118353 1.R1010

5'-most EST g501852
Method BLASTX
NCBI GI g4185141
BLAST score 552
E value 7.0e-57
Match length 127
% identity 87

NCBI Description (AC005724) putative calmodulin-binding protein [Arabidopsis



thaliana]

135283 Seq. No. 118354 1.R1010 Contig ID 5'-most EST jC-atXP2C79A3T7d1

Seq. No. 135284

118357 1.R1010 Contig ID $jC-atX\overline{P}30C140L5T7d2$ 5'-most EST

BLASTX Method g4666287 NCBI GI BLAST score 333 E value 4.0e-31 105 Match length 59 % identity

(D85764) cytosolic monodehydroascorbate reductase [Oryza NCBI Description

sativa]

Seq. No. 135285

118372 1.R1010 Contig ID $jC-atX\overline{P}30C141I15T7d2$ 5'-most EST

135286 Seq. No.

Contig ID 118374 1.R1010 5'-most EST jC-atXP30C141N11T7d2

135287 Seq. No. 118378 1.R1010 Contig ID

5'-most EST q2062849

135288 Seq. No.

118378 2.R1010 Contig ID

 $jC-atX\overline{P}30C142C14T7d2$ 5'-most EST

Method BLASTX q2392763 NCBI GI BLAST score 214 E value 4.0e-17 Match length 108 45 % identity

(AC002534) hypothetical protein [Arabidopsis thaliana] NCBI Description

135289 Seq. No.

118394 1.R1010 Contig ID

5'-most EST $g34497\overline{1}1$ Method BLASTX g4455295 NCBI GI BLAST score 256 E value 6.0e-22 Match length 118 % identity 47

(AL035528) isoflavone reductase-like protein [Arabidopsis NCBI Description

thaliana]

135290 Seq. No.

118394 2.R1010 Contig ID jC-atXP30C143N21T7d2 5'-most EST

BLASTX Method



73

64

Match length

% identity

```
q4455295
NCBI GI
BLAST score
                   337
                   6.0e-88
E value
                  197
Match length
% identity
                  (AL035528) isoflavone reductase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  135291
Seq. No.
                  118396 1.R1010
Contig ID
5'-most EST
                   jC-atXP30C142H16T7d2
                  BLASTN
Method
                  g4757401
NCBI GI
BLAST score
                   610
                   0.0e + 00
E value
Match length
                   657
                   100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGH6, complete sequence
                   135292
Seq. No.
                   118408 1.R1010
Contig ID
5'-most EST
                   jC-atX\overline{P}30C142K24T7d2
Seq. No.
                   135293
                   118414 1.R1010
Contig ID
5'-most EST
                   g3449702
                   135294
Seq. No.
                   118418 1.R1010
Contig ID
5'-most EST
                   q934789
                   BLASTX
Method
                   g1531758
NCBI GI
BLAST score
                   410
                   4.0e-40
E value
Match length
                   95
                   80
% identity
                   (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028)
NCBI Description
                   unknown protein [Arabidopsis thaliana]
                   135295
Seq. No.
                   118422 2.R1010
Contig ID
5'-most EST
                   g2393547
Seq. No.
                   135296
                   118423 1.R1010
Contig ID
5'-most EST
                   g2393319
Seq. No.
                   135297
Contig ID
                   118428 1.R1010
5'-most EST
                   q2763089
Method
                   BLASTX
                   q2465923
NCBI GI
                   228
BLAST score
E value
                   8.0e-19
```

```
(AF024648) receptor-like serine/threonine kinase
NCBI Description
                    [Arabidopsis thaliana]
                   135298
Seq. No.
                   118444 1.R1010
Contig ID
                   jC-atX\overline{P}30C143N4T7s2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2098575
BLAST score
                   312
                   1.0e-28
E value
                   91
Match length
                   64
% identity
\hbox{NCBI Description} \quad \hbox{(AC002115)} \quad \hbox{F25451\_2} \quad \hbox{[Homo sapiens]}
                   135299
Seq. No.
                   118445 1.R1010
Contig ID
                   jC-atXP30C143N6T7d2
5'-most EST
                   BLASTN
Method
NCBI GI
                   q3176693
                    331
BLAST score
                   0.0e + 00
E value
                   375
Match length
                   97
% identity
                   Arabidopsis thaliana chromosome I BAC T27I1 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   135300
Seq. No.
                   118465_1.R1010
Contig ID
5'-most EST
                   g2062885
                    135301
Seq. No.
                    118469 1.R1010
Contig ID
                    jC-atXP44C170K1T7093a1
5'-most EST
Method
                    BLASTX
                    g3941458
NCBI GI
BLAST score
                    779
E value
                    4.0e-83
                    157
Match length
% identity
                   (AF062883) putative transcription factor [Arabidopsis
NCBI Description
                    thaliana]
                    135302
Seq. No.
                    118482 1.R1010
Contig ID
5'-most EST
                    jC-atXP31C145E2T7d1
                    135303
Seq. No.
```

Contig ID 118493_1.R1010 5'-most EST jC-atXP31C146H5T7d2

Method BLASTX
NCBI GI g2388956
BLAST score 207
E value 4.0e-16
Match length 76
% identity 57

NCBI Description (Z98979) ribulose-phosphate 3-epimerase

[Schizosaccharomyces pombe]



```
135304
Seq. No.
                   118495 1.R1010
Contig ID
                   g2062915
5'-most EST
                   BLASTN
Method
                   g4585896
NCBI GI
BLAST score
                   449
                   0.0e + 00
E value
                   712
Match length
                   98
% identity
                   Arabidopsis thaliana chromosome II BAC F13I13 genomic
NCBI Description
                   sequence, complete sequence
                   135305
Seq. No.
                   118503 1.R1010
Contig ID
                   g2062921
5'-most EST
                   BLASTN
Method
NCBI GI
                   g4713943
BLAST score
                   588
                   0.0e+00
E value
                   636
Match length
                   98
% identity
                   Arabidopsis thaliana chromosome 1 BAC T8K14 sequence,
NCBI Description
                   complete sequence
                   135306
Seq. No.
                   118511 1.R1010
Contig ID
                   g2062937
5'-most EST
Method
                   BLASTN
                   q2582640
NCBI GI
                   36
BLAST score
                   2.0e-10
E value
                   40
Match length
                   97
% identity
                   Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   135307
Seq. No.
                   118513 1.R1010
Contig ID
                   jC-atX\overline{P}32C146P15T7s1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q1072328
BLAST score
                   49
E value
                   2.0e-18
Match length
                   183
                   81
% identity
NCBI Description B.campestris (ACP-SF1) gene for acyl carrier protein
Seq. No.
                   135308
                   118516 1.R1010
Contig ID
                   jC-atXP32C146P6T7s1
5'-most EST
                   BLASTX
Method
                   g3445207
NCBI GI
BLAST score
                   116
E value
                   6.0e-53
```

16074

110

81

Match length

% identity

BLAST score

E value

145 1.0e-30



```
(AC004786) unknown protein [Arabidopsis thaliana]
NCBI Description
                  135309
Seq. No.
                  118517 1.R1010
Contig ID
                  jC-atXP32C147D16T7s1
5'-most EST
                  135310
Seq. No.
                  118519 1.R1010
Contig ID
                  g1109722
5'-most EST
                  BLASTN
Method
                  g1946354
NCBI GI
BLAST score
                  339
E value
                  0.0e+00
Match length
                  354
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T06B20 genomic
NCBI Description
                  sequence, complete sequence
                  135311
Seq. No.
                  118522_1.R1010
Contig ID
5'-most EST
                  g2062934
                  135312
Seq. No.
Contig ID
                  118529_1.R1010
5'-most EST
                  g3449758
                  135313
Seq. No.
                  118532 1.R1010
Contig ID
5'-most EST
                   g2062935
Method
                  BLASTX
                   g3337348
NCBI GI
BLAST score
                   205
                   6.0e-16
E value
Match length
                   62
% identity
                   69
                   (AC004481) unknown protein, 5' partial [Arabidopsis
NCBI Description
                   thaliana]
                   135314
Seq. No.
Contig ID
                   118533 1.R1010
5'-most EST
                   q453715
                   BLASTX
Method
NCBI GI
                   g3367522
BLAST score
                   414
E value
                   2.0e-40
Match length
                   109
% identity
                   (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   135315
                   118548 1.R1010
Contig ID
                   g935320
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2462756
```



```
Match length 119 % identity 62
```

NCBI Description (AC002292) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 135316

Contig ID 118550_1.R1010

5'-most EST g2763551

Seq. No. 135317

Contig ID 118552 1.R1010

5'-most EST jC-atXP33C144023T7s2

Seq. No. 135318

Contig ID 118553_1.R1010

5'-most EST g2062953
Method BLASTN
NCBI GI g4587582
BLAST score 292
E value 1.0e-163
Match length 477
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T16B14 genomic

sequence, complete sequence

Seq. No. 135319

Contig ID 118553_2.R1010

5'-most EST g935270
Method BLASTX
NCBI GI g4587587
BLAST score 423
E value 2.0e-41
Match length 147
% identity 63

NCBI Description (AC007232) unknown protein [Arabidopsis thaliana]

Seq. No. 135320

Contig ID 118568_1.R1010 5'-most EST jC-atXP33C148C14T7d2

Method BLASTN
NCBI GI g3108025
BLAST score 237
E value 1.0e-130
Match length 485
% identity 99

NCBI Description Arabidopsis thaliana chromosome 1 BAC T13D8, complete

sequence [Arabidopsis thaliana]

Seq. No. 135321

Contig ID 118573_1.R1010 5'-most EST jC-atXP33C148C6T7d2

Method BLASTN
NCBI GI g3510336
BLAST score 384
E value 0.0e+00
Match length 470
% identity 33

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

Contig ID 5'-most EST



K18J17, complete sequence [Arabidopsis thaliana]

135322 Seq. No. 118588_1.R1010 Contig ID $g27635\overline{4}9$ 5'-most EST BLASTN Method g3243214 NCBI GI 199 BLAST score 1.0e-108 E value 321 Match length % identity Arabidopsis thaliana BAC T19B17 from chromsome IV, near NCBI Description 19.3 cM, complete sequence [Arabidopsis thaliana] Seq. No. 135323 118594 1.R1010 Contig ID g2062945 5'-most EST BLASTX Method g2500980 NCBI GI BLAST score 223 5.0e-18 E value 79 Match length 52 % identity GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE) (GLURS) NCBI Description >gi 1076718 pir__S51684 glutamate--tRNA ligase (EC 6.1.1.17) precursor - barley >gi_603849_emb_CAA58505_ (X83523) glutamate--tRNA ligase [Hordeum vulgare] 135324 Seq. No. 118594 2.R1010 Contig ID g2580690 5'-most EST Method BLASTX g2500981 NCBI GI BLAST score 418 4.0e-44 E value Match length 140 67 % identity GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE) (GLURS) NCBI Description >gi 1084418_pir S51685 glutamate--tRNA ligase (EC 6.1.1.17) - common tobacco >gi 603867 emb CAA58506 (X83524) glutamate--tRNA ligase [Nicotiana tabacum] 135325 Seq. No. 118610 1.R1010 Contig ID jC-atXP33C148H10T7s2 5'-most EST BLASTN Method q4589410 NCBI GI BLAST score 717 0.0e+00E value 745 Match length % identity 99 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description F2015, complete sequence Seq. No. 135326

16077

118617 1.R1010

g2763625



```
BLASTN
Method
                   g4376087
NCBI GI
                   144
BLAST score
                   3.0e-75
E value
                   344
Match length
                   96
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                   fragment No
                   135327
Seq. No.
                   118621_1.R1010
Contig ID
                   g935268
5'-most EST
                   BLASTN
Method
                   g2244788
NCBI GI
BLAST score
                   114
                   5.0e-57
E value
Match length
                   655
                   97
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   135328
Seq. No.
                   118623 1.R1010
Contig ID
                   jC-atXP33C148I21T7d2
5'-most EST
                   BLASTX
Method
                   g4371280
NCBI GI
BLAST score
                   321
                   1.0e-29
E value
Match length
                   131
                   50
% identity
                   (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   135329
Seq. No.
                   118624 1.R1010
Contig ID
                   jC-atX\overline{P}33C148I21T7s2
5'-most EST
                   135330
Seq. No.
Contig ID
                   118638 1.R1010
                   jC-atX\overline{P}33C148K6T7d2
5'-most EST
Seq. No.
                   135331
                   118649 1.R1010
Contig ID
                   g693032
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4538948
                   268
BLAST score
                   3.0e-23
E value
                   86
Match length
% identity
                   56
                   (AL049483) putative protein [Arabidopsis thaliana]
NCBI Description
                   135332
Seq. No.
                   118660 1.R1010
Contig ID
```

Contig ID 118660_1.R1010 5'-most EST jC-atXP33C149F9T7d2

Method BLASTX NCBI GI g2062171 BLAST score 419

% identity

NCBI Description

47



```
4.0e-41
E value
Match length
                   165
% identity
                   75
                   (ACO01645) DNA binding protein (CDC27SH) isolog
NCBI Description
                   [Arabidopsis thaliana]
                   135333
Seq. No.
                   118662 1.R1010
Contig ID
                   jC-atX\overline{P}33C150A10T7d2
5'-most EST
                   BLASTX
Method
                   g4335773
NCBI GI
                   220
BLAST score
                   1.0e-17
E value
Match length
                   110
% identity
                   49
                  (AC006284) unknown protein [Arabidopsis thaliana]
NCBI Description
                   135334
Seq. No.
                   118664 1.R1010
Contig ID
                   g2763742
5'-most EST
                   135335
Seq. No.
                   118667 1.R1010
Contig ID
5'-most EST
                   g3449789
Method
                   BLASTX
                   g4587525
NCBI GI
                   228
BLAST score
                   1.0e-18
E value
                   94
Match length
% identity
                   51
                   (AC007060) Contains the PF 00650 CRAL/TRIO
NCBI Description
                   phosphatidyl-inositol-transfer protein domain. ESTs
                   gb T76582, gb N06574 and gb_Z25700 come from this gene.
                   [Arabidopsis thaliana]
                   135336
Seq. No.
                   118679 1.R1010
Contig ID
                   q3449797
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1483222
BLAST score
                   170
                   6.0e-12
E value
Match length
                   64
                   70
% identity
                  (X99097) peroxidase [Arabidopsis thaliana]
NCBI Description
                   135337
Seq. No.
                   118680 1.R1010
Contig ID
                   jC-atXP33C151A16T7d2
5'-most EST
Method
                   BLASTX
                   q1706740
NCBI GI
                   263
BLAST score
                   8.0e-23
E value
                   107
Match length
```

16079

FLAVONOL 4'-SULFOTRANSFERASE (F4-ST) >gi 168169 (M84136)

flavonol 4'-sulfotransferase [Flaveria chloraefolia]



135338 Seq. No. 118682 1.R1010 Contig ID jC-atXP33C151A17T7d2 5'-most EST BLASTN Method g4580454 NCBI GI BLAST score 217 E value 1.0e-118 516 Match length 99 % identity Arabidopsis thaliana chromosome II BAC T2G17 genomic NCBI Description sequence, complete sequence Seq. No. 135339 118689 1.R1010 Contig ID jC-atXP33C151B20T7d2 5'-most EST BLASTX Method g481815 NCBI GI BLAST score 328 4.0e-30 E value 240 Match length 35 % identity vegetative storage protein - western balsam poplar x NCBI Description cottonwood >gi_309839 (L20233) vegetative storage protein [Populus trichocarpa x Populus deltoides] 135340 Seq. No. 118694_1.R1010 Contig ID 5'-most EST $jC-atX\overline{P}33C151C9T7s2$ Method BLASTX g2129575 NCBI GI 167 BLAST score 8.0e-26 E value Match length 80 79 % identity DNA repair protein homolog XPBara - Arabidopsis thaliana NCBI Description 135341 Seq. No. 118718 1.R1010 Contig ID jC-atXP34C149K12T7d1 5'-most EST BLASTX Method g4185136 NCBI GI BLAST score 616 2.0e-66 E value Match length 161 % identity (ACO05724) putative trehalose-6-phosphate synthase NCBI Description [Arabidopsis thaliana]

135342 Seq. No.

118723 1.R1010 Contig ID

g935683 5'-most EST

135343 Seq. No.

118724 1.R1010 Contig ID $jC-atX\overline{P}34C149P15T7d1$ 5'-most EST

BLASTX Method



```
q4263791
NCBI GI
BLAST score
                  712
                  3.0e-75
E value
                  156
Match length
% identity
                  (AC006068) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  135344
Seq. No.
                  118726_1.R1010
Contig ID
                  jC-atXP34C150D14T7d1
5'-most EST
                  135345
Seq. No.
Contig ID
                   118727 1.R1010
                   jC-atXP34C150E12T7d1
5'-most EST
                   135346
Seq. No.
                   118729 1.R1010
Contig ID
5'-most EST
                   jC-atXP34C150E20T7d1
                   BLASTN
Method
                   g3702732
NCBI GI
                   233
BLAST score
                   1.0e-128
E value
                   448
Match length
% identity
                   100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MGF10, complete sequence [Arabidopsis thaliana]
                   135347
Seq. No.
                   118732 1.R1010
Contig ID
                   jC-atX\overline{P}34C150G20T7d1
5'-most EST
                   BLASTN
Method
                   g4726109
NCBI GI
BLAST score
                   161
                   3.0e-85
E value
                   385
Match length
                   83
% identity
                   Arabidopsis thaliana chromosome II BAC F13J11 genomic
NCBI Description
                   sequence, complete sequence
                   135348
Seq. No.
                   118735 1.R1010
Contig ID
                   jC-atXP34C150I21T7d1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2245031
                   355
BLAST score
                   0.0e + 00
E value
                   433
Match length
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
```

Seq. No. 135349

Contig ID 118749_1.R1010 5'-most EST g2580787 Method BLASTN NCBI GI g3985931 BLAST score 0.0e + 00E value 402 Match length 88 % identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K21H1, complete sequence [Arabidopsis thaliana] 135350 Seq. No. 118749 2.R1010 Contig ID g935709 5'-most EST BLASTN Method g3985931 NCBI GI 184 BLAST score 5.0e-99 E value Match length 316 99 % identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K21H1, complete sequence [Arabidopsis thaliana] 135351 Seq. No. 118750 1.R1010 Contig ID jC-atXP34C150N9T7d1 5'-most EST BLASTX Method g4335751 NCBI GI 573 BLAST score 4.0e-59 E value 158 Match length % identity 76 (AC006284) putative methyltransferase [Arabidopsis NCBI Description thaliana] 135352 Seq. No. 118755 2.R1010 Contig ID g935414 5'-most EST 135353 Seq. No. 118759 1.R1010 Contig ID $jC-atX\overline{P}34C151H10T7d1$ 5'-most EST BLASTN Method q3241923 NCBI GI

Method BLASTN
NCBI GI g3241923
BLAST score 277
E value 1.0e-154
Match length 301
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MMN10, complete sequence [Arabidopsis thaliana]

Seq. No. 135354

Contig ID 118780_1.R1010

5'-most EST g2047812
Method BLASTN
NCBI GI g1946354
BLAST score 287
E value 1.0e-160
Match length 369
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC T06B20 genomic



sequence, complete sequence

```
135355
Seq. No.
                  118811 1.R1010
Contig ID
                  g935790
5'-most EST
                  BLASTX
Method
                  g2281085
NCBI GI
                   562
BLAST score
                   8.0e-58
E value
                   126
Match length
% identity
                   (AC002333) CTR1 protein kinase isolog [Arabidopsis
NCBI Description
                   thaliana]
                   135356
Seq. No.
                   118812 1.R1010
Contig ID
                   jC-atXP35C153F18T7s2
5'-most EST
                   {\tt BLASTN}
Method
                   q2281081
NCBI GI
                   266
BLAST score
                   1.0e-148
E value
                   313
Match length
% identity
                   96
                   Arabidopsis thaliana chromosome II BAC F18019 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   135357
Seq. No.
                   118813_1.R1010
Contig ID
                   q935791
5'-most EST
                   BLASTX
Method
                   g3858935
NCBI GI
                   249
BLAST score
                   5.0e-24
E value
                   77
Match length
                   75
% identity
                   (AL021636) synaptobrevin-like protein [Arabidopsis
NCBI Description
                   thaliana] >gi_4103357 (AF025332) vesicle-associated
                   membrane protein 7C; synaptobrevin 7C [Arabidopsis
                   thaliana]
                   135358
Seq. No.
                    118818 1.R1010
Contig ID
5'-most EST
                    g935794
Seq. No.
                    135359
                    118820 1.R1010
Contig ID
                    jC-atX\overline{P}37C158B21T7d2
5'-most EST
                    BLASTN
Method
                    g2264311
NCBI GI
                    523
BLAST score
E value
                    0.0e + 00
                    531
Match length
                    100
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                    MLN1, complete sequence [Arabidopsis thaliana]
```

Seq. No. 135360



```
118820 3.R1010
Contig ID
                   jC-atXP35C153G13T7d1
5'-most EST
                   BLASTN
Method
                   a2264311
NCBI GI
                   209
BLAST score
                   1.0e-114
E value
                   490
Match length
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MLN1, complete sequence [Arabidopsis thaliana]
                   135361
Seq. No.
                   118822 1.R1010
Contig ID
                   jC-atX\overline{P}35C153G15T7d1
5'-most EST
                   BLASTN
Method
                   q3004543
NCBI GI
                   290
BLAST score
                   1.0e-162
E value
                   511
Match length
                   100
% identity
                   Arabidopsis thaliana chromosome II BAC F19F24 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   135362
Seq. No.
                   118822 2.R1010
Contig ID
                   jC-atX\overline{P}64C207B6T7d1
5'-most EST
                   BLASTN
Method
                   g3004543
NCBI GI
                   332
BLAST score
                   0.0e + 00
E value
                   340
Match length
                   100
% identity
                   Arabidopsis thaliana chromosome II BAC F19F24 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   135363
Seq. No.
                   118831 1.R1010
Contig ID
                   jC-atXP35C153K12T7d1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q4589421
                   35
BLAST score
E value
                    6.0e-10
                    158
Match length
                   87
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
 NCBI Description
                   K5K13, complete sequence
                    135364
 Seq. No.
                    118833_1.R1010
 Contig ID
                    g935467
```

5'-most EST

135365 Seq. No.

118834 1.R1010 Contig ID

jC-atXP35C153I12T7s2 5'-most EST

135366 Seq. No.

118848 1.R1010 Contig ID

```
q2763762
5'-most EST
                  BLASTN
Method
                  g3335331
NCBI GI
                   41
BLAST score
                   2.0e-13
E value
                   99
Match length
                   97
% identity
                  Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   135367
Seq. No.
                   118852 1.R1010
Contig ID
                   g935474
5'-most EST
Seq. No.
                   135368
                   118854 1.R1010
Contig ID
                   jC-atX\overline{P}35C153M19T7d1
5'-most EST
                   BLASTX
Method
                   q627071
NCBI GI
                   144
BLAST score
                   1.0e-08
E value
                   136
Match length
                   11
% identity
                   histidine-rich protein - Plasmodium lophurae (fragment)
NCBI Description
                   >gi 552196 (M15317) histidine-rich protein [Plasmodium
                   lophurae]
                   135369
Seq. No.
                   118854_3.R1010
Contig ID
5'-most EST
                   q2048322
                   BLASTN
Method
                   g3335331
NCBI GI
                   257
BLAST score
                   1.0e-142
E value
                   284
Match length
                   98
% identity
                   Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   135370
Seq. No.
                   118880 1.R1010
Contig ID
5'-most EST
                   g2047844
Seq. No.
                   135371
                   118884 1.R1010
Contig ID
                   jC-atXP35C154F12T7d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4263820
BLAST score
                   177
                   1.0e-14
E value
Match length
                    92
                    40
% identity
                   (AC006067) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

135372 Seq. No.

118917 1.R1010 Contig ID g2763852 5'-most EST

Method

NCBI GI

BLASTN g2828185



```
135373
Seq. No.
                  118921 1.R1010
Contig ID
                  jC-atXP36C154N7T7d1
5'-most EST
                  BLASTX
Method
                  g1935909
NCBI GI
                  174
BLAST score
                  2.0e-12
E value
                  89
Match length
                  38
% identity
NCBI Description (U77345) lethal leaf-spot 1 [Zea mays]
                  135374
Seq. No.
                   118926 1.R1010
Contig ID
                   jC-atXP36C154P1T7d1
5'-most EST
                   BLASTX
Method
                   g4389444
NCBI GI
                   159
BLAST score
                   1.0e-10
E value
                   61
Match length
% identity
                   (AE001574) hypothetical 23.1kd-like protein [Drosophila
NCBI Description
                   melanogaster]
                   135375
Seq. No.
                   118927 1.R1010
Contig ID
                   q509459
5'-most EST
                   135376
Seq. No.
                   118929 1.R1010
Contig ID
                   jC-atXP80C232F19T7d1
5'-most EST
                   BLASTX
Method
                   g4587987
NCBI GI
                   661
BLAST score
                   1.0e-72
E value
                   188
Match length
% identity
                   (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   135377
Seq. No.
Contig ID
                   118935 1.R1010
                   jC-atXP36C155B7T7d1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q3980374
                   275
BLAST score
                   1.0e-153
E value
                   475
Match length
                   97
 % identity
                   Arabidopsis thaliana chromosome II BAC F16P2 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   135378
 Seq. No.
                   118939 1.R1010
 Contig ID
                   jC-atX\overline{P}36C155C20T7d1
 5'-most EST
```

```
BLAST score
                  0.0e + 00
E value
                   530
Match length
                   96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUD21, complete sequence [Arabidopsis thaliana]
                   135379
Seq. No.
                   118948_1.R1010
Contig ID
                   g2047869
5'-most EST
                   BLASTN
Method
                   g4519187
NCBI GI
                   275
BLAST score
                   1.0e-153
E value
Match length
                   358
                   95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                   K1G2, complete sequence
                   135380
Seq. No.
                   118952_1.R1010
Contig ID
                   jC-atX\overline{P}36C156A11T7d1
5'-most EST
                   BLASTX
Method
                   g4467147
NCBI GI
BLAST score
                   67
                   3.0e-19
E value
                   84
Match length
                   67
% identity
                   (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                   135381
Seq. No.
                   118952 2.R1010
Contig ID
                   g2722580
5'-most EST
                   BLASTN
Method
                   q4467131
NCBI GI
                   286
BLAST score
                   1.0e-160
E value
                   429
Match length
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13
NCBI Description
                    (ESSA project)
                    135382
Seq. No.
                    118965 1.R1010
Contig ID
                    jC-atXP86CG9G6T7d2
 5'-most EST
                    BLASTN
Method
                    q3873174
NCBI GI
BLAST score
                    442
                    0.0e + 00
E value
                    672
Match length
 % identity
                    100
                    Genomic sequence for Arabidopsis thaliana BAC F14N23,
NCBI Description
                    complete sequence [Arabidopsis thaliana]
```

Seq. No. 135383

Contig ID 118967_1.R1010 5'-most EST g3719095

Match length

% identity

341

99



```
BLASTN
Method
                  g2564051
NCBI GI
                  273
BLAST score
                  1.0e-152
E value
                  619
Match length
                  96
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MWD9, complete sequence [Arabidopsis thaliana]
                  135384
Seq. No.
                  118970 1.R1010
Contig ID
                  jC-atXP22C114P4T7043a1
5'-most EST
                  BLASTN
Method
                  g2462264
NCBI GI
                  57
BLAST score
                  5.0e-23
E value
                  57
Match length
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   135385
Seq. No.
                   118978 1.R1010
Contig ID
                   jC-atXP36C156F18T7d1
5'-most EST
                   BLASTN
Method
                   q3297806
NCBI GI
BLAST score
                   279
                   1.0e-155
E value
Match length
                   906
                   99
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5
NCBI Description
                   (ESSA project)
                   135386
Seq. No.
                   118980_1.R1010
Contig ID
                   g2763803
5'-most EST
                   BLASTX
Method
                   g2760830
NCBI GI
                   341
BLAST score
                   5.0e-32
E value
Match length
                   63
                   100
% identity
                   (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
                   135387
Seq. No.
                   118997 1.R1010
Contig ID
 5'-most EST
                   g936012
                   135388
Seq. No.
                   119001 1.R1010
 Contig ID
 5'-most EST
                   g936016
                   BLASTN
Method
                   g2570223
NCBI GI
                   228
 BLAST score
 E value
                   1.0e-125
```





NCBI Description Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana]

135389 Seq. No.

119007 1.R1010 Contig ID

jC-atXP36C157D13T7d1 5'-most EST

BLASTX Method g1246823 NCBI GI 292 BLAST score 1.0e-44 E value 176 Match length 60 % identity

NCBI Description (X89865) unknown [Phoenix dactylifera]

135390 Seq. No.

119008 1.R1010 Contig ID

g2047896 5'-most EST BLASTX Method g1246823 NCBI GI 217 BLAST score 2.0e-17 E value 43 Match length 93 % identity

NCBI Description (X89865) unknown [Phoenix dactylifera]

135391 Seq. No.

119021 1.R1010 Contig ID

 $jC-atX\overline{P}37C157G14T7d2$ 5'-most EST

BLASTN Method g2462264 NCBI GI 48 BLAST score 1.0e-17 E value 56 Match length 96 % identity

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

135392 Seq. No.

119027 1.R1010 Contig ID

 $jC-atX\overline{P}37C157H10T7d2$ 5'-most EST

BLASTX Method q2252833 NCBI GI 330 BLAST score 2.0e-30 E value Match length 144 57 % identity

(AF013293) A_IG005I10.12 gene product [Arabidopsis NCBI Description

thaliana]

135393 Seq. No.

119028 1.R1010 Contig ID jC-atXP37C157H12T7d2 5'-most EST

Method BLASTN q2462264 NCBI GI BLAST score 51 2.0e-19 E value Match length 51 % identity 100

E value

Match length

% identity

6.0e-64

189

64



```
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   135394
Seq. No.
                   119034 1.R1010
Contig ID
                   jC-atX\overline{P}37C157I7T7d2
5'-most EST
                   BLASTX
Method
                   q1504008
NCBI GI
                   177
BLAST score
                   2.0e-12
E value
                   120
Match length
                   38
% identity
                  (D86967) Containing ATP/GTP-binding site motif A(P-loop):
NCBI Description
                   Similar to C.elegans protein(P1:CEC47E128); Similar to Mouse
                   alpha-mannosidase(P1:B54407) [Homo sapiens]
                   135395
Seq. No.
                   119040 1.R1010
Contig ID
                   jC-atXP37C157K20T7d2
5'-most EST
                   BLASTX
Method
                   g4406763
NCBI GI
                   700
BLAST score
                   8.0e-74
E value
                   147
Match length
                   93
% identity
                   (AC006836) unknown protein [Arabidopsis thaliana]
NCBI Description
                   135396
Seq. No.
                   119058 1.R1010
Contig ID
                   jC-atX\overline{P}37C157P23T7d2
5'-most EST
                   BLASTN
Method
                   q2462264
NCBI GI
                   59
BLAST score
                   4.0e-24
E value
                   59
Match length
                   100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   135397
Seq. No.
                   119059 1.R1010
Contig ID
                   jC-atXP37C157P3T7d2
5'-most EST
                   BLASTN
Method
                   q2462264
NCBI GI
                   44
BLAST score
E value
                   3.0e-15
Match length
                   44
                   100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                   135398
                   119064 1.R1010
Contig ID
                   jC-atXP37C158A15T7d2
 5'-most EST
                   BLASTX
Method
NCBI GI
                   q4200165
BLAST score
                   285
```



```
NCBI Description (Y16262) neutral invertase [Daucus carota]
```

 Seq. No.
 135399

 Contig ID
 119068_1.R1010

 5'-most EST
 jC-atXP37C158C8T7s2

 Method
 BLASTX

 NCBI GI
 g2829900

BLAST score 769 E value 5.0e-82 Match length 148 % identity 99

NCBI Description (AC002311) similar to ripening-induced protein, gp AJ001449 2465015 and major latex protein, gp X91961 1107495 [Arabidopsis thaliana]

Seq. No. 135400

Contig ID 119069_1.R1010 5'-most EST jC-atXP37C159A22T7d2

Method BLASTN
NCBI GI g3785968
BLAST score 182
E value 1.0e-97
Match length 434

% identity 95
NCBI Description Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135401

Contig ID 119071_1.R1010 5'-most EST jC-atXP37C159B14T7d2

Method BLASTX
NCBI GI g2498731
BLAST score 598
E value 8.0e-62
Match length 173
% identity 66

NCBI Description PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1

>gi_1362013_pir__S57611 zeta-crystallin homolog -

Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)

zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No. 135402

Contig ID 119080_1.R1010 5'-most EST jC-atXP37C159D4T7d2

Method BLASTX
NCBI GI g4006886
BLAST score 361
E value 5.0e-34
Match length 160
% identity 49

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 135403

Contig ID 119091_1.R1010

5'-most EST g2047708 Method BLASTX NCBI GI g3603473

5'-most EST

Method

NCBI GI

g2047929

BLASTN g3059018



```
BLAST score
                  6.0e-49
E value
                  143
Match length
                  63
% identity
                 (AF090698) elicitor-responsive gene-3 [Oryza sativa]
NCBI Description
                  135404
Seq. No.
                  119092 1.R1010
Contig ID
                  g937527
5'-most EST
                  BLASTX
Method
                  g3643602
NCBI GI
                  407
BLAST score
                  1.0e-39
E value
Match length
                  134
% identity
                   (AC005395) putative tonoplast intrinsic protein
NCBI Description
                   [Arabidopsis thaliana]
                   135405
Seq. No.
                   119099 1.R1010
Contig ID
                   g2047925
5'-most EST
                   BLASTX
Method
                   g3702620
NCBI GI
                   118
BLAST score
                   2.0e-13
E value
                   75
Match length
                   63
% identity
                  (Y17329) calnexin [Pisum sativum]
NCBI Description
Seq. No.
                   135406
                   119099 2.R1010
Contig ID
                   g936089
5'-most EST
                   BLASTX
Method
                   g473878
NCBI GI
BLAST score
                   383
                   6.0e-37
E value
                   119
Match length
                   72
% identity
                   (U08315) calnexin homolog [Arabidopsis thaliana]
NCBI Description
                   135407
Seq. No.
                   119121 1.R1010
Contig ID
                   g930568
5'-most EST
                   BLASTN
Method
NCBI GI
                   q3059018
                   328
BLAST score
                   0.0e + 00
E value
                   385
Match length
 % identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12
NCBI Description
                   (ESSAII project)
                   135408
 Seq. No.
                   119122 1.R1010
 Contig ID
```

```
BLAST score 199
E value 1.0e-108
Match length 109
% identity 97
NCRI Description Arabidopsis thaliana DNA chromosom
```

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project)

Seq. No. 135409

Contig ID 119123_1.R1010

5'-most EST jC-atXP38C158J17T7d1

Seq. No. 135410

Contig ID 119125_1.R1010

NCBI Description Arabidopsis thaliana chromosome 1 BAC T1F15 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 135411

Contig ID 119125_2.R1010

5'-most EST jC-atXP38C158J19T7d1

Method BLASTX
NCBI GI g3176663
BLAST score 629
E value 6.0e-66
Match length 123
% identity 97

NCBI Description (AC004393) Contains similarity to S-receptor kinase 8

precursor gb_D38563 from Brassica rapa. ESTs gb_T88253 and

gb_AA394649 come from this gene. [Arabidopsis thaliana]

Seq. No. 135412

Contig ID 119136_1.R1010

5'-most EST g2047933
Method BLASTN
NCBI GI g3046854
BLAST score 399
E value 0.0e+00
Match length 439
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRG7, complete sequence [Arabidopsis thaliana]

Seq. No. 135413

Contig ID 119143_1.R1010 5'-most EST jC-atXP38C158K4T7d1

Method BLASTX
NCBI GI g3335363
BLAST score 162
E value 4.0e-11
Match length 131
% identity 19



n [Arabidonsis thal:

```
(AC003028) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  135414
Seq. No.
                  119152 1.R1010
Contig ID
                  jC-atXP38C159G21T7d1
5'-most EST
                  135415
Seq. No.
                  119155 1.R1010
Contig ID
                  jC-atX\overline{P}81C240M14T7s1
5'-most EST
                  135416
Seq. No.
                  119155 2.R1010
Contig ID
5'-most EST
                  jC-atXP38C159G2T7s2
                  135417
Seq. No.
                  119162 1.R1010
Contig ID
                  jC-atXP38C160E8T7s2
5'-most EST
                  BLASTX
Method
                  g2245014
NCBI GI
                   442
BLAST score
                  8.0e-44
E value
                  84
Match length
                  100
% identity
NCBI Description (Z97341) glucosyltransferase homolog [Arabidopsis thaliana]
                   135418
Seq. No.
                   119166 1.R1010
Contig ID
                   g936117
5'-most EST
                   BLASTN
Method
                   g4585952
NCBI GI
                   408
BLAST score
                   0.0e+00
E value
                   440
Match length
                   98
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F26F24,
                   complete sequence
                   135419
Seq. No.
                   119171_1.R1010
Contig ID
5'-most EST
                   g2763832
                   BLASTX
Method
                   q4584546
NCBI GI
                   526
BLAST score
                   1.0e-53
E value
                   141
Match length
                   67
% identity
NCBI Description (AL049608) putative protein [Arabidopsis thaliana]
Seq. No.
                   135420
                   119184 1.R1010
Contig ID
 5'-most EST
                   g2749168
                   BLASTN
Method
                   q4589445
 NCBI GI
                   311
 BLAST score
 E value
                   1.0e-175
 Match length
                   439
```

16094

95

% identity



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No. 135421

Contig ID 119185_1.R1010

5'-most EST g936451

Seq. No. 135422

Contig ID 119190_1.R1010 5'-most EST jC-atXP55C186O1T7s2

Method BLASTN
NCBI GI g3985954
BLAST score 405
E value 0.0e+00
Match length 445
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRG21, complete sequence [Arabidopsis thaliana]

Seq. No. 135423

Contig ID 119193_1.R1010

5'-most EST jC-atXP38C160J23T7d1

Method BLASTN
NCBI GI 94490324
BLAST score 338
E value 0.0e+00
Match length 365
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14

(ESSA project)

Seq. No. 135424

Contig ID 119195_1.R1010 5'-most EST jC-atXP38C160J3T7d1

Method BLASTN
NCBI GI 94589437
BLAST score 314
E value 1.0e-176
Match length 362
% identity 97

% identity 97 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MPN9, complete sequence

Seq. No. 135425

Contig ID 119196_1.R1010

5'-most EST g2749171
Method BLASTN
NCBI GI g4589437
BLAST score 344
E value 0.0e+00
Match length 421
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MPN9, complete sequence

Seq. No. 135426

Contig ID 119203_1.R1010

E value



```
g2764258
5'-most EST
                   135427
Seq. No.
                   119205 1.R1010
Contig ID
                   g27491\overline{5}7
5'-most EST
                   BLASTN
Method
                   q3702735
NCBI GI
                   313
BLAST score
                   1.0e-176
E value
                   354
Match length
                   97
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MQL5, complete sequence [Arabidopsis thaliana]
Seq. No.
                   135428
                   119206 1.R1010
Contig ID
                   jC-atX\overline{P}39C161H6T7d1
5'-most EST
                   BLASTN
Method
                   g2924734
NCBI GI
                   442
BLAST score
                   0.0e + 00
E value
                   495
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXE10, complete sequence [Arabidopsis thaliana]
                   135429
Seq. No.
                   119216 1.R1010
Contig ID
                   jC-atXP39C160L5T7s1
5'-most EST
                   {\tt BLASTX}
Method
                   g4835244
NCBI GI
                   396
BLAST score
                   4.0e-38
E value
                   180
Match length
                   48
% identity
                   (AL049862) putative mitochondrial protein [Arabidopsis
NCBI Description
                   thaliana]
                   135430
Seq. No.
                   119225 1.R1010
Contig ID
5'-most EST
                   g936475
                   BLASTX
Method
                   g4218120
NCBI GI
                   286
BLAST score
                   1.0e-25
E value
Match length
                    112
                    54
 % identity
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                    thaliana]
                    135431
 Seq. No.
                    119229 1.R1010
 Contig ID
                    q936477
 5'-most EST
                    BLASTN
 Method
                    g4220643
 NCBI GI
 BLAST score
                    259
```

16096

1.0e-143



Match length 370 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 135432

Contig ID 119248 1.R1010

5'-most EST g2749187

Method BLASTN

NCBI GI g4415905

BLAST score 276

E value 1.0e-154

Match length 395

% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC F13K3 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135433

Contig ID 119248 2.R1010

5'-most EST g936187
Method BLASTN
NCBI GI g4415905
BLAST score 256
E value 1.0e-142
Match length 395
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC F13K3 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135434

Contig ID 119259_1.R1010

5'-most EST jC-atXP39C161D14T7d1

Method BLASTN
NCBI GI g4589439
BLAST score 319
E value 1.0e-179
Match length 879
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQM1, complete sequence

Seq. No. 135435

Contig ID 119263_1.R1010 5'-most EST jC-atXP39C161D17T7d1

Method BLASTX
NCBI GI g3860262
BLAST score 347
E value 3.0e-53
Match length 158
% identity 70

NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 135436

Contig ID 119265_1.R1010 5'-most EST jC-atXP39C161D1T7s1

Seq. No. 135437



```
119284 1.R1010
Contig ID
                   iC-atXP39C162G7T7d1
5'-most EST
                   BLASTX
Method
                   g2708331
NCBI GI
BLAST score
                   703
E value
                   2.0e-74
                   164
Match length
% identity
                   82
                   (AF038557) ligand gated channel-like protein [Arabidopsis
NCBI Description
Seq. No.
                   135438
                   119285 1.R1010
Contig ID
5'-most EST
                   jC-atXP39C161F12T7s1
Method
                   BLASTN
                   q3080406
NCBI GI
BLAST score
                   294
E value
                   1.0e-164
Match length
                   352
                   95
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12
NCBI Description
                   (ESSA project)
Seq. No.
                   135439
                   119288 1.R1010
Contig ID
5'-most EST
                   q936526
                   BLASTN
Method
NCBI GI
                   q4589439
BLAST score
                   419
E value
                   0.0e+00
Match length
                   455
                   98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MQM1, complete sequence
                   135440
Seq. No.
                   119292 1.R1010
Contig ID
5'-most EST
                   g936528
                   135441
Seq. No.
                   119298 1.R1010
Contig ID
                   jC-atX\overline{P}39C161G17T7s1
5'-most EST
                   BLASTN
Method
                   g2924730
NCBI GI
BLAST score
                   137
                   7.0e-71
E value
Match length
                   361
% identity
                   93
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MPI7, complete sequence [Arabidopsis thaliana]
```

135442 Seq. No.

119308 1.R1010 Contig ID

5'-most EST g936546 BLASTN Method NCBI GI g3983533 BLAST score 243

```
1.0e-134
E value
                  452
Match length
% identity
                  97
                  Arabidopsis thaliana BAC T24G3 from chromosome V near 70
NCBI Description
                  cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  135443
                  119309 1.R1010
Contig ID
5'-most EST
                  g2749202
Method
                  BLASTX
NCBI GI
                  q4586245
BLAST score
                  248
E value
                  5.0e-21
Match length
                  109
% identity
                  (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  135444
                  119334 1.R1010
Contig ID
5'-most EST
                  jC-atXP39C162H19T7s1
                  135445
Seq. No.
Contig ID
                  119353 1.R1010
                  jC-atXP3C81E4T7d1
5'-most EST
                  BLASTX
Method
                  g2244964
NCBI GI
BLAST score
                  456
E value
                  4.0e-55
Match length
                  150
                  77
% identity
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  135446
                  119354 1.R1010
Contig ID
5'-most EST
                  jC-atXP3C81E6T7d1
Method
                  BLASTX
NCBI GI
                  g2244866
                  226
BLAST score
E value
                  2.0e-18
                  146
Match length
                  38
% identity
                  (297337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   135447
                  119357 1.R1010
Contig ID
                  g501917
5'-most EST
Method
                  BLASTX
```

NCBI GI g2827715 BLAST score 313 7.0e-29 E value 103 Match length 60 % identity

(AL021684) receptor protein kinase - like protein NCBI Description

[Arabidopsis thaliana]

135448 Seq. No.

119359 1.R1010 Contig ID

```
5'-most EST
                   q933622
                  BLASTN
Method
                   q862320
NCBI GI
                   125
BLAST score
                   2.0e-63
E value
Match length
                   145
% identity
                   97
NCBI Description Arabidopsis thaliana tRNA-Met gene (clone pAtM-8)
Seq. No.
                   135449
                   119361 1.R1010
Contig ID
                   g933625
5'-most EST
Method
                   BLASTX
                   g3980402
NCBI GI
BLAST score
                   584
E value
                   3.0e-60
Match length
                   184
% identity
                   72
                   (AC004561) putative tropinone reductase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   135450
Contig ID
                   119362 1.R1010
5'-most EST
                   g933627
                   BLASTX
Method
NCBI GI
                   q4263791
BLAST score
                   486
E value
                   8.0e-49
Match length
                   176
                   44
% identity
                   (AC006068) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   135451
Seq. No.
                   119373 1.R1010
Contig ID
5'-most EST
                   g933664
                   BLASTX
Method
                   q1173624
NCBI GI
                   367
BLAST score
                   6.0e-35
E value
                   133
Match length
                   59
% identity
                   (U34744) cytochrome P-450 [Phalaenopsis sp. 'hybrid
NCBI Description
                   SM9108']
                   135452
Seq. No.
                   119378 1.R1010
Contig ID
                   g933681
5'-most EST
                   BLASTX
Method
                   g4522012
NCBI GI
BLAST score
                   635
                   4.0e-69
E value
Match length
                   135
                   93
% identity
                   (AC007069) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   135453
```



```
119379 1.R1010
Contig ID
5'-most EST
                   jC-atXP3C83G7T7d1
                  BLASTX
Method
                   g2281085
NCBI GI
BLAST score
                   468
E value
                   7.0e-47
Match length
                   149
% identity
                   55
                   (AC002333) CTR1 protein kinase isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   135454
                   119384 1.R1010
Contig ID
5'-most EST
                   g933692
Seq. No.
                   135455
Contig ID
                   119385 1.R1010
5'-most EST
                   g933695
Method
                  BLASTX
                   g1524370
NCBI GI
BLAST score
                   262
E value
                   1.0e-22
Match length
                   93
                   57
% identity
                  (X92491) TOM20 [Solanum tuberosum]
NCBI Description
Seq. No.
                   135456
Contig ID
                   119392 1.R1010
5'-most EST
                   jC-atXP108C170H10T7005d1
Method
                   BLASTN
NCBI GI
                   g4519186
BLAST score
                   129
                   7.0e-66
E value
Match length
                   749
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K18B18, complete sequence
                   135457
Seq. No.
                   119392 3.R1010
Contig ID
5'-most EST
                   g958091
Method
                   BLASTN
NCBI GI
                   g4519186
BLAST score
                   77
E value
                   4.0e-35
Match length
                   170
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K18B18, complete sequence
                   135458
Seq. No.
Contig ID
                   119393 1.R1010
```

5'-most EST jC-atXP3C85A9T7d1

Method BLASTX NCBI GI q2739389 BLAST score 806 E value 4.0e-86

```
Match length
% identity
                   32
NCBI Description
                  (AC002505) Cf-2.2 like protein [Arabidopsis thaliana]
Seq. No.
                  135459
                  119393 2.R1010
Contig ID
5'-most EST
                  g2393575
Method
                  BLASTX
NCBI GI
                  g2739389
BLAST score
                  266
E value
                   4.0e-23
Match length
                  121
% identity
                   49
NCBI Description
                  (AC002505) Cf-2.2 like protein [Arabidopsis thaliana]
Seq. No.
                  135460
                  119404 1.R1010
```

Contig ID 119404_1.R1010
5'-most EST g937048

Method BLASTX

NCBI GI g99772

BLAST score 417

E value 6.0e-41

Match length 107 % identity 79

NCBI Description ubiquitin 81-aa extension protein 2 - Arabidopsis thaliana

>gi_166936 (J05540) ubiquitin extension protein (UBQ6)
[Arabidopsis thaliana] >gi_3522953 (AC004411) ubiquitin

extension protein (UBQ6) [Arabidopsis thaliana]

Seq. No. 135461

Contig ID 119416 1.R1010

5'-most EST g937078

Method BLASTN

NCBI GI g3297806

BLAST score 119

E value 3.0e-60

Match length 355

% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F1715

(ESSA project)

Seq. No. 135462

Contig ID 119417 1.R1010

5'-most EST jC-atXP40C161N2T7035a1

Method BLASTX
NCBI GI g3176726
BLAST score 506
E value 5.0e-51
Match length 108
% identity 94

NCBI Description (AC002392) putative serine proteinase [Arabidopsis

thaliana]

Seq. No. 135463

Contig ID 119417_2.R1010 5'-most EST jC-atXP75C225N23T7d1

Method BLASTX



```
NCBI GI
                  q3176726
BLAST score
                  772
E value
                  2.0e-82
Match length
                  149
                  100
% identity
NCBI Description
                  (AC002392) putative serine proteinase [Arabidopsis
                  thaliana]
Seq. No.
                  135464
Contig ID
                  119423 1.R1010
5'-most EST
                  g2723035
Method
                  BLASTX
NCBI GI
                  g2146835
BLAST score
                  163
E value
                  6.0e-11
Match length
                  80
% identity
NCBI Description
                  hypothetical protein YCL039w - yeast (Saccharomyces
                  cerevisiae) >gi_1907121_emb_CAA42377_ (X59720) YCL039w,
                  len:745 [Saccharomyces cerevisiae]
Seq. No.
                  135465
Contig ID
                  119434 1.R1010
5'-most EST
                  q1520564
Method
                  BLASTN
NCBI GI
                  q3228389
BLAST score
                  265
E value
                  1.0e-147
Match length
                  486
                  95
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F17L21,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  135466
Contig ID
                  119436 1.R1010
5'-most EST
                  g936620
Seq. No.
                  135467
Contig ID
                  119438 1.R1010
5'-most EST
                  jC-atXP40C162L8T7d1
Method
                  BLASTN
NCBI GI
                  g4371278
BLAST score
                  397
                  0.0e+00
E value
Match length
                  421
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T2N18 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  135468
                  119441 1.R1010
Contig ID
```

5'-most EST jC-atXP40C162M4T7d1

Method BLASTX NCBI GI g4539380 BLAST score 720 E value 8.0e-76 Match length 161



% identity 82
NCBI Description (AL035526) putative protein [Arabidopsis thaliana]
Seq. No. 135469
Contig ID 119443 1.R1010
5'-most EST g936637
Method BLASTX
NCBI GI g3522938

NCBI GI g3522938 BLAST score 326 E value 3.0e-30 Match length 103 % identity 68

NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 135470

Contig ID 119462_1.R1010 5'-most EST jC-atXP40C164E1T7d1

Seq. No. 135471

Contig ID 119463_1.R1010 5'-most EST jC-atXP40C164E5T7d1

Method BLASTN
NCBI GI g3869065
BLAST score 283
E value 1.0e-158
Match length 473
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K24M7, complete sequence [Arabidopsis thaliana]

Seq. No. 135472

Contig ID 119464 1.R1010

NCBI Description (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase

with GDSL-motif family. [Arabidopsis thaliana]

Seq. No. 135473

Contig ID 119468_1.R1010 5'-most EST jC-atXP41C162015T7d1

Seq. No. 135474

Contig ID 119469_1.R1010 5'-most EST jC-atXP41C162015T7s1

Seq. No. 135475

Contig ID 119471_1.R1010 5'-most EST jC-atXP41C16208T7d1

Method BLASTX
NCBI GI g4154352
BLAST score 75
E value 3.0e-20



Match length 114 % identity 51

NCBI Description (AF110333) PrMC3 [Pinus radiata]

Seq. No. 135476

Contig ID 119479_1.R1010

5'-most EST g936653

Method BLASTX

NCBI GI g4502897

BLAST score 282

E value 5.0e-25

Match length 96
% identity 54

NCBI Description cleft lip and palate associated transmembrane protein 1

>gi_4039014 (AF037338) cleft lip and palate transmembrane protein 1 [Homo sapiens] >gi_4063033 (AF037339) cleft lip

and palate transmembrane protein 1 [Homo sapiens]

Seq. No. 135477

Contig ID 119496_1.R1010 5'-most EST jC-atXP41C163F3T7s1

Method BLASTX
NCBI GI g2498892
BLAST score 183
E value 1.0e-13
Match length 66
% identity 33

NCBI Description SEC13-RELATED PROTEIN

Seq. No. 135478

Contig ID 119497 1.R1010

5'-most EST g936696

Seq. No. 135479

Contig ID 119498_1.R1010

5'-most EST g2047945

Seq. No. 135480

Contig ID 119501_1.R1010 5'-most EST jC-atXP41C163G4T7d1

Method BLASTX
NCBI GI g4063743
BLAST score 276
E value 3.0e-24
Match length 93
% identity 63

NCBI Description (AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135481

Contig ID 119533_1.R1010

5'-most EST jC-atXP41C164I22T7s1

Method BLASTN
NCBI GI g2618677
BLAST score 149
E value 4.0e-78
Match length 272
% identity 93



Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 135482

NCBI Description

% identity

Contig ID 119539_1.R1010 5'-most EST jC-atXP41C164J14T7s1

Method BLASTX
NCBI GI g2462754
BLAST score 49
E value 3.0e-24
Match length 117

NCBI Description (AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No. 135483

Contig ID 119549 1.R1010

5'-most EST jC-atXP41C164L10T7s1

66

Method BLASTN
NCBI GI g2494106
BLAST score 203
E value 1.0e-110
Match length 314
% identity 98

NCBI Description Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 135484

Contig ID 119561_1.R1010

5'-most EST g936762

Method BLASTX

NCBI GI g1706189

BLAST score 155

E value 6.0e-10

Match length 51

% identity 51

NCBI Description LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2)

(CAT2) (TEA PROTEIN) (T-CELL EARLY ACTIVATION PROTEIN) (20.5) >gi_627850_pir__A54011 CAT1/ecoR protein - mouse >gi 293315 (L11600) cationic amino acid transporter-2 [Mus

musculus] >gi 517493 (L29006) membrane protein [Mus

musculus]

Seq. No. 135485

Contig ID 119568 1.R1010

5'-most EST g2047971
Method BLASTX
NCBI GI g4539004
BLAST score 142
E value 1.0e-08
Match length 48
% identity 50

NCBI Description (AL049481) putative protein kinase [Arabidopsis thaliana]

Seq. No.

135486

Contig ID 119572 1.R1010

5'-most EST $g93677\overline{2}$ Method BLASTX



```
NCBI GI
                   q2047324
BLAST score
                   745
E value
                   4.0e-79
                  152
Match length
                   89
% identity
NCBI Description (U80192) HAL3 homolog [Arabidopsis thaliana]
                  135487
Seq. No.
                  119594_1.R1010
Contig ID
                  g695433
5'-most EST
Method
                  BLASTN
NCBI GI
                  g3047074
BLAST score
                   517
E value
                  0.0e + 00
Match length
                   643
                  100
% identity
NCBI Description Arabidopsis thaliana BAC F21E10
Seq. No.
                   135488
                   119601_1.R1010
Contig ID
5'-most EST
                  g936797
Seq. No.
                   135489
Contig ID
                   119605 1.R1010
                   jC-atX\overline{P}41C166A2T7d1
5'-most EST
Method
                  BLASTN
              ×.,
NCBI GI
                   q2477521
                   27
BLAST score
E value
                   3.0e-05
                   403
Match length
                   75
% identity
                  Arabidopsis thaliana chromosome I BAC F22K2O genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   135490
Seq. No.
Contig ID
                   119638 1.R1010
5'-most EST
                   g2749315
Method
                   BLASTX
NCBI GI
                   q4138265
BLAST score
                   248
                   6.0e-52
E value
Match length
                   221
% identity
                   49
                   (AJ006228) Avr9 elicitor response protein [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   135491
                   119645 1.R1010
Contig ID
5'-most EST
                   q2749298
                   BLASTX
Method
```

g2464905 NCBI GI BLAST score 61 E value 8.0e-21

Match length 82 80 % identity

(Z99708) minor allergen [Arabidopsis thaliana] NCBI Description

```
Seq. No.
                   119652 1.R1010
Contig ID
5'-most EST
                   jC-atXP43C169D23T7s1
Method
                   BLASTN
NCBI GI
                   q4454004
BLAST score
                   647
E value
                   0.0e + 00
                   709
Match length
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6
                   (ESSAII project)
Seq. No.
                   135493
Contig ID
                   119655 1.R1010
                   jC-atX\overline{P}43C170D15T7s1
                   BLASTN
```

5'-most EST jC-atXP43C170D15T7.

Method BLASTN

NCBI GI g2088638

BLAST score 113

E value 1.0e-56

Match length 342

E value 1.0e
Match length 342
% identity 93
NCBI Description Arab

NCBI Description Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135494 Contig ID 119667_1.R1010 5'-most EST g2749281

Seq. No. 135495

Contig ID 119677_1.R1010 5'-most EST g2580700 Method BLASTN

Method BLASTN
NCBI GI g2815519
BLAST score 240
E value 1.0e-132
Match length 272
% identity 97

NCBI Description Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm,

complete sequence [Arabidopsis thaliana]

Seq. No. 135496 Contig ID 119684_1.R1010

5'-most EST jC-atXP43C171A2T7s1

Seq. No. 135497

Contig ID 119686 1.R1010

5'-most EST g937423
Method BLASTX
NCBI GI g2828293
BLAST score 205
E value 4.0e-16
Match length 131
% identity 44

NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No. 135498

Contig ID 119687 1.R1010

E value

Match length

% identity

0.0e+00

398

92



```
5'-most EST
                  q2764196
Method
                  BLASTX
NCBI GI
                  q3482910
BLAST score
                   480
E value
                  2.0e-48
Match length
                  110
% identity
                  79
NCBI Description
                   (AC003970) Similar to rice water stress induced protein
                  gi_537404 [Arabidopsis thaliana]
Seq. No.
                  135499
Contig ID
                  119691 1.R1010
5'-most EST
                  q773548
Method
                  BLASTX
NCBI GI
                  q4454025
BLAST score
                  309
E value
                  3.0e-72
Match length
                  154
% identity
NCBI Description
                   (AL035394) putative cellulase [Arabidopsis thaliana]
                  135500
Seq. No.
Contig ID
                  119694_1.R1010
5'-most EST
                  q937545
Method
                  BLASTN
NCBI GI
                  q4519182
BLAST score
                  156
E value
                  3.0e-82
Match length
                  460
% identity
                  97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K13H13, complete sequence
Seq. No.
                  135501
                  119695 1.R1010
Contig ID
5'-most EST
                  jC-atXP44C170H19T7d1
Method
                  BLASTX
NCBI GI
                  g4586246
BLAST score
                  193
E value
                  4.0e-15
Match length
                  41
% identity
                  90
                  (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  135502
Contig ID
                  119698 1.R1010
5'-most EST
                  g473340
Seq. No.
                  135503
                  119717 1.R1010
Contig ID
5'-most EST
                  q937878
Method
                  BLASTN
NCBI GI
                  g4756963
BLAST score
                  394
```



```
Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
NCBI Description
                  (ESSA project)
Seq. No.
                  135504
                  119719 2.R1010
Contig ID
5'-most EST
                  g2764237
Method
                  BLASTX
                  g2262162
NCBI GI
BLAST score
                  266
E value
                  5.0e-25
Match length
                  149
% identity
                  46
NCBI Description
                  (AC002329) hypothetical protein similar to A. thaliana
                  protein F19K23.19 [Arabidopsis thaliana]
                  135505
Seq. No.
```

119722 1.R1010 Contig ID 5'-most EST g1053458 Method BLASTX NCBI GI g4006899 BLAST score 622 E value 5.0e-65 Match length 133 % identity 89

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

135506 Seq. No. Contig ID 119727 1.R1010 5'-most EST $q93790\overline{4}$ Method BLASTN NCBI GI g2760166 BLAST score 120 8.0e-61 E value

Match length 449 % identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBK20, complete sequence [Arabidopsis thaliana]

Seq. No. 135507

Contig ID 119734 1.R1010

5'-most EST g937978

Seq. No. 135508

Contig ID 119739 1.R1010

5'-most EST g937600

Seq. No. 135509

Contig ID 119761 1.R1010

5'-most EST g2749396 Method BLASTN NCBI GI g4733984 BLAST score 184 E value 5.0e-99

Match length 271 % identity 98

Arabidopsis thaliana chromosome II BAC F1404 genomic NCBI Description

sequence, complete sequence

Match length

% identity

386 93



```
Seq. No.
                  135510
Contig ID
                  119764 1.R1010
5'-most EST
                  g905521
Method
                  BLASTX
NCBI GI
                  g2911067
BLAST score
                  499
E value
                  1.0e-50
Match length
                  138
% identity
                  70
NCBI Description
                   (AL021960) UV-damaged DNA-binding protein-like [Arabidopsis
                  thaliana]
                  135511
Seq. No.
Contig ID
                  119770 1.R1010
5'-most EST
                  g2596241
Method
                  BLASTX
                  g100225
NCBI GI
BLAST score
                  393
                  4.0e-38
E value
Match length
                  96
                  73
% identity
NCBI Description
                  heat shock transcription factor 8 - tomato
                  >gi_19260_emb_CAA47868_ (X67599) heat stress transcription
                  factor 8 [Lycopersicon esculentum]
Seq. No.
                  135512
                  119771_1.R1010
Contig ID
5'-most EST
                  g905530
Method
                  BLASTX
NCBI GI
                  g3047125
BLAST score
                  155
E value
                  4.0e-55
Match length
                  120
% identity
                  100
NCBI Description
                  (AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.
                  135513
Contig ID
                  119773 1.R1010
5'-most EST
                  q905533
Method
                  BLASTX
                  g3785995
NCBI GI
BLAST score
                  665
E value
                  6.0e-70
Match length
                  136
% identity
                  95
NCBI Description
                  (AC005499) unknown protein [Arabidopsis thaliana]
                  135514
Seq. No.
                  119774 1.R1010
Contig ID
5'-most EST
                  g2749400
Method
                  BLASTN
                  q3785992
NCBI GI
BLAST score
                  284
                  1.0e-158
E value
```



NCBI Description Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135515

Contig ID 119775_1.R1010

5'-most EST g2749401

Seq. No. 135516

Contig ID 119779_1.R1010

5'-most EST g905539
Method BLASTX
NCBI GI g434765
BLAST score 159
E value 2.0e-10
Match length 113
% identity 39

NCBI Description (D21262) ORF [Homo sapiens]

Seq. No. 135517

Contig ID 119783_1.R1010

5'-most EST g905961 Method BLASTX NCBI GI g2708743 BLAST score 257 E value 4.0e-22 Match length 141 % identity 38

NCBI Description (AC003952) putative Tal-1-like reverse transcriptase

[Arabidopsis thaliana]

Seq. No. 135518

Contig ID 119784 1.R1010

5'-most EST $g27494\overline{0}3$

Seg. No. 135519

Contig ID 119790 1.R1010

5'-most EST g2749405
Method BLASTN
NCBI GI g4220634
BLAST score 312
E value 1.0e-175
Match length 688
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9H21, complete sequence [Arabidopsis thaliana]

Seq. No. 135520

Contig ID 119791 1.R1010

5'-most EST q2749366

Seq. No. 135521

Contig ID 119797 1.R1010

5'-most EST g3449832

Seq. No. 135522

Contig ID 119801_1.R1010

5'-most EST $q90564\overline{4}$



```
Method
  NCBI GI
                     q627580
  BLAST score
                     226
  E value
                     3.0e-19
  Match length
                     127
                     41
  % identity
  NCBI Description
                     prolyl oligopeptidase (EC 3.4.21.26) - human
                     >gi 904214 dbj BAA04661 (D21102) prolyl endopeptidase
                     [Homo sapiens]
  Seq. No.
                     135523
  Contig ID
                     119802 1.R1010
  5'-most EST
                     g2749435
  Method
                     BLASTX
  NCBI GI
                     q4506043
  BLAST score
                     74
  E value
                     2.0e-23
  Match length
                     106
                     53
  % identity
                     prolyl endopeptidase >gi 1346769 sp P48147 PPCE HUMAN
  NCBI Description
                     PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE)
                     >gi_558596_emb_CAA52605_ (X74496) prolyl oligopeptidase
                     [Homo sapiens] >gi_1585155_prf 2124300A Pro oligopeptidase
                     [Homo sapiens]
                     135524
  Seq. No.
  Contig ID
                     119815 1.R1010
  5'-most EST
                     g906056
  Seq. No.
                     135525
  Contig ID
                     119819 1.R1010
  5'-most EST
                     g906064
  Method
                     BLASTN
  NCBI GI
                     g2924733
  BLAST score
                     168
E value
                     2.0e-89
  Match length
                     191
                     97
  % identity
  NCBI Description
                     Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                     MUF9, complete sequence [Arabidopsis thaliana]
  Seq. No.
                     135526
                     119820_1.R1010
  Contig ID
                     g2749442
  5'-most EST
  Method
                     BLASTN
  NCBI GI
                     g4220636
  BLAST score
                     260
                     1.0e-144
  E value
  Match length
                     437
                     96
  % identity
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
  NCBI Description
                     MFB16, complete sequence [Arabidopsis thaliana]
```

Seq. No. 135527

Contig ID 119833_1.R1010 5'-most EST q2749446

5'-most EST g274944 Method BLASTN



```
NCBI GI
                   q2182286
BLAST score
                   335
E value
                   0.0e + 00
Match length
                   382
% identity
NCBI Description
                  Sequence of BAC F20P5 from Arabidopsis thaliana chromosome
                   1, complete sequence [Arabidopsis thaliana]
                   135528
Seq. No.
Contig ID
                   119847 1.R1010
5'-most EST
                   jC-atXP47C176E11T7d2
Method
                   BLASTX
NCBI GI
                   q4835226
BLAST score
                   456
E value
                   3.0e-45
Match length
                   178
% identity
                   55
NCBI Description
                   (AL049862) putative protein [Arabidopsis thaliana]
Seq. No.
                   135529
                   119848_1.R1010
Contig ID
                   jC-atX\overline{P}47C176E11T7s2
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4835223
BLAST score
                   419
E value
                   0.0e + 00
Match length
                   485
                   99
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3
                   (ESSA project)
Seq. No.
                   135530
Contig ID
                   119856 1.R1010
5'-most EST
                   g905793
Seq. No.
                   135531
Contig ID
                   119860 1.R1010
5'-most EST
                   q2749469
Seq. No.
                   135532
                   119869 1.R1010
Contig ID
                   jC-atXP44C171E11T7087a1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2462264
BLAST score
                   56
                   2.0e-22
E value
Match length
                   56
% identity
                   100
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                   135533
Seq. No.
                   119888 1.R1010
Contig ID
```

5'-most EST g2733455

BLASTX Method NCBI GI g4115386 BLAST score 589 E value 4.0e-61



Match length 122 % identity 98

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 135534

Contig ID 119900 1.R1010

5'-most EST g905778

Method BLASTX

NCBI GI g2088661

BLAST score 192

E value 2.0e-14

Match length 129

% identity 33

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135535

Contig ID 119903_1.R1010

5'-most EST g2597363
Method BLASTX
NCBI GI g3687833
BLAST score 561
E value 2.0e-57
Match length 172
% identity 19

NCBI Description (AF069737) notchless [Xenopus laevis]

Seq. No. 135536

Contig ID 119918_1.R1010

5'-most EST g2733511
Method BLASTX
NCBI GI g3915463
BLAST score 155
E value 4.0e-10
Match length 80
% identity 44

NCBI Description HYPOTHETICAL 33.1 KD PROTEIN SLR1592

>gi 1652063 dbj BAA16988 (D90902) hypothetical protein

[Synechocystis sp.]

Seq. No. 135537

Contig ID 119919 1.R1010

5'-most EST g2749484
Method BLASTX
NCBI GI g3915463
BLAST score 146
E value 4.0e-09
Match length 57
% identity 56

NCBI Description HYPOTHETICAL 33.1 KD PROTEIN SLR1592

>gi_1652063_dbj_BAA16988_ (D90902) hypothetical protein

[Synechocystis sp.]

Seq. No. 135538

Contig ID 119920 1.R1010

5'-most EST $g90622\overline{4}$ Method BLASTN NCBI GI g2245031



```
BLAST score 258
E value 1.0e-143
Match length 341
% identity 94
```

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 135539

Contig ID 119921 1.R1010

5'-most EST g905845

Method BLASTN

NCBI GI g3033373

BLAST score 367

E value 0.0e+00

Match length 400
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135540

Contig ID 119922 1.R1010

5'-most EST g2749488

Method BLASTN

NCBI GI g3033373

BLAST score 187

E value 1.0e-100

Match length 341

% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135541

Contig ID 119925 1.R1010

5'-most EST g905852

Method BLASTN

NCBI GI g4580732

BLAST score 298

E value 1.0e-167

Match length 333

% identity 98

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F5J5,

complete sequence

Seq. No. 135542

Contig ID 119935 1.R1010

5'-most EST g2749491
Method BLASTN
NCBI GI g3402745
BLAST score 271
E value 1.0e-151
Match length 366
% identity 94

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5

(ESSAII project)

Seg. No. 135543

Contig ID 119961 1.R1010



```
5'-most EST
                  iC-atXP49C177O9T7d2
Method
                  BLASTX
                  q3123712
NCBI GI
                  190
BLAST score
E value
                  2.0e-32
Match length
                  171
% identity
NCBI Description
                  (D89051) ERD6 protein [Arabidopsis thaliana]
                  135544
Seq. No.
                  119973 1.R1010
                  g2733463
```

Contig ID 5'-most EST Method BLASTX NCBI GI q3928862 BLAST score 348

E value 3.0e - 33Match length 133 % identity 61

(AF089710) disease resistance protein RPP8 [Arabidopsis NCBI Description

thaliana]

Seq. No. 135545

119978 1.R1010 Contig ID

5'-most EST q906286

Seq. No. 135546

Contig ID 119984 1.R1010

5'-most EST iC-atXP49C178M11T7d2

Method BLASTX NCBI GI g2119846 BLAST score 378 2.0e-36 E value Match length 71 100 % identity

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi 3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 135547

119988 1.R1010 Contig ID

5'-most EST q905880 Method BLASTX NCBI GI g3212868 BLAST score 621 1.0e-64 E value 146 Match length % identity

(AC004005) unknown protein [Arabidopsis thaliana] NCBI Description

135548 Seq. No.

120004_1.R1010 Contig ID

5'-most EST q906839 Method BLASTX



```
NCBI GI
                   q1698548
BLAST score
                   472
                  7.0e-48
E value
                  130
Match length
% identity
                  71
NCBI Description
                  (U58971) calmodulin-binding protein [Nicotiana tabacum]
Seq. No.
                  135549
                  120008 1.R1010
Contig ID
5'-most EST
                  jC-atXP4C85D7T7d1
Method
                  BLASTN
NCBI GI
                  g2351071
BLAST score
                  131
E value
                  5.0e-67
Match length
                  183
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MVA3, complete sequence [Arabidopsis thaliana]
                  135550
Seq. No.
                  120010 1.R1010
Contig ID
5'-most EST
                  jC-atXP4C85D9T7d1
Seq. No.
                  135551
Contig ID
                  120012 1.R1010
5'-most EST
                  q949358
Method
                  BLASTN
NCBI GI
                  q1632775
BLAST score
                   65
E value
                  7.0e-28
Match length
                  287
% identity
                  84
NCBI Description A.thaliana t5r gene
Seq. No.
                  135552
                  120019 1.R1010
Contig ID
5'-most EST
                  q2393588
Method
                  BLASTN
NCBI GI
                  q4580365
BLAST score
                  310
                  1.0e-174
E value
Match length
                  341
                  72
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F3F20 genomic
                  sequence, complete sequence
                  135553
Seq. No.
Contig ID
                  120021 1.R1010
5'-most EST
                  g2393592
                  BLASTX
Method
NCBI GI
                  g4455349
                  308
```

BLAST score E value 5.0e-28 Match length 68 % identity 87

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]



```
Seq. No.
                   135554
Contig ID
                   120022 1.R1010
5'-most EST
                   g501992
Method
                   BLASTX
NCBI GI
                   g2160185
BLAST score
                   411
E value
                   2.0e-40
Match length
                   120
% identity
                   61
                   (ACO00132) Similar to S. pombe ISP4 (gb D83992).
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   135555
                   120034 1.R1010
Contig ID
5'-most EST
                   g2393599
Method
                   BLASTX
NCBI GI
                   g2213615
BLAST score
                   280
E value
                   2.0e-25
Match length
                   75
% identity
                   61
NCBI Description
                  (AC000103) F21J9.9 [Arabidopsis thaliana]
Seq. No.
                   135556
Contig ID
                   120043 1.R1010
5'-most EST
                   g502017
Method
                   BLASTN
NCBI GI
                   g2623294
BLAST score
                   168
E value
                   2.0e-89
Match length
                   382
% identity
                   71
                  Arabidopsis thaliana chromosome II BAC T20B5 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   135557
Contig ID
                   120049 1.R1010
5'-most EST
                   g15657\overline{2}9
Seq. No.
                   135558
Contig ID
                   120051 1.R1010
5'-most EST
                   jC-atX\overline{P}4C88I3T7d1
Method
                   BLASTN
NCBI GI
                   g3063438
BLAST score
                   213
E value
                   1.0e-116
Match length
                   542
                   99
% identity
                  Complete sequence of Arabidopsis F22013, complete sequence
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   135559
Contig ID
                   120054 1.R1010
```

5'-most EST $q50204\overline{5}$ Method BLASTN NCBI GI q3695386 BLAST score 386



E value 0.0e+00 Match length 616 % identity 98

NCBI Description Arabidopsis thaliana BAC T2L5

Seq. No. 135560

Contig ID 120069_1.R1010

5'-most EST g2749522

Method BLASTN

NCBI GI g4756963

BLAST score 163

E value 2.0e-86

Match length 278

% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23

(ESSA project)

Seq. No. 135561

Contig ID 120074 1.R1010

5'-most EST $g50707\overline{6}$

Seq. No. 135562

Contig ID 120081 1.R1010

5'-most EST g2749531
Method BLASTN
NCBI GI g3702722
BLAST score 262
E value 1.0e-145
Match length 383
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K12B20, complete sequence [Arabidopsis thaliana]

Seq. No. 135563

Contig ID 120090_1.R1010 5'-most EST jC-atXP50C180F1T7s1

Method BLASTN
NCBI GI 94468103
BLAST score 144
E value 4.0e-75
Match length 380
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9

(ESSA project)

Seq. No. 135564

Contig ID 120093_1.R1010 5'-most EST jC-atXP50C180F8T7s1

Seq. No. 135565

Contig ID 120100 1.R1010

5'-most EST g2749558
Method BLASTX
NCBI GI g3063691
BLAST score 428
E value 4.0e-42
Match length 124



% identity 60

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 135566

Contig ID 120105 1.R1010

Match length 312 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRB17, complete sequence [Arabidopsis thaliana]

Seq. No. 135567

Contig ID 120110_1.R1010 5'-most EST jC-atXP50C181A7T7s1

Seq. No. 135568

Contig ID 120125 1.R1010

5'-most EST g2749580

Seq. No. 135569

Contig ID 120135_1.R1010

5'-most EST $g27495\overline{8}7$

Seq. No. 135570

Contig ID 120144 1.R1010

5'-most EST jC-atXP76C226O24T7s1

Method BLASTN
NCBI GI g3004543
BLAST score 376
E value 0.0e+00
Match length 420
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F19F24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135571

Contig ID 120150_1.R1010

5'-most EST g17063 Method BLASTX NCBI GI g2529659 BLAST score 496 E value 7.0e-50 Match length 145 % identity 68

NCBI Description (AC002535) putative pectinesterase [Arabidopsis thaliana]

>gi 3738281 (AC005309) putative pectinesterase [Arabidopsis

thaliana]

Seq. No. 135572

Contig ID 120154 1.R1010

5'-most EST jC-atXP40C161K4T7081a1

Method BLASTN NCBI GI g2264307



BLAST score 57 E value 7.0e-23 Match length 205 % identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MED24, complete sequence [Arabidopsis thaliana]

Seq. No. 135573

Contig ID 120154_2.R1010

5'-most EST jC-atXP52C181K21T7d2

Method BLASTN
NCBI GI g2264307
BLAST score 63
E value 2.0e-26
Match length 115
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MED24, complete sequence [Arabidopsis thaliana]

Seq. No. 135574

Contig ID 120156 1.R1010

5'-most EST jC-atXP52C181K22T7s2

Seq. No. 135575

Contig ID 120171_1.R1010 5'-most EST jC-atXP52C181M6T7d2

Seq. No. 135576

Contig ID 120192 1.R1010

5'-most EST jC-atXP52C181P11T7s2

Seq. No. 135577

Contig ID 120198_1.R1010

5'-most EST jC-atXP52C182F18T7d2

Method BLASTX
NCBI GI 94337198
BLAST score 276
E value 3.0e-24
Match length 101
% identity 61

NCBI Description (AC006403) putative auxin-induced protein [Arabidopsis

thaliana]

Seq. No. 135578

Contig ID 120199_1.R1010

5'-most EST jC-atXP52C182F18T7s2

Method BLASTX
NCBI GI g4337198
BLAST score 49
E value 3.0e-28
Match length 87
% identity 78

NCBI Description (AC006403) putative auxin-induced protein [Arabidopsis

thaliana]

Seq. No. 135579

Contig ID 120201 1.R1010



```
5'-most EST
                  jC-atXP52C182G15T7d2
                  135580
Seq. No.
```

Contig ID 120212 1.R1010

5'-most EST jC-atXP52C182J18T7d2

Method BLASTX NCBI GI g126201 BLAST score 52 2.0e-19 E value Match length 76 % identity 67

NCBI Description 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM

> DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi_81676 pir S20510 3-isopropylmalate dehydrogenase (EC $\overline{1}.1.1.\overline{8}5$) $\overline{\text{precursor}}$ rape >gi_17827_emb_CAA42596_ (X59970) 3-isopropylmalate

dehydrogenase [Brassica napus]

Seq. No. 135581

Contig ID 120215 1.R1010 5'-most EST jC-atXP52C182J3T7s2

Seq. No. 135582

Contig ID 120218 1.R1010 5'-most EST jC-atXP98CH2G10T7b1

Method BLASTN NCBI GI q3097257 BLAST score 52 4.0e-20 E value Match length 56 % identity 98

NCBI Description Platichthys flesus Ki-ras gene (exons 1 to 4)

Seq. No. 135583

120218 3.R1010 Contig ID

5'-most EST jC-atXP52C182K23T7d2

Method BLASTX NCBI GI g1706319 BLAST score 397 2.0e-38 E value

Match length 150 52 % identity

NCBI Description HISTIDINE DECARBOXYLASE (HDC) (TOM92)

>gi_481829 pir S39554 histidine decarboxylase (EC 4.1.1.22) - tomato >gi 416534 emb CAA50719 (X71900) histidine decarboxylase [Lycopersicon esculentum]

135584 Seq. No.

Contig ID 120224 1.R1010 5'-most EST jC-atXP52C182L21T7d2

Seq. No. 135585

Contig ID 120226 1.R1010 5'-most EST $jC-atX\overline{P}52C182L2T7d2$

Method BLASTX NCBI GI g2982444 BLAST score 633 E value 3.0e-66



Match length 148 % identity 86

NCBI Description (AL022224) CLV1 receptor kinase like protein [Arabidopsis

thaliana]

Seq. No. 135586

Contig ID 120227 1.R1010

5'-most EST jC-atXP52C182M18T7d2

Seq. No. 135587

Contig ID 120234_1.R1010

5'-most EST g2749636

Seq. No. 135588

Contig ID 120236 1.R1010

5'-most EST g907039

Method BLASTX

NCBI GI g2129581

BLAST score 225

E value 2.0e-18

Match length 90

% identity 50

NCBI Description envelope Ca2+-ATPase precursor - Arabidopsis thaliana

>gi 471089 dbj BAA03091 (D13984) chloroplast envelope

Ca2+-ATPase precursor [Arabidopsis thaliana]

>gi_4165448_emb_CAA49558_ (X69940) envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 135589

Contig ID 120237 1.R1010

5'-most EST jC-at \overline{XP} 52C183B23T7d2

Method BLASTX
NCBI GI 94457221
BLAST score 172
E value 5.0e-12
Match length 50
% identity 62

NCBI Description (AF127797) putative bZIP DNA-binding protein [Capsicum

chinense]

Seq. No. 135590

Contig ID 120239_1.R1010

5'-most EST jC-atXP52C183C13T7d2

Seq. No. 135591

Contig ID 120242_1.R1010

5'-most EST g2749637
Method BLASTX
NCBI GI g3413710
BLAST score 164
E value 4.0e-11
Match length 77
% identity 48

NCBI Description (AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135592

Contig ID 120242 2.R1010



5'-most EST iC-atXP52C183D14T7d2 Method BLASTX NCBI GI q3834319 BLAST score 242 3.0e-20 E value Match length 139 % identity 43 (AC005679) Similar to gi_2244754 heat shock transcription NCBI Description factor HSF30 homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97335. [Arabidopsis thaliana] Seq. No. 135593 Contig ID 120244 1.R1010 $q27496\overline{3}8$ 5'-most EST Method BLASTX NCBI GI q2244740 BLAST score 144 E value 8.0e-09 Match length 69 % identity 42 NCBI Description (D88417) endo-1,4-beta-glucanase [Gossypium hirsutum] Seq. No. 135594 Contig ID 120244 2.R1010 5'-most EST jC-atXP52C183E12T7d2 Seq. No. 135595 Contig ID 120247 1.R1010 5'-most EST q906582 Seq. No. 135596 Contig ID 120250 1.R1010 5'-most EST jC-atXP52C183F22T7s2 Method BLASTN NCBI GI q4325336 BLAST score 286 E value 1.0e-160 Match length 455 % identity 99 NCBI Description Arabidopsis thaliana BAC F15P23 Seq. No. 135597 120256 1.R1010 Contig ID 5'-most EST jC-atXP52C183G24T7s2 Seq. No. 135598

120276 1.R1010 Contig ID

5'-most EST g957510 Method BLASTN NCBI GI g2351063 BLAST score 357 0.0e + 00E value Match length 400 98 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MCL19, complete sequence [Arabidopsis thaliana]



```
Seq. No.
Contig ID
                  120276 2.R1010
                  jC-atXP55C186J7T7d2
5'-most EST
Method
                  BLASTN
NCBI GI
                  q2351063
BLAST score
                  551
E value
                  0.0e+00
Match length
                  965
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCL19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  135600
                  120278 1.R1010
Contig ID
                  g957486
5'-most EST
Method
                  BLASTX
                  g4454051
NCBI GI
BLAST score
                  265
                  6.0e-24
E value
Match length
                  133
% identity
                  46
                  (AL035394) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  135601
                  120279_1.R1010
Contig ID
5'-most EST
                  g2445918
Method
                  BLASTN
                  g3449313
NCBI GI
BLAST score
                  42
                  4.0e-14
E value
Match length
                  118
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K21P3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  135602
Contig ID
                  120285 1.R1010
5'-most EST
                  jC-atXP55C186L2T7s2
Seq. No.
                  135603
Contig ID
                  120288 1.R1010
5'-most EST
                  g957499
Method
                  BLASTX
NCBI GI
                  g4218535
BLAST score
                  593
E value
                  2.0e-61
Match length
                  154
% identity
                   69
NCBI Description
                  (AJ010829) GRAB1 protein [Triticum sp.]
```

135604 Seq. No.

120290 1.R1010 Contig ID

5'-most EST g587049

135605 Seq. No.

Contig ID 120302 1.R1010



```
5'-most EST
                  q2412870
Method
                  BLASTX
                  q4115936
NCBI GI
BLAST score
                  282
E value
                  4.0e-25
Match length
                  54
                  100
% identity
                  (AF118223) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  135606
                  120311 1.R1010
Contig ID
5'-most EST
                  jC-atXP55C187E8T7d2
Method
                  BLASTN
NCBI GI
                  q4589427
BLAST score
                  392
E value
                  0.0e + 00
Match length
                  459
% identity
                  97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFG13, complete sequence
Seq. No.
                  135607
Contig ID
                  120327 1.R1010
5'-most EST
                  jC-atXP55C187I20T7d2
Method
                  BLASTN
                  g3885325
NCBI GI
BLAST score
                  609
E value
                  0.0e + 00
Match length
                  776
% identity
                  98
                  Arabidopsis thaliana chromosome II BAC T20P8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  135608
                  120333 1.R1010
Contig ID
5'-most EST
                  g2733294
Seq. No.
                  135609
                  120343 1.R1010
Contig ID
5'-most EST
                  jC-atXP55C187L17T7d2
Method
                  BLASTX
NCBI GI
                  g4753882
BLAST score
                  350
                  5.0e-33
E value
Match length
                  141
% identity
                  52
                  (AL049754) putative aspartate aminotransferase
NCBI Description
                  [Streptomyces coelicolor]
Seq. No.
                  135610
                  120373 1.R1010
Contig ID
```

 5'-most EST
 g958166

 Method
 BLASTX

 NCBI GI
 g2781359

 BLAST score
 658

 E value
 4.0e-72

 Match length
 163



% identity 88
NCBI Description (AC003113) F2501.15 [Arabidopsis thaliana]

Seq. No. 135611

Contig ID 120378 1.R1010

5'-most EST g2733952
Method BLASTX
NCBI GI g4218991
BLAST score 443
E value 8.0e-44
Match length 99
% identity 91

NCBI Description (AF098632) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 135612

Contig ID 120380 1.R1010

5'-most EST $g95769\overline{3}$

Seq. No. 135613

Contig ID 120391_1.R1010

5'-most EST $q95817\overline{5}$

Seq. No. 135614

Contig ID 120393 1.R1010

5'-most EST g957707

Seq. No. 135615

Contig ID 120395 1.R1010

5'-most EST g870878
Method BLASTX
NCBI GI g2851455
BLAST score 86
E value 3.0e-12
Match length 106
% identity 43

NCBI Description DYNAMIN-LIKE PROTEIN >gi 2267213 (L36939) dynamin-like GTP

binding protein [Arabidopsis thaliana]

Seq. No. 135616

Contig ID 120396 1.R1010

5'-most EST g958176
Method BLASTX
NCBI GI g3269287
BLAST score 509
E value 1.0e-51
Match length 141
% identity 76

NCBI Description (AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No. 135617

Contig ID 120399 1.R1010

 5'-most EST
 g957716

 Method
 BLASTX

 NCBI GI
 g4508076

 BLAST score
 160

 E value
 1.0e-10

 Match length
 101



```
% identity
NCBI Description
                  (AC005882) 55659 [Arabidopsis thaliana]
Seq. No.
                  135618
                  120418 1.R1010
Contig ID
5'-most EST
                  q958228
                  BLASTN
Method
NCBI GI
                  g3449321
BLAST score
                  351
E value
                  0.0e + 00
Match length
                  415
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MTG10, complete sequence [Arabidopsis thaliana]
                  135619
Seq. No.
                  120433 1.R1010
Contig ID
5'-most EST
                  g957861
Method
                  BLASTN
NCBI GI
                  g3510343
BLAST score
                  362
                  0.0e+00
E value
Match length
                  421
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MJC20, complete sequence [Arabidopsis thaliana]
                  135620
Seq. No.
                  120442 1.R1010
Contig ID
5'-most EST
                  g2047453
                  BLASTN
Method
NCBI GI
                  g4220643
BLAST score
                  248
E value
                  1.0e-137
Match length
                  501
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MWD22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  135621
                  120443 1.R1010
Contig ID
5'-most EST
                  jC-atXP58C191M1T7s3
Seq. No.
                  135622
Contig ID
                  120445 1.R1010
5'-most EST
                  jC-atXP58C191L8T7s3
                  135623
Seq. No.
Contig ID
                  120470 1.R1010
5'-most EST
                  jC-atXP58C192F7T7s3
```

Method BLASTX
NCBI GI g1174470
BLAST score 176
E value 2.0e-12
Match length 53
% identity 60

NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)



(INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A integral membrane protein [Mus musculus]

Seq. No. 135624 120481 1.R1010 Contig ID 5'-most EST jC-atXP58C194E8T7s3 Method BLASTN NCBI GI g2341023 BLAST score 302 E value 1.0e-169 Match length 362 % identity 96

NCBI Description Sequence of BAC F19P19 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 135625

Contig ID 120482 1.R1010

5'-most EST g2749702

Seq. No. 135626

Contig ID 120483 1.R1010

5'-most EST jC-atXP117C141N21T7a1

Method BLASTX
NCBI GI g4512701
BLAST score 532
E value 4.0e-54
Match length 136
% identity 73

NCBI Description (AC006569) putative tyrosine decarboxylase [Arabidopsis

thaliana]

Seq. No. 135627

Contig ID 120492_1.R1010

5'-most EST jC-atXP58C194A16T7s3

Method BLASTX
NCBI GI g4501901
BLAST score 146
E value 4.0e-09
Match length 63
% identity 44

NCBI Description aminoacylase 1 >gi 461466 sp Q03154 ACY1 HUMAN

AMINOACYLASE-1 (N-ACYL-L-AMINO-ACID AMIDOHYDROLASE) (ACY-1) >gi 1082202 pir A47488 aminoacylase (EC 3.5.1.14) - human

>qi 178071 (L07548) aminoacylase-1 [Homo sapiens]

>gi_285903_dbj_BAA03397_ (D14524) aminoacylase-1 [Homo sapiens] >gi_303595_dbj_BAA03814_ (D16307) 45kDa protein

[Homo sapiens]

Seq. No. 135628

Contig ID 120501_1.R1010

5'-most EST g2749724
Method BLASTN
NCBI GI g2760165
BLAST score 269
E value 1.0e-150
Match length 289



% identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MAC9, complete sequence [Arabidopsis thaliana]

135629 Seq. No.

120510 1.R1010 Contig ID 5'-most EST jC-atXP58C194K8T7s3

Seq. No. 135630

120513 1.R1010 Contig ID

5'-most EST jC-atXP59C194N2T7d1

Method BLASTX NCBI GI g3080426 BLAST score 294 3.0e-26 E value Match length 170 % identity 38

(AL022604) putative protein [Arabidopsis thaliana] NCBI Description

135631 Seq. No.

120603 1.R1010 Contig ID

5'-most EST g2446231 Method BLASTN NCBI GI g2462264 BLAST score 42

5.0e-14 E value Match length 42 % identity 100

Cucumis sativus mRNA for patatin-like protein, partial NCBI Description

135632 Seq. No.

Contig ID 120615 1.R1010

5'-most EST g2756855 Method BLASTN NCBI GI g2182289 BLAST score 352 0.0e + 00E value 356 Match length % identity 100

Arabidopsis thaliana chromosome I BAC F11P17 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

135633 Seq. No.

Contig ID 120617 1.R1010

5'-most EST g2756837 Method BLASTN NCBI GI g2275194 BLAST score 359 E value 0.0e + 00Match length 464 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC T08I13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135634

Contig ID 120621 1.R1010

5'-most EST g931440



```
Method
                   BLASTX
NCBI GI
                  g2959358
BLAST score
                   640
                   1.0e-66
E value
Match length
                   129
% identity
                   97
NCBI Description (X96758) clathrin coat assembly protein AP17 [Zea mays]
                   135635
Seq. No.
Contig ID
                   120624 1.R1010
5'-most EST
                  q502091
Method
                  BLASTX
NCBI GI
                  q4584521
BLAST score
                   471
E value
                   5.0e-56
Match length
                   144
                   89
% identity
NCBI Description
                  (AL049607) putative protein [Arabidopsis thaliana]
Seq. No.
                   135636
                   120630 1.R1010
Contig ID
5'-most EST
                   q2756848
Method
                   BLASTX
NCBI GI
                   q2435514
BLAST score
                   607
E value
                   5.0e-63
Match length
                   147
                   83
% identity
NCBI Description
                   (AF024504) Similar to serine/threonine protein kinase;
                   coded for by A. thaliana cDNA T20930; coded for by A.
                   thaliana cDNA T43472 [Arabidopsis thaliana]
Seq. No.
                   135637
                   120632 1.R1010
Contig ID
5'-most EST
                   g2756852
                   135638
Seq. No.
                   120633 1.R1010
Contig ID
5'-most EST
                   g2756853
Method
                   BLASTX
NCBI GI
                   g4539335
BLAST score
                   131
                   3.0e-49
E value
Match length
                   208
% identity
                   54
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   135639
                   120635 1.R1010
Contig ID
                   jC-atX\overline{P}5C89I19T7039a1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g16397
BLAST score
                   470
                   0.0e+00
E value
Match length
                   634
% identity
                   99
```

16132

NCBI Description A.thaliana gene for nucleoside diphosphate kinase, exons



```
135640
Seq. No.
                  120639 1.R1010
Contig ID
                  jC-atXP5C90C12T7d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2811031
BLAST score
                  588
E value
                  5.0e-61
Match length
                  142
```

79

% identity NCBI Description BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH)

>gi_2109299_gb_AAB58165.1_ (AF000132) betaine aldehyde

dehydrogenase [Amaranthus hypochondriacus]

135641 Seq. No.

120644 1.R1010 Contig ID

5'-most EST q958208

135642 Seq. No.

Contig ID 120650 1.R1010

5'-most EST jC-atXP61C201E15T7d1

Seq. No. 135643

Contig ID 120658 1.R1010 5'-most EST jC-atXP61C199P11T7d1

BLASTX Method

NCBI GI q3152614 BLAST score 614 9.0e-64 E value Match length 163 80 % identity

NCBI Description (AC004482) unknown protein [Arabidopsis thaliana]

Seq. No. 135644

120666 2.R1010 Contig ID

5'-most EST q1053908 Method BLASTN NCBI GI q3510343 BLAST score 333 E value 0.0e + 00Match length 333 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJC20, complete sequence [Arabidopsis thaliana]

Seq. No. 135645

Contig ID 120678 1.R1010 jC-atXP61C200F5T7d1 5'-most EST

Method BLASTX q4539335 NCBI GI BLAST score 76 1.0e-40 E value Match length 82 99 % identity

(AL035539) putative protein [Arabidopsis thaliana] NCBI Description



```
135646
  Seq. No.
                    120698 1.R1010
  Contig ID
  5'-most EST
                    jC-atXP61C200K24T7d1
                    BLASTX
  Method
                    q82231
  NCBI GI
  BLAST score
                    435
                    4.0e-43
  E value
                    82
  Match length
                    100
  % identity
NCBI Description
                    hypothetical protein 82 - common tobacco chloroplast
                    >gi 225200 prf 1211235AE ORF 82 [Nicotiana tabacum]
  Seq. No.
                    135647
                    120704 1.R1010
  Contig ID
  5'-most EST
                    q1053798
  Method
                    BLASTX
  NCBI GI
                    g4406818
  BLAST score
                    378
  E value
                    3.0e-36
  Match length
                    114
  % identity
  NCBI Description
                     (AC006201) putative transcription factor-like protein
                     [Arabidopsis thaliana]
  Seq. No.
                    135648
                    120710 1.R1010
  Contig ID
  5'-most EST
                    jC-atXP61C200024T7d1
  Method
                    BLASTX
                    g2909448
  NCBI GI
                    212
  BLAST score
                    9.0e-17
  E value
                    64
  Match length
  % identity
                    64
                    (AL021929) fadE5 [Mycobacterium tuberculosis]
  NCBI Description
                    135649
  Seq. No.
                    120712 1.R1010
  Contig ID
  5'-most EST
                    jC-atXP100C268G12T7b1
  Method
                    BLASTX
                    g2462834
  NCBI GI
                    185
  BLAST score
                    9.0e-25
  E value
                    179
  Match length
  % identity
                    39
                    (AF000657) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
                    135650
  Seq. No.
  Contig ID
                    120722 1.R1010
  5'-most EST
                    g1053911
                    135651
  Seq. No.
                    120725 1.R1010
  Contig ID
```

5'-most EST g2413820 Method BLASTX NCBI GI g2194118 BLAST score 166 2.0e-11 E value



Match length 72 % identity

(AC002062) F20P5.4 gene product [Arabidopsis thaliana] NCBI Description

Seq. No. 135652

120739 1.R1010 Contig ID 5'-most EST jC-atXP61C201E2T7d1

Seq. No. 135653

Contig ID 120749 1.R1010 5'-most EST jC-atXP61C201F7T7d1

Method BLASTN NCBI GI q1871173 BLAST score 476 E value 0.0e + 00Match length 501 98 % identity

Arabidopsis thaliana chromosome II BAC T06D20 genomic NCBI Description

sequence, complete sequence

135654 Seq. No.

Contig ID 120754 1.R1010 5'-most EST iC-atXP61C201H9T7d1

Method BLASTN NCBI GI q4510360 BLAST score 210 E value 1.0e-114 Match length 398 % identity 100

Arabidopsis thaliana chromosome II BAC F11F19 genomic NCBI Description

sequence, complete sequence

Seq. No. 135655

120757 1.R1010 Contiq ID

5'-most EST jC-atXP61C201H24T7d1

Seq. No. 135656

120766 1.R1010 Contig ID

5'-most EST jC-atXP2C77F12T7061a1

Method BLASTX g4191788 NCBI GI BLAST score 836 8.0e-90 E value Match length 157 100 % identity

(AC005917) putative 1-aminocyclopropane-1-carboxylate NCBI Description

oxidase [Arabidopsis thaliana]

135657 Seq. No.

120802 1.R1010 Contig ID $jC-atX\overline{P}62C201P3T7d2$ 5'-most EST

Method BLASTX g1817535 NCBI GI BLAST score 144 1.0e-08 E value Match length 54 52 % identity



(D78508) YfiK [Bacillus subtilis] >gi 2633154 emb CAB12659 NCBI Description (Z99108) similar to two-component response regulator [YfiJ] [Bacillus subtilis]

"(. -

135658 Seq. No.

Contig ID 120817 1.R1010

5'-most EST jC-atXP71CF1E2T7096d1

Method BLASTX NCBI GI q2909583 34€ BLAST score E value 1.0e-31 Match length 146 % identity 50

NCBI Description (AL021926) oxcA [Mycobacterium tuberculosis]

135659 Seq. No.

120821 1.R1010 Contig ID

5'-most EST $jC-atX\overline{P}62C202M24T7d2$

BLASTX Method NCBI GI q4104561 BLAST score 289 5.0e-47 E value Match length 242 % identity 41

(AF036960) subtilisin-like protease [Glycine max] NCBI Description

Seq. No. 135660

120821 2.R1010 Contig ID

5'-most EST g2758403 Method BLASTX NCBI GI g4104561 BLAST score 363 E value 2.0e-34 Match length 130 55

% identity

(AF036960) subtilisin-like protease [Glycine max] NCBI Description

135661 Seq. No.

120828 1.R1010 Contig ID jC-atXP62C202P6T7d2 5'-most EST

Method BLASTX g3193309 NCBI GI BLAST score 475 2.0e-47 E value 169 Match length % identity 57

(AF069300) No definition line found [Arabidopsis thaliana] NCBI Description

135662 Seq. No.

120851 1.R1010 Contig ID

jC-atXP62C203F16T7d2 5'-most EST

Method BLASTX g4587607 NCBI GI 521 BLAST score 7.0e-53 E value 212 Match length 81 % identity



NCBI Description (AC006951) putative antisense basic fibroblast growth factor [Arabidopsis thaliana]

Seq. No. 135663 120855 1.R1010 Contia ID 5'-most EST g1054093 Method BLASTX NCBI GI q2979551 BLAST score 219 1.0e-17 E value Match length 102 % identity

NCBI Description (AC003680) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 135664

Contig ID 120858_1.R1010 5'-most EST g1054395 Method BLASTN NCBI GI g2760316 BLAST score 271

BLAST score 271 E value 1.0e-151 Match length 424 % identity 98

NCBI Description The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 135665

Contig ID 120870_1.R1010

5'-most EST g1054409

Method BLASTN

NCBI GI g3080352

BLAST score 285

E value 1.0e-159

Match length 343

% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18

(ESSAII project)

Seq. No. 135666

Contig ID 120876_1.R1010

5'-most EST g1054039
Method BLASTX
NCBI GI g4415924
BLAST score 418
E value 4.0e-41
Match length 95
% identity 83

NCBI Description (AC006282) putative glucosyl transferase [Arabidopsis

thaliana]

Seq. No. 135667

Contig ID 120877_1.R1010

5'-most EST $g24460\overline{3}6$ Method BLASTN NCBI GI g4415905 BLAST score 45



E value 6.0e-16 Match length 547 % identity 52

NCBI Description Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

- 、

Seq. No. 135668

Contig ID 120879 1.R1010

5'-most EST jC-atXP63C2O3I13T7s2

Method BLASTN
NCBI GI g2058275
BLAST score 162
E value 3.0e-86
Match length 162
% identity 100

NCBI Description A.thaliana atran2 gene

Seq. No. 135669

Contig ID 120882 1.R1010

NCBI Description Arabidopsis thaliana chromosome I BAC F21M11 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135670

Contig ID 120898_1.R1010

5'-most EST jC-atXP63C2O3N14T7d2

Method BLASTX
NCBI GI g2460200
BLAST score 124
E value 4.0e-15
Match length 137
% identity 38

NCBI Description (AF020833) eukaryotic translation initiation factor 3

subunit [Homo sapiens]

Seq. No. 135671

Contig ID 120904_1.R1010 5'-most EST jC-atXP63C203O6T7d2

Seq. No. 135672

Contig ID 120910 1.R1010

5'-most EST $g24460\overline{4}6$

Seq. No. 135673

Contig ID 120915 2.R1010

5'-most EST jC-atXP20C116B6T7088a1

Seq. No. 135674

Contig ID 120920_1.R1010 5'-most EST jC-atXP63C204G7T7d2



```
135675
   Seq. No.
                      120922 1.R1010
   Contig ID
                      g2446061
   5'-most EST
   Method
                     BLASTX
   NCBI GI
                      g3269297
   BLAST score
                      61
                      2.0e-16
   E value
   Match length
                      77
NCBI Description
                      58
                      (AL030978) putative protein [Arabidopsis thaliana]
   Seq. No.
                      135676
                      120922 2.R1010
   Contig ID
                      q1054096
   5'-most EST
                      BLASTN
   Method
                      a3046855
   NCBI GI
   BLAST score
                      354
   E value
                      0.0e + 00
                      515
   Match length
                      97
   % identity
                     Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
   NCBI Description
                      MSL1, complete sequence [Arabidopsis thaliana]
   Seq. No.
                      135677
                      120944 1.R1010
   Contig ID
                      jC-atXP63C204K18T7d2
   5'-most EST
                      BLASTN
   Method
                      a4468103
   NCBI GI
   BLAST score
                      315
                      1.0e-177
   E value
                      556
   Match length
                      98
   % identity
                      Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9
   NCBI Description
                      (ESSA project)
   Seq. No.
                      135678
                      120946 1.R1010
   Contig ID
                      jC-atXP63C204K1T7d2
   5'-most EST
                      135679
   Seq. No.
                      120948 2.R1010
   Contig ID
                      jC-atXP63C204K9T7d2
   5'-most EST
   Method
                      BLASTX
   NCBI GI
                      g1617270
   BLAST score
                      791
                      2.0e-84
   E value
   Match length
                      197
                      73
   % identity
                      (X94624) acyl-CoA synthetase [Brassica napus]
   NCBI Description
                      135680
   Seq. No.
                      120953 1.R1010
   Contig ID
   5'-most EST
                      g906756
```

Seq. No. 135681

Contig ID 120956_1.R1010 5'-most EST g2446068

Contig ID



```
Method
                     BLASTX
  NCBI GI
                     q2880054
  BLAST score
                     389
  E value
                     1.0e-37
  Match length
                     76
                     96
  % identity
                    (AC002340) putative cytochrome P450 [Arabidopsis thaliana]
  NCBI Description
                     135682
  Seq. No.
                    ·120961 1.R1010
  Contig ID
5'-most EST
                     g2446070
  Method
                     BLASTX
  NCBI GI
                     q3892059
  BLAST score
                     49
  E value
                     3.0e-36
  Match length
                     101
                     79
  % identity
                     (AC002330) predicted protein of unknown function
  NCBI Description
                     [Arabidopsis thaliana]
                     135683
  Seq. No.
  Contig ID
                     120961 2.R1010
                     jC-atX\overline{P}63C205D17T7d2
  5'-most EST
  Method
                     BLASTX
                     g3892059
  NCBI GI
  BLAST score
                     778
                     4.0e-83
  E value
  Match length
                     182
  % identity
                     88
                     (AC002330) predicted protein of unknown function
  NCBI Description
                     [Arabidopsis thaliana]
                     135684
  Seq. No.
  Contig ID
                     120969 1.R1010
  5'-most EST
                     g2446076
  Method
                     BLASTN
  NCBI GI
                     g3337347
  BLAST score
                     202
  E value
                     1.0e-109
  Match length
                     406
  % identity
                     98
                     Arabidopsis thaliana chromosome II BAC F13P17 genomic
  NCBI Description
                     sequence, complete sequence [Arabidopsis thaliana]
                     135685
  Seq. No.
                     120974 1.R1010
  Contig ID
  5'-most EST
                     jC-atXP63C205A3T7s2
  Method
                     BLASTX
                     g2342736
  NCBI GI
  BLAST score
                     343
                     3.0e - 32
  E value
  Match length
                     65
                     100
  % identity
                     (AC002341) unknown protein [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
                     135686
```

16140

120979 1.R1010



```
g1054441
5'-most EST
                  BLASTN
Method
                  g2342717
NCBI GI
                  272
BLAST score
                  1.0e-151
E value
Match length
                  329
% identity
                  98
                  Arabidopsis thaliana chromosome II BAC T14G11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   135687
Contig ID
                  120986 1.R1010
5'-most EST
                   jC-atXP63C205C13T7s2
Method
                  BLASTN
                   q2795802
NCBI GI
BLAST score
                   339
E value
                   0.0e + 00
Match length
                   423
% identity
                  Arabidopsis thaliana chromosome II BAC F17A14 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   135688
Seq. No.
                   120997 1.R1010
Contig ID
5'-most EST
                   q2413482
                   135689
Seq. No.
Contia ID
                   121013 1.R1010
                   iC-atXP65C206L10T7049d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4585877
                   399
BLAST score
E value
                   2.0e-38
Match length
                   277
% identity
                  (AC005850) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   135690
Seq. No.
                   121020 1.R1010
Contig ID
                   jC-atX\overline{P}64C205K1T7d1
5'-most EST
                   BLASTN
Method
                   g2264312
NCBI GI
BLAST score
                   333
E value
                   0.0e+00
                   384
Match length
                   97
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MOK16, complete sequence [Arabidopsis thaliana]
                   135691
Seq. No.
                   121027 1.R1010
```

Contig ID 121027_1.R1010 5'-most EST jC-atXP64C205L7T7s1

Seq. No. 135692

Contig ID 121034 1.R1010 5'-most EST jC-atXP64C205M23T7d1

Method BLASTX

```
q3063691
NCBI GI
BLAST score
                  515
E value
                   2.0e-52
Match length
                  145
% identity
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                  135693
                  121037 1.R1010
Contig ID
5'-most EST
                  g11586\overline{8}5
Seq. No.
                   135694
                   121044 1.R1010
Contig ID
5'-most EST
                  q1199979
                   135695
Seq. No.
                   121053 1.R1010
Contig ID
5'-most EST
                  g1158300
                   135696
Seq. No.
Contig ID
                   121068 1.R1010
5'-most EST
                   g906121
Method
                   BLASTX
                   g4432854
NCBI GI
                   158
BLAST score
                   2.0e-10
E value
                   106
Match length
% identity
                   36
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]
                   135697
Seq. No.
Contig ID
                   121070 1.R1010
5'-most EST
                   q1565842
Method
                   BLASTX
                   g2809246
NCBI GI
BLAST score
                   294
E value
                 -1.0e-26
Match length
                   163
% identity
NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]
                   135698
Seq. No.
                   121073 1.R1010
Contig ID
5'-most EST
                   g1158781
Method
                   BLASTX
NCBI GI
                   g3337361
BLAST score
                   1042
E value
                   1.0e-114
                   194
Match length
                   97
% identity
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]
```

135699 Seq. No.

121074 1.R1010 Contig ID g2413829 5'-most EST

BLASTX Method g3337361 NCBI GI



```
BLAST score
E value
                   3.0e-18
                   63
Match length
                   75
% identity
                   (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
                   135700
Seq. No.
                   121096 1.R1010
Contig ID
5'-most EST
                   jC-atX\overline{P}65C206O16T7s1
Method
                  BLASTN
NCBI GI
                   g4757414
BLAST score
                   349
E value
                   0.0e + 00
Match length
                   406
                   95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MYF24, complete sequence
                   135701
Seq. No.
Contig ID
                   121105 1.R1010
5'-most EST
                   g2047492
                   135702
Seq. No.
Contig ID
                   121114_1.R1010
5'-most EST
                   g2048687
Method
                   BLASTN
                   g4757412
NCBI GI
BLAST score
                   336
E value
                   0.0e + 00
Match length
                   482
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXK23, complete sequence
                   135703
Seq. No.
                   121119_1.R1010
Contig ID
5'-most EST
                   q2062775
                   BLASTX
Method
NCBI GI
                   q2983814
BLAST score
                   511
E value
                   1.0e-51
Match length
                   197
% identity
                   54
                   (AE000739) tryptophan synthase beta subunit [Aquifex
NCBI Description
                   aeolicus]
Seq. No.
                   135704
                   121124 1.R1010
Contig ID
5'-most EST
                   g936461
Method
                   BLASTX
                   g2832641
NCBI GI
                   335
BLAST score
                   2.0e-31
E value
Match length
                   68
                   97
% identity
                   (AL021710) glycolate oxidase - like protein [Arabidopsis
NCBI Description
```

thaliana]

Method

NCBI GI



```
135705
Seq. No.
                  121125 1.R1010
Contig ID
                  jC-atXP65C208J23T7071d1
5'-most EST
                  BLASTX
Method
                  g4741197
NCBI GI
                  281
BLAST score
                  8.0e-25
E value
Match length
                  145
% identity
                  43
                  (AL049746) aldose 1-epimerase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  135706
Seq. No.
                  121141 1.R1010
Contig ID
                  jC-atXP66C208N17T7d1
5'-most EST
                  BLASTN
Method
                  g2564045
NCBI GI
                  277
BLAST score
                  1.0e-154
E value
                  415
Match length
                  94
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K8K14, complete sequence [Arabidopsis thaliana]
                  135707
Seq. No.
                  121144 1.R1010
Contig ID
                  g1158479
5'-most EST
                  BLASTX
Method
                  g136125
NCBI GI
BLAST score
                  150
                  1.0e-09
E value
                  92
Match length
                   35
% identity
                  PUTATIVE AC TRANSPOSASE (ORFA) >gi_22113_emb_CAA29005_
NCBI Description
                   (X05424) ORFa [Zea mays]
                   135708
Seq. No.
Contig ID
                   121145 1.R1010
5'-most EST
                   q1158846
Method
                   BLASTX
                   g3367537
NCBI GI
                   147
BLAST score
                   4.0e-16
E value
Match length
                   106
% identity
                   48
                   (AC004392) Contains similarity to ANK repeat region of
NCBI Description
                   Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi_485107
                   from Caenorhabditis elegans cosmid gb U00049. This gene is
                   continued from unannotated gene on BAC F19K23 gb_AC000375.
                   [Arabid
                   135709
Seq. No.
                   121149 1.R1010
Contig ID
5'-most EST
                   jC-atXP66C209H10T7d1
```

BLASTN

g2828184

E value Match length

% identity

```
BLAST score
                   9.0e-39
E value
Match length
                   383
                   55
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSN9, complete sequence [Arabidopsis thaliana]
                   135710
Seq. No.
                   121161 1.R1010
Contig ID
                   jC-atXP66C210F5T7d1
5'-most EST
                    135711
Seq. No.
                    121163 1.R1010
Contig ID
5'-most EST
                    jC-atXP66C210G15T7d1
                    135712
Seq. No.
                    121168 1.R1010
Contig ID
                    g11585\overline{2}6
5'-most EST
                    BLASTX
Method
                    q4455158
NCBI GI
BLAST score
                    551
                    2.0e-56
E value
                    169
Match length
                    70
 % identity
                   (AL021687) kinase-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    135713
                    121173 1.R1010
Contig ID
                    jC-atXP66C211F3T7d1
5'-most EST
                    135714
 Seq. No.
                    121181 1.R1010
 Contig ID
 5'-most EST
                    g1159030
                    BLASTX
Method
 NCBI GI
                    g2829899
 BLAST score
                    194
                    1.0e-14
 E value
 Match length
                    64
                    59
 % identity
                    (AC002311) similar to ripening-induced protein,
 NCBI Description
                    gp AJ001449 2465015 and major#latex protein,
                    gp X91961 1107495 [Arabidopsis thaliana]
                    135715
 Seq. No.
 Contig ID
                    121185 1.R1010
                    g1159007
 5'-most EST
                    135716
 Seq. No.
 Contig ID
                    121191 1.R1010
                    g11590\overline{1}1
 5'-most EST
 Method
                    BLASTX
                    q266922
 NCBI GI
 BLAST score
                    148
```

16145

NCBI Description 50S RIBOSOMAL PROTEIN L13 >gi_97861_pir__S23063 ribosomal

2.0e-09

92



protein L13 - Staphylococcus carnosus
>gi_46912_emb_CAA45367_ (X63912) ribosomal protein L13
[Staphylococcus carnosus] >gi_383760_prf__1904196A
ribosomal protein L13 [Staphylococcus carnosus]

Seq. No. 135717 Contig ID 121192 1.R1010

5'-most EST g1159012

Seq. No. 135718

Contig ID 121194 1.R1010

5'-most EST g1158591
Method BLASTX
NCBI GI g2864615
BLAST score 367
E value 1.0e-40

Match length 138 % identity 70

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 135719

Contig ID 121213_1.R1010

5'-most EST g1158626

Method BLASTN

NCBI GI g2182285

BLAST score 116

E value 2.0e-58

Match length 384

% identity 96

NCBI Description Sequence of BAC F5I14 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 135720

Contig ID 121221_1.R1010

5'-most EST g1158640
Method BLASTX
NCBI GI g3249096
BLAST score 453
E value 4.0e-45
Match length 110
% identity 27

NCBI Description (AC003114) Match to mRNA for importin alpha-like protein 4

(impa4) gb_Y14616 from A. thaliana. ESTs gb_N96440, gb_N37503, gb_N37498 and gb_T42198 come from this gene.

[Arabidopsis thaliana]

Seq. No. 135721

Contig ID 121224 1.R1010

5'-most EST g1159062
Method BLASTX
NCBI GI g1931652
BLAST score 514
E value 3.0e-52
Match length 114
% identity 87

NCBI Description (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog

[Arabidopsis thaliana]

NCBI Description



```
Seq. No.
                     135722
                     121228 1.R1010
 Contig ID
                     g11590\overline{6}7
 5'-most EST
                     135723
 Seq. No.
                     121231 1.R1010
 Contig ID
 5'-most EST
                     g1159073
                     BLASTN
 Method
                     g3063690
NCBI GI
 BLAST score
                     316
                     1.0e-178
 E value
 Match length
                     463
 % identity
                     93
                    Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11
 NCBI Description
                     (ESSAII project)
                     135724
 Seq. No.
                     121255_1.R1010
 Contig ID
 5'-most EST
                     g11586\overline{6}5
                     135725
 Seq. No.
                     121258 1.R1010
 Contig ID
 5'-most EST
                     jC-atX\overline{P}68C214F17T7s1
                     BLASTN
 Method
                     g4159705
 NCBI GI
 BLAST score
                     520
                     0.0e+00
 E value
 Match length
                     610
 % identity
                     98
                     Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
 NCBI Description
                     MGD8, complete sequence
                     135726
 Seq. No.
                     121290_1.R1010
 Contig ID
                     g11591<del>6</del>1
 5'-most EST
 Method
                     BLASTN
                     g4757388
 NCBI GI
 BLAST score
                     361
 E value
                     0.0e + 00
 Match length
                     462
                     95
  % identity
                     Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                     F15L12, complete sequence
                     135727
 Seq. No.
                     121294 1.R1010
 Contig ID
 5'-most EST
                     q3449412
 Method
                     BLASTN
 NCBI GI
                     q4159706
 BLAST score
                     184
 E value
                     5.0e-99
 Match length
                     309
  % identity
                     96
                     Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
```

MGL6, complete sequence



```
135728
Seq. No.
                   121299 1.R1010
Contig ID
5'-most EST
                   g1159549
Seq. No.
                   135729
                   121307 1.R1010
Contiq ID
                   q550267
5'-most EST
                   BLASTN
Method
                   g2564046
NCBI GI
BLAST score
                   309
                   1.0e-173
E value
Match length
                   349
                   98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MGI19, complete sequence [Arabidopsis thaliana]
Seq. No.
                   135730
                   121338 1.R1010
Contig ID
                   g1159231
5'-most EST
Seq. No.
                   135731
                   121347 1.R1010
Contig ID
5'-most EST
                   g1159610
Method
                   BLASTX
                   g1730107
NCBI GI
BLAST score
                   174
                   2.0e-12
E value
Match length
                   108
% identity
                   36
                   LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN
NCBI Description
                   HYDROXYLASE) >gi_421870_pir__S33144 anthocyanidin
hydroxylase - apple tree >gi_296844_emb_CAA50498_ (X71360)
                   anthocyanidin hydroxylase [Malus sp.]
                   >gi_4588783_gb_AAD26205.1_AF117269_1 (AF117269)
                   anthocyanidin synthase [Malus domestica]
                   135732
Seq. No.
                   121359 1.R1010
Contig ID
5'-most EST
                   g2596253
Method
                   BLASTX
                   g4128197
NCBI GI
BLAST score
                    142
                    1.0e-08
E value
                    49
Match length
                    61
% identity
                   (U75273) acyl-CoA binding protein [Arabidopsis thaliana]
NCBI Description
                    135733
Seq. No.
                    121360_1.R1010
Contig ID
5'-most EST
                    jC-atXP6C90H3T7s1
Seq. No.
                    135734
```

Contig ID 121371 1.R1010

5'-most EST g2393647
Method BLASTN
NCBI GI g4678705
BLAST score 238



```
1.0e-131
E value
Match length
                   322
% identity
                   93
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
NCBI Description
                   (ESSA project)
                   135735
Seq. No.
Contig ID
                   121383 1.R1010
                   jC-atXP6C90L24T7d1
5'-most EST
                   BLASTN
Method
                   g3702737
NCBI GI
BLAST score
                   283
                   1.0e-158
E value
Match length
                   327
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSN2, complete sequence [Arabidopsis thaliana]
                   135736
Seq. No.
                   121385_1.R1010
Contig ID
5'-most EST
                   g773541
                   BLASTX
Method
                   g2213601
NCBI GI
BLAST score
                   840
E value
                   2.0e-90
                   196
Match length
% identity
                   81
                   (AC000348) T7N9.21 [Arabidopsis thaliana]
NCBI Description
                   135737
Seq. No.
                   121391 1.R1010
Contig ID
                   g23936<del>5</del>1
5'-most EST
                   BLASTN
Method
                   g3702737
NCBI GI
BLAST score
                   171
                   3.0e-91
E value
Match length
                   345
                   97
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSN2, complete sequence [Arabidopsis thaliana]
                   135738
Seq. No.
                   121396 1.R1010
Contig ID
5'-most EST
                   jC-atXP6C90M3T7d1
                   135739
Seq. No.
Contig ID
                   121422 1.R1010
```

5'-most EST g2756858

Seq. No. 135740

Contig ID 121432 1.R1010

 5'-most EST
 g2393657

 Method
 BLASTN

 NCBI GI
 g4584387

 BLAST score
 324

 E value
 0.0e+00

 Match length
 446



% identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project) 135741 Seq. No. 121445 1.R1010 Contig ID 5'-most EST jC-atXP6C91C2T7d1 BLASTN Method g2696018 NCBI GI BLAST score 405 0.0e+00E value Match length 506 % identity 96 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana] 135742 Seq. No. 121451 1.R1010 Contig ID 5'-most EST jC-atXP6C91C4T7d1 Seq. No. 135743 121459 1.R1010 Contig ID 5'-most EST jC-atXP44C170H13T7036a1 Method ${\tt BLASTX}$ NCBI GI g2565436 BLAST score 218 3.0e-17 E value Match length 115 42 % identity NCBI Description (AF028842) DegP protease precursor [Arabidopsis thaliana] 135744 Seq. No. 121484 1.R1010 Contig ID 5'-most EST jC-atXP6C91E5T7d2 Method BLASTX NCBI GI g4056500 477 BLAST score 1.0e-53 E value Match length 127 94 % identity (AC005896) putative acetyltransferase [Arabidopsis NCBI Description thaliana] 135745 Seq. No. Contig ID 121487_1.R1010 q15657825'-most EST BLASTX Method NCBI GI q1723376

BLAST score 77 E value 4.0e-18

Match length 125 % identity NCBI Description

HYPOTHETICAL 20.1 KD PROTEIN IN YCF37-PSAF INTERGENIC REGION (ORF174) >gi_2147509_pir__S73113 hypothetical protein 174 - Porphyra purpurea chloroplast >gi_1276658

(U38804) ORF174 [Porphyra purpurea]

```
Seq. No.
                  135746
Contig ID
                  121497 1.R1010
                  g2747887
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2827541
BLAST score
                  495
                  6.0e-50
E value
Match length
                  106
% identity
                  92
                  (AL021635) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 135747

Contig ID 121528_1.R1010 5'-most EST jC-atXP70C221C16T7d1

Method BLASTN
NCBI GI g2914688
BLAST score 463
E value 0.0e+00
Match length 499
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

 Seq. No.
 135748

 Contig ID
 121547_1.R1010

 5'-most EST
 jC-atXP71C221H24T7s2

 Method
 BLASTX

 NCBI GI
 g4249403

 BLAST score
 617

NCBI GI g4249403
BLAST score 617
E value 3.0e-64
Match length 140
% identity 89

NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 135749

Contig ID 121565_1.R1010

5'-most EST jC-atXP71C222J18T7089d1

Seq. No. 135750

Contig ID 121571 1.R1010 5'-most EST jC-atXP71C222M14T7s2

Method BLASTN
NCBI GI g3449313
BLAST score 153
E value 4.0e-80

Match length 539 % identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21P3, complete sequence [Arabidopsis thaliana]

Seq. No. 135751

Contig ID 121574_1.R1010 5'-most EST jC-atXP71C222M6T7s2

Method BLASTN
NCBI GI g2924651
BLAST score 274
E value 1.0e-153



Match length 349 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K2A18, complete sequence [Arabidopsis thaliana]

Seq. No. 135752

Contig ID 121584_1.R1010 5'-most EST jC-atXP71C22209T7s2

Seq. No. 135753

Contig ID 121589_1.R1010

5'-most EST g1159394

Seq. No. 135754

Contig ID 121591_1.R1010

5'-most EST jC-atXP72C221M23T7d1

Method BLASTX
NCBI GI g2078350
BLAST score 612
E value 1.0e-63
Match length 160
% identity 77

NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 135755

Contig ID 121604_1.R1010

5'-most EST g1216552
Method BLASTX
NCBI GI g2492519
BLAST score 613
E value 1.0e-72
Match length 152

% identity 93

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT

7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase

subunit [Spinacia oleracea]

Seq. No. 135756

Contig ID 121618_1.R1010 5'-most EST jC-atXP72C221O6T7d1

Method BLASTN
NCBI GI g2264305
BLAST score 306
E value 1.0e-172
Match length 409
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBK23, complete sequence [Arabidopsis thaliana]

Seq. No. 135757

Contig ID 121645 1.R1010

5'-most EST jC-atXP121C95J22T7068d1

Method BLASTX
NCBI GI g4454032
BLAST score 189
E value 5.0e-14
Match length 131



```
% identity
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
                   135758
Seq. No.
                   121722 1.R1010
Contig ID
5'-most EST
                   g2393388
Seq. No.
                   135759
Contig ID
                   121727 1.R1010
                   jC-atXP75C226L2T7d1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q2570223
BLAST score
                   556
                   0.0e + 00
E value
                   614
Match length
                   100
% identity
                  Arabidopsis thaliana chromosome 1 BAC F20D22 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   135760
Seq. No.
                   121745 1.R1010
Contig ID
                   jC-atX\overline{P}75C228D21T7d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2982464
                   225
BLAST score
                   3.0e-18
E value
Match length
                   112
% identity
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]
                   135761
Seq. No.
                   121756 1.R1010
Contig ID
5'-most EST
                   jC-atXP75C228F20T7d1
Method
                   BLASTN
NCBI GI
                   q3241927
BLAST score
                   676
E value
                   0.0e+00
Match length
                   684
% identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MTE17, complete sequence [Arabidopsis thaliana]
                   135762
Seq. No.
                   121803 1.R1010
Contig ID
5'-most EST
                   jC-atX\overline{P}76C226021T7s1
```

BLASTN Method NCBI GI q4586098 BLAST score 333

E value 0.0e + 00389 Match length % identity

Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 NCBI Description

(ESSA project)

135763 Seq. No.

121809 1.R1010 Contig ID 5'-most EST g2412862



```
Method BLASTX
NCBI GI g2618691
BLAST score 406
E value 1.0e-39
Match length 111
% identity 75
```

NCBI Description (AC002510) putative chloroplast envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No. 135764

Contig ID 121899_1.R1010

5'-most EST jC-atXP76C227L17T7d1
Method BLASTX

Method BLASTX
NCBI GI g3776567
BLAST score 336
E value 9.0e-84
Match length 183
% identity 86

NCBI Description (AC005388) Strong similarity to F21B7.33 gi_2809264 from A.

thaliana BAC gb_AC002560. EST gb_N65119 comes from this

gene. [Arabidopsis thaliana]

Seq. No. 135765

Contig ID 121903_1.R1010

5'-most EST g1216747
Method BLASTN
NCBI GI g3869067
BLAST score 372
E value 0.0e+00
Match length 459
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCK7, complete sequence [Arabidopsis thaliana]

Seq. No. 135766

Contig ID 121905 1.R1010

5'-most EST g1216749
Method BLASTX
NCBI GI g3912919
BLAST score 597
E value 9.0e-70
Match length 142
% identity 97

NCBI Description (AF001308) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135767

Contig ID 121926 1.R1010

5'-most EST g2749655
Method BLASTX
NCBI GI g3738296
BLAST score 247
E value 7.0e-21
Match length 112
% identity 46

NCBI Description (AC005309) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135768

```
121926 2.R1010
Contig ID
5'-most EST
                  q958238
Method
                   BLASTN
                  g2656026
NCBI GI
BLAST score
                   458
                  0.0e+00
E value
                   526
Match length
% identity
                   98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   135769
Seq. No.
Contig ID
                   121944_1.R1010
                   g12173\overline{3}9
5'-most EST
Method
                   BLASTN
                  q3608126
NCBI GI
BLAST score
                   211
E value
                   1.0e-115
Match length
                   430
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC T32F12 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   135770
                   121948 1.R1010
Contig ID
                   g1217334
5'-most EST
Method
                   BLASTX
                   q2832618
NCBI GI
BLAST score
                   512
                   5.0e-52
E value
                   138
Match length
                   43
% identity
NCBI Description
                   (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                   135771
                   121955 1.R1010
Contig ID
                   g2749507
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2117725
BLAST score
                   371
                   2.0e-35
E value
                   87
Match length
% identity
                   80
                   1,4-alpha-glucan branching enzyme (EC 2.4.1.18) isoform
NCBI Description
                   SBE2.2 precursor - Arabidopsis thaliana (fragment)
                   >gi 726490 (U22428) starch branching enzyme class II
                   [Arabidopsis thaliana]
Seq. No.
                   135772
                   121978 1.R1010
Contig ID
5'-most EST
                   q1217107
                   135773
```

Seq. No.

121979 1.R1010 Contig ID

5'-most EST g2749283

135774 Seq. No.



```
122004 1.R1010
Contig ID
                   jC-atXP77C230H20T7d1
5'-most EST
                  BLASTN
Method
                   q2656032
NCBI GI
                   152
BLAST score
                   6.0e-80
E value
Match length
                   425
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
Seq. No.
                   135775
Contig ID
                   122019 1.R1010
                   jC-atXP77C230K17T7d1
5'-most EST
                   135776
Seq. No.
                   122045 1.R1010
Contig ID
5'-most EST
                   jC-atXP7C91I21T7d1
                   135777
Seq. No.
Contig ID
                   122065 1.R1010
                   jC-atXP7C91K17T7d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3337352
BLAST score
                   250
E value
                   2.0e-29
Match length
                   138
% identity
                   59
                   (AC004481) putative chromatin structural protein Supt5hp
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   135778
Contig ID
                   122067 1.R1010
5'-most EST
                   q3450510
                   BLASTN
Method
NCBI GI
                   g4581103
BLAST score
                   150
E value
                   1.0e-78
Match length
                   393
% identity
                   93
                   Arabidopsis thaliana chromosome II BAC T24I21 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   135779
                   122072 1.R1010
Contig ID
                   jC-atXP7C91L10T7s1
5'-most EST
Method
                   BLASTX
                   g2194119
NCBI GI
BLAST score
                   445
                   2.0e-44
E value
                   86
Match length
                   94
% identity
                  (AC002062) No definition line found [Arabidopsis thaliana]
NCBI Description
```

45

135780

122073 1.R1010

jC-atXP7C91L2T7d1

Seq. No.

Contig ID 5'-most EST



```
BLASTX
Method
NCBI GI
                  g2252851
                                                , T.
BLAST score
                  689
                  1.0e-72
E value
                  171
Match length
                  87
% identity
                  (AF013294) No definition line found [Arabidopsis thaliana]
NCBI Description
                  135781
Seq. No.
                  122076 1.R1010
Contig ID
5'-most EST
                  jC-atXP7C91M17T7d1
Method
                  BLASTX
NCBI GI
                  q4056462
                  662
BLAST score
E value
                  9.0e-70
Match length
                  128
% identity
                  (AC005990) Strong similarity to gb Y09876 aldehyde
NCBI Description
                  dehydrogenase (NAD+) from Nicotiana tabacum and a member of
                   the aldehyde dehydrogenase family PF_00171. ESTs
                   gb F15117, gb R83958 and gb 586262 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  135782
Contig ID
                  122077 1.R1010
                  q2393671
5'-most EST
Method
                  BLASTX
                  q3337352
NCBI GI
BLAST score
                   59
                   8.0e-15
E value
                   70
Match length
                   64
% identity
                   (AC004481) putative chromatin structural protein Supt5hp
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   135783
                   122083 1.R1010
Contig ID
5'-most EST
                   q2393673
                   BLASTN
Method
NCBI GI
                   q2252848
BLAST score
                   354
E value
                   0.0e + 00
                   390
Match length
% identity
                   98
                  Arabidopsis thaliana BAC TM018A10
NCBI Description
Seq. No.
                   135784
                   122087 1.R1010
Contig ID
```

5'-most EST q2393679 Method BLASTX g2495120 NCBI GI 207 BLAST score 3.0e-16 E value Match length 102 40 % identity

POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THOF NCBI Description >gi 1652979 dbj BAA17896_ (D90910) thiophen and furan



oxidation protein [Synechocystis sp.]

```
135785
Seq. No.
                   122089 1.R1010
Contig ID
5'-most EST
                   g2393677
Seq. No.
                   135786
                   122094 1.R1010
Contig ID
5'-most EST
                  g2757021
                   135787
Seq. No.
Contig ID
                   122095 1.R1010
5'-most EST
                   jC-atXP7C91P20T7d1
                   BLASTX
Method
                   a1524359
NCBI GI
                   408
BLAST score
                   7.0e-40
E value
Match length
                   135
% identity
                   60
                  (X98090) GTPase [Synechocystis PCC6803]
NCBI Description
                   135788
Seq. No.
Contig ID
                   122098 1.R1010
5'-most EST
                   q2047552
                   BLASTX
Method
                   q4581117
NCBI GI
                   554
BLAST score
                   2.0e-58
E value
```

Match length 121 93 % identity

(AC005825) putative ubiquitin-conjugating enzyme NCBI Description

E2;GB:T21483 appears to be a partially-spliced transcript

from this gene [Arabidopsis thaliana]

Seq. No. 135789 Contig ID 122109 1.R1010

5'-most EST q1565823 Method BLASTX NCBI GI g1709358 BLAST score 176 1.0e-12 E value Match length 98 38 % identity

NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE NCBI Description

PHOSPHOHYDROLASE) (NTPASE) >gi_629638_pir__S48859

nucleoside triphosphatase - garden pea

>gi 2129890 pir S65147 nucleoside triphosphatase

precursor, chromatin-associated - garden pea

>qi 563612 emb CAA83655 (Z32743) nucleoside triphosphatase

[Pisum satīvum] >qi 4519173 dbj BAA75506.1 (AB022319)

nucleoside triphosphatase (NTPase) [Pisum sativum]

135790 Seq. No.

NCBI GI

122126 1.R1010 Contig ID $g34504\overline{8}2$ 5'-most EST BLASTN Method

q2980787



```
BLAST score
E value
                   1.0e-157
Match length
                   459
% identity
                   62
                  Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2
NCBI Description
                   (ESSAII project)
                   135791
Seq. No.
                   122131 1.R1010
Contig ID
5'-most EST
                   g2747550
                   BLASTX
Method
NCBI GI
                   g3335374
BLAST score
                   605
                   6.0e-63
E value
Match length
                   123
                   95
% identity
                  (ACO03028) glutaredoxin-like protein [Arabidopsis thaliana]
NCBI Description
                   135792
Seq. No.
                   122144 1.R1010
Contig ID
5'-most EST
                   jC-atXP7C92D2T7s1
                   BLASTX
Method
                   g3386565
NCBI GI
BLAST score
                   218
                   1.0e-17
E value
Match length
                   69
                   64
% identity
                   (AF079588) 1-aminocyclopropane-1-carboxylate oxidase
NCBI Description
                   [Sorghum bicolor]
                   135793
Seq. No.
                   122150 1.R1010
Contig ID
5'-most EST
                   q27483\overline{9}4
Method
                   BLASTX
                   q3080441
NCBI GI
BLAST score
                   185
E value
                   9.0e-14
                   96
Match length
                   50
% identity
NCBI Description
                   (AL022605) putative protein [Arabidopsis thaliana]
                   135794
Seq. No.
                   122152 1.R1010
Contig ID
5'-most EST
                   jC-atX\overline{P}80C231L1T7d1
Method
                   BLASTN
NCBI GI
                   q4220644
BLAST score
                   404
E value
                   0.0e + 00
Match length
                   453
                   98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MXL8, complete sequence [Arabidopsis thaliana]
```

Seq. No. 135795

Contig ID 122184_1.R1010

5'-most EST g1217470 Method BLASTN



```
q3510344
NCBI GI
BLAST score
                   203
                   1.0e-110
E value
                   495
Match length
% identity
                   98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MJG14, complete sequence [Arabidopsis thaliana]
                   135796
Seq. No.
                   122213 1.R1010
Contig ID
                   g2047786
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2244898
BLAST score
                   127
                   8.0e-07
E value
Match length
                   81
% identity
                   50
                   (Z97338) strong similarity to protein phosphatase 2A
NCBI Description
                   regulatory chain, 74K [Arabidopsis thaliana]
                   135797
Seq. No.
Contig ID
                   122274 1.R1010
5'-most EST
                   jC-atXP80C240I16T7d1
Method
                   BLASTN
                   g2244870
NCBI GI
BLAST score
                   447
E value
                   0.0e + 00
Match length
                   506
% identity
                   98
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
Seq. No.
                   135798
                   122298 1.R1010
Contig ID
5'-most EST
                   g396863
Method
                   BLASTN
                   g4589409
NCBI GI
                   317
BLAST score
                   1.0e-178
E value
                   325
Match length
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   F17P19, complete sequence
                   135799
Seq. No.
                   122303 1.R1010
Contig ID
                   jC-atXP29C138K22T7095d1
5'-most EST
                   BLASTX
Method
                   g3128184
NCBI GI
```

4.

151 BLAST score E value 2.0e-99 204 Match length 90 % identity

(AC004521) unknown protein [Arabidopsis thaliana] NCBI Description

135800 Seq. No.

Contig ID 122303 2.R1010



```
g1217247
5'-most EST
Method
                  BLASTX
                  q3128184
NCBI GI
BLAST score
                  501
E value
                  1.0e-50
Match length
                  141
% identity
                  (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
                  135801
Seq. No.
Contig ID
                  122312 1.R1010
5'-most EST
                  jC-atXP12C103A10T7042a1
Method
                  BLASTN
NCBI GI
                  q3766106
BLAST score
                   371
E value
                  0.0e + 00
                  564
Match length
% identity
                   99
                  Arabidopsis thaliana chromosome 1 BAC F9K20 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   135802
Contig ID
                   122322 1.R1010
5'-most EST
                   g2048559
                   135803
Seq. No.
                   122323 1.R1010
Contig ID
5'-most EST
                   iC-atXP81C240J5T7d1
Method
                   BLASTX
NCBI GI
                   g4191791
BLAST score
                   368
E value
                   4.0e-66
Match length
                   129
% identity
                   99
                   (AC005917) putative sf21 {Helianthus annuus} protein
NCBI Description
                   [Arabidopsis thaliana]
                   135804
Seq. No.
                   122328 1.R1010
Contig ID
                   jC-atXP81C240K17T7d1
5'-most EST
                   BLASTX
Method
                   g4589123
NCBI GI
                   293
BLAST score
                   3.0e-26
E value
Match length
                   125
% identity
                   52
NCBI Description (AF126374) At14a protein [Arabidopsis thaliana]
                   135805
Seq. No.
Contig ID
                   122337 1.R1010
5'-most EST
                   g493432
                   BLASTX
Method
NCBI GI
                   g4539416
BLAST score
                   741
                   2.0e-80
E value
```

16161

196

85

Match length % identity



NCBI Description (AL049171) 1-aminocyclopropane-1-carboxylate synthase-like protein [Arabidopsis thaliana]

Seq. No. 135806

Contig ID 122338 1.R1010

5'-most EST g507023
Method BLASTX
NCBI GI g4539416
BLAST score 149
E value 9.0e-12
Match length 39
% identity 97

NCBI Description (AL049171) 1-aminocyclopropane-1-carboxylate synthase-like

protein [Arabidopsis thaliana]

Seq. No. 135807

Contig ID 122348_1.R1010 5'-most EST jC-atXP81C240L8T7d1

Method BLASTN
NCBI GI g4510360
BLAST score 453
E value 0.0e+00
Match length 509
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic

sequence, complete sequence

Seq. No. 135808

Contig ID 122352 1.R1010 5'-most EST jC-atXP81C240M10T7s1

Method BLASTN
NCBI GI g2827538
BLAST score 283
E value 1.0e-158
Match length 363
% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17

(ESSAII project)

Seq. No. 135809

Contig ID 122457 1.R1010

5'-most EST g1269287
Method BLASTN
NCBI GI g4165340
BLAST score 276
E value 1.0e-154
Match length 463
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F11M15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135810

Contig ID 122460_1.R1010 5'-most EST jC-atXP88C241P11T7s1

Method BLASTN
NCBI GI g4581084
BLAST score 354

```
E value 0.0e+00 Match length 409 % identity 96
```

NCBI Description Arabidopsis thaliana chromosome I BAC T30F21 genomic

sequence, complete sequence

Seq. No. 135811

Contig ID 122482_1.R1010

5'-most EST g1269300

Method BLASTX

NCBI GI g2288985

BLAST score 330

E value 1.0e-30

Match length 119
% identity 54

NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135812

Contig ID 122486_1.R1010

 5'-most EST
 g496838

 Method
 BLASTX

 NCBI GI
 g3618316

 BLAST score
 224

 E value
 3.0e-24

 Match length
 99

% identity 46

NCBI Description (AB001886) zinc finger protein [Oryza sativa]

Seq. No. 135813

Contig ID 122501_1.R1010

5'-most EST g1269312

Method BLASTN

NCBI GI g4589439

BLAST score 262

E value 1.0e-145

Match length 416

% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQM1, complete sequence

Seq. No. 135814

Contig ID 122555_1.R1010 5'-most EST jC-atXP88C242G7T7d1

Method BLASTN
NCBI GI g4732167
BLAST score 178
E value 2.0e-95
Match length 392
% identity 92

NCBI Description Arabidopsis thaliana BAC F28D6

Seq. No. 135815

Contig ID 122572 1.R1010 5'-most EST g1269355

Method BLASTX
NCBI GI g4581143
BLAST score 234

NCBI GI

E value

BLAST score

Match length



```
E value
Match length
                   109
% identity
                   (AC006919) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   135816
Seq. No.
Contig ID
                   122580 1.R1010
                   jC-atX\overline{P}123C162F21T7081d1
5'-most EST
                   BLASTN
Method
                   g3047060
NCBI GI
BLAST score
                   195
                   1.0e-105
E value
Match length
                   478
% identity
                   95
NCBI Description Arabidopsis thaliana BAC F7N22
                   135817
Seq. No.
                   122587 1.R1010
Contig ID
5'-most EST
                   g1269365
                   BLASTN
Method
                   g1313929
NCBI GI
                   268
BLAST score
                   1.0e-149
E value
Match length
                   624
% identity
                   86
NCBI Description B.oleracea mRNA for IFA binding protein
                   135818
Seq. No.
                   122591 1.R1010
Contig ID
                   g12694\overline{3}4
5'-most EST
                   BLASTX
Method
                   q3080446
NCBI GI
                   439
BLAST score
E value
                   2.0e-43
                   153
Match length
% identity
                   63
                   (AL022605) puative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   135819
Contig ID
                   122602 1.R1010
5'-most EST
                   q16700
Method
                   BLASTX
NCBI GI
                   g2505874
BLAST score
                   639
E value
                   7.0e-67
Match length
                   123
% identity
                   (Y12776) putative kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   135820
                   122604 1.R1010
Contig ID
                   q12694\overline{4}3
5'-most EST
                   BLASTN
Method
```

16164

g4519195

7.0e-77

147



Seq. No. 135821 Contig ID 122611_1.R1010

5'-most EST jC-atXP89C242J19T7d1

Seq. No. 135822

Contig ID 122618 1.R1010

5'-most EST jC-atXP122C159G13T7008a1

Method BLASTX
NCBI GI g3269285
BLAST score 394
E value 7.0e-38
Match length 215
% identity 44

NCBI Description (AL030978) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135823

Contig ID 122714_1.R1010 5'-most EST jC-atXP89C245E18T7d1

Seq. No. 135824

Contig ID 122723_1.R1010 5'-most EST jC-atXP8C92D17T7d1

Method BLASTN
NCBI GI g1707006
BLAST score 336
E value 0.0e+00
Match length 375
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135825

Contig ID 122734 1.R1010

5'-most EST g2393682
Method BLASTX
NCBI GI g3135277
BLAST score 157
E value 3.0e-10
Match length 119
% identity 38

NCBI Description (AC003058) hypothetical protein [Arabidopsis thaliana] >gi 4191776 (AC005917) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 135826

Contig ID 122736_1.R1010

5'-most EST g3450543
Method BLASTN
NCBI GI g3928074
BLAST score 317
E value 1.0e-178
Match length 366
% identity 98



NCBI Description Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135827

Contig ID 122755_1.R1010 5'-most EST jC-atXP8C92H10T7d1

Seq. No. 135828

Contig ID 122762_1.R1010 5'-most EST jC-atXP8C92H24T7s1

Method BLASTX
NCBI GI g3355480
BLAST score 91
E value 1.0e-12
Match length 137
% identity 44

NCBI Description (AC004218) Medicago nodulin N21-like protein [Arabidopsis

thaliana]

Seq. No. 135829

Contig ID 122775_1.R1010 5'-most EST jC-atXP8C92J13T7d1

Seq. No. 135830

Contig ID 122779_1.R1010 5'-most EST jC-atXP8C92J24T7d1

Method BLASTN
NCBI GI 94220468
BLAST score 404
E value 0.0e+00
Match length 506
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC T8011 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135831

Contig ID 122783_1.R1010 5'-most EST jC-atXP8C92K11T7d1

Method BLASTX
NCBI GI 94056432
BLAST score 865
E value 3.0e-93
Match length 167
% identity 100

NCBI Description (AC005990) Similar to gi_2245014 glucosyltransferase

homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97341. ESTs gb_T20778 and gb_AA586281 come from this

gene. [Arabidopsis thaliana]

Seq. No. 135832

Contig ID 122787_1.R1010 5'-most EST jC-atXP8C92K15T7s1

Method BLASTN
NCBI GI g4678340
BLAST score 400
E value 0.0e+00
Match length 468

```
% identity
                   Arabidopsis thaliana DNA chromosome 3, BAC clone T29H11
NCBI Description
                   (ESSA project)
                   135833
Seq. No.
                   122791 1.R1010
Contig ID
5'-most EST
                   jC-atX\overline{P}8C92K1T7s1
Seq. No.
                   135834
                   122792 1.R1010
Contig ID
                   g23936<del>9</del>7
5'-most EST
Method
                   BLASTN
                   g2833627
NCBI GI
BLAST score
                   415
                   0.0e+00
E value
Match length
                   519
                   96
% identity
                   Arabidopsis thaliana chromosome 1 BAC F1707 complete
NCBI Description
                   sequence [Arabidopsis thaliana]
                   135835
Seq. No.
                   122797_1.R1010
Contig ID
                   jC-atX\overline{P}8C92L10T7s1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2351069
BLAST score
                   163
                   2.0e-86
E value
                   412
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

MSH12, complete sequence [Arabidopsis thaliana]

135836 Seq. No. Contig ID 122802 1.R1010 5'-most EST q2393700 Method BLASTN NCBI GI q4220632 BLAST score 383 E value 0.0e + 00Match length 513

82 % identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K6M13, complete sequence [Arabidopsis thaliana]

Seq. No. 135837 122802 2.R1010 Contig ID 5'-most EST jC-atXP8C92L5T7s1 Method BLASTX

q4835236 NCBI GI BLAST score 387 2.0e-37 E value Match length 133 % identity 62

(AL049862) putative protein [Arabidopsis thaliana] NCBI Description

135838 Seq. No. 122804 1.R1010 Contig ID

E value

Match length



```
5'-most EST
                   jC-atXP8C92L7T7s1
                   BLASTN
Method
                   q3873174
NCBI GI
BLAST score
                   341
E value
                   0.0e+00
Match length
                   453
% identity
                   Genomic sequence for Arabidopsis thaliana BAC F14N23,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   135839
Contig ID
                   122810 1.R1010
5'-most EST
                   jC-atXP8C92M22T7d1
                   BLASTX
Method
                   q3892714
NCBI GI
                   83
BLAST score
                   2.0e-30
E value
Match length
                   99
% identity
                   (AL033545) trehalose-6-phosphate phosphatase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   135840
Seq. No.
Contig ID
                   122819 1.R1010
5'-most EST
                   g12160\overline{2}4
                   BLASTN
Method
                   q4757678
NCBI GI
                   35
BLAST score
E value
                   4.0e-10
                   123
Match length
% identity
                   Arabidopsis thaliana chromosome I BAC F9H16 genomic
NCBI Description
                   sequence, complete sequence
                   135841
Seq. No.
                   122822 1.R1010
Contig ID
5'-most EST
                   jC-atXP8C92N21T7s1
Seq. No.
                   135842
                   122823 1.R1010
Contig ID
5'-most EST
                   g3450557
Method
                   BLASTX
                   g872116
NCBI GI
BLAST score
                   57
                   7.0e-18
E value
                   82
Match length
% identity
                   58
                   (X79770) sti (stress inducible protein) [Glycine max]
NCBI Description
                   135843
Seq. No.
                   122824 1.R1010
Contig ID
                   jC-atX\overline{P}104CE10D11T7b1
5'-most EST
Method
                   BLASTX
                   g872116
NCBI GI
                   687
BLAST score
```

16168

3.0e-72



```
% identity
                   (X79770) sti (stress inducible protein) [Glycine max]
NCBI Description
                   135844
Seq. No.
                   122830 1.R1010
Contig ID
5'-most EST
                   jC-atX\overline{P}8C92018T7d1
                   135845
Seq. No.
                   122834 1.R1010
Contig ID
                   jC-atXP8C92O4T7d1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3869065
BLAST score
                   448
E value
                   0.0e + 00
Match length
                   517
                   97
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K24M7, complete sequence [Arabidopsis thaliana]
                   135846
Seq. No.
                   122838 1.R1010
Contig ID
5'-most EST
                   q23937\overline{1}2
Method
                   BLASTX
NCBI GI
                   q4388834
BLAST score
                   351
                   5.0e-33
E value
                   107
Match length
% identity
                   60
                   (ACO06528) putative disease resistance protein RPP1, 3'
NCBI Description
                   partial [Arabidopsis thaliana]
                   135847
Seq. No.
                   122838 2.R1010
Contig ID
5'-most EST
                   q2748854
Method
                   BLASTX
                   g3757516
NCBI GI
BLAST score
                   439
E value
                   2.0e-43
Match length
                   144
% identity
                   58
                    (AC005167) putative TMV resistance protein [Arabidopsis
NCBI Description
                   thaliana]
                   135848
Seq. No.
                   122859 1.R1010
Contig ID
                   q12693\overline{9}1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3337347
BLAST score
                   446
```

0.0e + 00E value 462 Match length 99 % identity.

Arabidopsis thaliana chromosome II BAC F13P17 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

135849 Seq. No.

122887 1.R1010 Contig ID

Seq. No.

135856



```
5'-most EST
                   g1269399
Seq. No.
                   135850
                   122889 1.R1010
Contig ID
5'-most EST
                   jC-atXP90C245F10T7d2
Seq. No.
                   135851
                   122893 1.R1010
Contig ID
5'-most EST
                   g1269500
Method
                   BLASTX
NCBI GI
                   q2344900
BLAST score
                   509
E value
                   9.0e-52
Match length
                   107
% identity
                   91
                  (AC002388) EREBP isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   135852
                   122919 1.R1010
Contig ID
5'-most EST
                   q12695\overline{17}
                   BLASTX
Method
                   q2104951
NCBI GI
BLAST score
                   307
E value
                   6.0e-28
                   88
Match length
                   66
% identity
                  (U96717) MAP kinase-like protein [Selaginella lepidophylla]
NCBI Description
Seq. No.
                   135853
                   122919 3.R1010
Contig ID
5'-most EST
                   jC-atXP90C245J15T7s2
Seq. No.
                   135854
Contig ID
                   122931 1.R1010
5'-most EST
                   g2576644
Method
                   BLASTX
                   g4559366
NCBI GI
BLAST score
                   508
E value
                   2.0e-51
Match length
                   99
% identity
                   99
                   (AC006585) putative tyrosine transaminase [Arabidopsis
NCBI Description
                   thaliana]
                   135855
Seq. No.
                   122931 3.R1010
Contig ID
5'-most EST
                   g1054021
Method
                   BLASTX
NCBI GI
                   q4559366
BLAST score
                   432
                   1.0e-42
E value
                   87
Match length
                   99
% identity
NCBI Description
                   (AC006585) putative tyrosine transaminase [Arabidopsis
                   thaliana]
```



```
Contig ID
                   122963 1.R1010
                   jC-atXP90C246C11T7d2
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3293582
BLAST score
                   125
                   7.0e-64
E value
Match length
                   342
                   99
% identity
NCBI Description Arabidopsis thaliana BAC T15F16
Seq. No.
                   135857
Contig ID
                   122964 1.R1010
5'-most EST
                   jC-atXP90C246C16T7d2
                   135858
Seq. No.
                   122973 1.R1010
Contig ID
5'-most EST
                   q27484\overline{1}9
Method
                   BLASTX
                   g3068714
NCBI GI
BLAST score
                   419
                   4.0e-41
E value
Match length
                   157
                   60
% identity
NCBI Description
                  (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                   135859
Contig ID
                   122992 1.R1010
                   jC-atX\overline{P}90C246G18T7d2
5'-most EST
Method
                   BLASTX
                   q2344894
NCBI GI
BLAST score
                   186
                   7.0e-36
E value
                   144
Match length
% identity
                   65
                  (AC002388) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   135860
Contig ID
                   123008 1.R1010
5'-most EST
                   q1269596
Method
                   BLASTX
                   q3688188
NCBI GI
BLAST score
                   726
E value
                   5.0e-77
Match length
                   141
% identity
                   (AL031804) pyruvate decarboxylase-1 (Pdc1) [Arabidopsis
NCBI Description
                   thaliana]
                   135861
Seq. No.
Contig ID
                   123009 1.R1010
5'-most EST
                   g510754
                   BLASTX
Method
                   g3688188
NCBI GI
BLAST score
                   125
E value
                   1.0e-44
                   90
Match length
```

16171

100

% identity



```
(AL031804) pyruvate decarboxylase-1 (Pdc1) [Arabidopsis
NCBI Description
                   thaliana]
                   135862
Seq. No.
                   123020 1.R1010
Contig ID
                   q20479\overline{3}5
5'-most EST
                  BLASTX
Method
                  g2190547
NCBI GI
BLAST score
                   253
E value
                   1.0e-21
Match length
                   128
                   49
% identity
NCBI Description
                  (AC001229) ESTs
                   gb T43256,gb 46316,gb N64930,gb AA395255,gb AA404382 come
                   from this gene. [Arabidopsis thaliana]
                   135863
Seq. No.
                   123024 1.R1010
Contig ID
5'-most EST
                   g12696\overline{0}9
                   BLASTN
Method
                   g3241925
NCBI GI
BLAST score
                   309
                   1.0e-173
E value
Match length
                   342
% identity
                   97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MOK9, complete sequence [Arabidopsis thaliana]
                   135864
Seq. No.
Contig ID
                   123034 1.R1010
                   jC-atXP91C247G10T7d1
5'-most EST
                   BLASTN
Method
                   q3335331
NCBI GI
BLAST score
                   372
                   0.0e + 00
E value
Match length
                   404
% identity
                   70
                   Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   135865
Contig ID
                   123042 1.R1010
5'-most EST
                   jC-atXP91C247H16T7d1
Seq. No.
                   135866
                   123052 1.R1010
Contig ID
5'-most EST
                   g2722056
Method
                   BLASTX
```

q4835234 NCBI GI BLAST score 429 3.0e-42E value Match length 89 % identity 93

(AL049862) putative cold acclimation protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 135867

Ö,



```
Contig ID
                  123071 1.R1010
                  iC-atXP92C247N12T7074d1
5'-most EST
                  BLASTN
Method
NCBI GI
                  q3941523
                  40
BLAST score
                  7.0e-13
E value
Match length
                  40
                  100
% identity
                  Arabidopsis thaliana putative transcription factor (MYB92)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  135868
Contig ID
                  123072 1.R1010
                  jC-atXP92C247N23T7082d1
5'-most EST
                  BLASTX
Method
                  a3426051
NCBI GI
                  428
BLAST score
E value
                  7.0e-42
                  185
Match length
                  49
% identity
                  (AC005168) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  135869
Seq. No.
Contig ID
                  123073 1.R1010
                   jC-atXP92C246O22T7052d1
5'-most EST
                  BLASTX
Method
                  q3980385
NCBI GI
                   605
BLAST score
E value
                   3.0e-66
                  145
Match length
                   92
% identity
                   (AC004561) putative 18 kDa class I heat shock protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   135870
                   123094 1.R1010
Contig ID
5'-most EST
                   jC-atXP92C249C14T7053d1
                   BLASTX
Method
                   q2244817
NCBI GI
BLAST score
                   635
                   3.0e-66
E value
                   207
Match length
                   69
% identity
                   (Z97336) disease resistance protein RPS2 homolog
NCBI Description
                   [Arabidopsis thaliana]
                   135871
Seq. No.
                   123095 1.R1010
Contig ID
                   jC-atXP94CG11A10T7b1
5'-most EST
                   BLASTN
Method
                   g4589440
NCBI GI
BLAST score
                   159
E value
                   7.0e-84
                   582
Match length
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
```

MSD21, complete sequence



```
Seq. No.
                  135872
                  123098 1.R1010
Contig ID
                  jC-atXP92C249D16T7077d1
5'-most EST
                  BLASTX
Method
                  q2129641
NCBI GI
BLAST score
                  609
                  3.0e-63
E value
                  152
Match length
% identity
                  71
NCBI Description
                  major latex protein type 1 - Arabidopsis thaliana
                  >gi_1107493_emb_CAA63026_ (X91960) major latex protein
                  typel [Arabidopsis thaliana]
                  135873
Seq. No.
                  123102 1.R1010
Contig ID
5'-most EST
                  jC-atXP92C246018T7028d1
Method
                  BLASTN
NCBI GI
                  q4589446
BLAST score
                  415
                  0.0e + 00
E value
Match length
                  487
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  T12B11, complete sequence
                  135874
Seq. No.
                  123109 1.R1010
Contig ID
5'-most EST
                  jC-atXP96C248A15T7b1
                  BLASTN
Method
NCBI GI
                  q3941523
BLAST score
                  52
E value
                   4.0e-20
Match length
                  52
% identity
                  100
                  Arabidopsis thaliana putative transcription factor (MYB92)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  135875
                  123111 1.R1010
Contig ID
                   jC-atXP96C248C23T7b1
5'-most EST
Method
                  BLASTN
                  g3941523
NCBI GI
BLAST score
                  51
                   2.0e-19
E value
                  51
Match length
% identity
                  100
                  Arabidopsis thaliana putative transcription factor (MYB92)
NCBI Description
                  mRNA, complete cds
                  135876
Seg. No.
                  123113 1.R1010
Contig ID
```

5'-most EST jC-at \overline{XP} 96C248B22T7b1

Method BLASTX
NCBI GI g2264368
BLAST score 457
E value 2.0e-45



Match length 91 % identity 100

NCBI Description (AC002354) putative tetracycline transporter-like protein

[Arabidopsis thaliana]

Seq. No. 135877

Contig ID 123118_1.R1010

5'-most EST jC-atXP96C248D13T7b1

Method BLASTN
NCBI GI g3800746
BLAST score 50
E value 7.0e-19
Match length 50

Match length 50 % identity 100

NCBI Description Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA,

complete cds

Seq. No. 135878

Contig ID 123126_1.R1010 5'-most EST jC-atXP96C248I16T7b1

Method BLASTX
NCBI GI g2072720
BLAST score 368
E value 6.0e-35
Match length 181
% identity 46

NCBI Description (Z95121) hypothetical protein Rv3253c [Mycobacterium

tuberculosis

Seq. No. 135879

Contig ID 123128 1.R1010

5'-most EST jC-atXP96C248J10T7b1

Method BLASTX
NCBI GI g2660673
BLAST score 545
E value 1.0e-55
Match length 184
% identity 26

NCBI Description (AC002342) unknown protein [Arabidopsis thaliana]

Seq. No. 135880

Contig ID 123137_1.R1010 5'-most EST jC-atXP96C248E9T7b1

Method BLASTN
NCBI GI g3461810
BLAST score 197
E value 1.0e-106
Match length 376
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T17M13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135881

Contig ID 123150_1.R1010 5'-most EST jC-atXP96C250A3T7b1

Method BLASTN NCBI GI g2656028



BLAST score 124 E value 5.0e-63 Match length 574 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

, 5.2

MNF13

Seq. No. 135882

Contig ID 123161_1.R1010 5'-most EST jC-atXP96C250F9T7d1

Method BLASTN
NCBI GI g1707006
BLAST score 210
E value 1.0e-114
Match length 254
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135883

Contig ID 123162_1.R1010 5'-most EST jC-atXP97C249M14T7d1

Method BLASTN
NCBI GI g4519188
BLAST score 670
E value 0.0e+00
Match length 713
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21L19, complete sequence

Seq. No. 135884

Contig ID 123163_1.R1010

5'-most EST jC-atXP13C104C2T7042a1

Method BLASTN
NCBI GI g2290120
BLAST score 57
E value 5.0e-23
Match length 61
% identity 98

NCBI Description HIV-1 strain MO2 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No. 135885

Contig ID 123165_1.R1010

5'-most EST g1327783
Method BLASTX
NCBI GI g1628622
BLAST score 317
E value 3.0e-29
Match length 95
% identity 61

NCBI Description (U72631) flavonol synthase [Arabidopsis thaliana]

>gi_1805305 (U84258) flavonol synthase [Arabidopsis
thaliana] >gi_1805307 (U84259) flavonol synthase
[Arabidopsis thaliana] >gi_1805309 (U84260) flavonol

synthase [Arabidopsis thaliana]



```
135886
Seq. No.
                  123173 1.R1010
Contig ID
                  g1520687
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4490718
BLAST score
                  1123
E value
                  1.0e-123
Match length
                  261
                  84
% identity
                  (AL035709) bZIP transcription factor-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  135887
Seq. No.
                  123177_1.R1010
Contig ID
5'-most EST
                  g1520694
                  BLASTX
Method
NCBI GI
                  g2723477
BLAST score
                  499
E value
                  2.0e-50
                  167
Match length
                   63
% identity
NCBI Description (D89824) GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                  135888
Contig ID
                  123183 1.R1010
                   jC-atX\overline{P}97C251F20T7d1
5'-most EST
                  BLASTN
Method
NCBI GI
                   q4589440
BLAST score
                   331
                   0.0e + 00
E value
                   767
Match length
% identity
                   83
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSD21, complete sequence
Seq. No.
                   135889
                   123191 1.R1010
Contig ID
5'-most EST
                   a2393715
Method
                   BLASTX
                   q4056480
NCBI GI
BLAST score
                   197
E value
                   3.0e-19
Match length
                   103
% identity
                   54
                  (AC005896) putative adenylate kinase [Arabidopsis thaliana]
NCBI Description
                   135890
Seq. No.
Contig ID
                   123195 1.R1010
5'-most EST
                   g2596342
Method
                   BLASTX
NCBI GI
                   g3249077
BLAST score
                   509
E value
                   1.0e-51
Match length
                   95
```

% identity 100
NCBI Description (AC004473) Similar to prunasin hydrolase precursor



gb_U50201 from Prunus serotina. ESTs gb_T21225 and gb_AA586305 come from this gene. [Arabidopsis thaliana]

 Seq. No.
 135891

 Contig ID
 123200_1.R1010

 5'-most EST
 jC-atXP9C93E19T7s1

Seq. No. 135892

Contig ID 123212 1.R1010

5'-most EST g2596378
Method BLASTN
NCBI GI g3510343
BLAST score 144
E value 3.0e-75
Match length 341
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJC20, complete sequence [Arabidopsis thaliana]

Seq. No. 135893

Contig ID 123213_1.R1010 5'-most EST jC-atXP9C93I10T7s1

Method BLASTN
NCBI GI g3510343
BLAST score 114
E value 4.0e-57
Match length 475
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJC20, complete sequence [Arabidopsis thaliana]

Seq. No. 135894

Contig ID 123217_1.R1010 5'-most EST jC-atXP9C93I15T7d1

Seq. No. 135895

Contig ID 123229 1.R1010

5'-most EST g2757051
Method BLASTN
NCBI GI g3241925
BLAST score 502
E value 0.0e+00
Match length 518
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOK9, complete sequence [Arabidopsis thaliana]

Seq. No. 135896

Contig ID 123236 1.R1010

5'-most EST g2048822
Method BLASTN
NCBI GI g4263373
BLAST score 231
E value 1.0e-127
Match length 479
% identity 97

NCBI Description Arabidopsis thaliana BAC T15G18 from chromosome IV, near 25



cM, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                   135897
                   123253 1.R1010
Contig ID
                   jC-atXP74C223N13T7004d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4507229
BLAST score
                   517
                   3.0e-52
E value
Match length
                   160
% identity
                   62
                   Succinic semialdehyde dehydrogenase
NCBI Description
                   >gi 3766467 emb_CAA72076_ (Y11192) NAD+ dependent succinic
                   semialdehyde dehydrogenase [Homo sapiens]
                   >gi_4164365_emb_CAA20248_ (AL031230) dJ73M23.2
(NAD+-dependent succinic semialdehyde dehydrogenase (SSADH,
                   EC 1.2.1.24)) [Homo sapiens]
                   135898
Seq. No.
                   123253 2.R1010
Contig ID
5'-most EST
                   g20488<u>2</u>5
                   BLASTX
Method
                   g1800047
NCBI GI
BLAST score
                   264
E value
                   6.0e-23
Match length
                   69
                   68
% identity
                   (D90890) SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (EC
NCBI Description
                   1.2.1.16) (SSDH). [Escherichia coli]
                   135899
Seq. No.
Contig ID
                   123255 1.R1010
                    jC-atXP9C93P6T7s1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4589425
BLAST score
                    436
E value
                    0.0e + 00
Match length
                    616
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MBA10, complete sequence
                    135900
Seq. No.
Contig ID
                    123256 1.R1010
5'-most EST
                    g2756934
Method
                    BLASTX
NCBI GI
                    g1172498
BLAST score
                    375
                    6.0e-45
E value
Match length
                    132
% identity
                   PHYTOCHROME E >gi 1076376 pir S46313 phytochrome E -
NCBI Description
                    Arabidopsis thaliana >gi \overline{452817} emb CAA54075 (X76610)
```

Seq. No. 135901

Contig ID 123265_1.R1010

phytochrome E [Arabidopsis thaliana]



```
iC-atXP122C152I4T7007a1
5'-most EST
                   BLASTX
Method
                   q4490737
NCBI GI
                   340
BLAST score
                   1.0e-31
E value
                   148
Match length
% identity
                   (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                   135902
Seq. No.
                   123267 1.R1010
Contig ID
                   g2047780
5'-most EST
                   BLASTN
Method
                   g2341023
NCBI GI
                   290
BLAST score
                   1.0e-162
E value
                   481
Match length
                   98
% identity
                   Sequence of BAC F19P19 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
                   135903
Seq. No.
                   123271 1.R1010
Contig ID
                   jC-atXP9C94C4T7d1
5'-most EST
                   BLASTX
Method
                   g133356
NCBI GI
BLAST score
                   170
                   6.0e-12
E value
                   108
Match length
                    35
% identity
                   DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT (C160)
NCBI Description
                    >gi_66978_pir__RNBY3L DNA-directed RNA polymerase (EC
                   2.7.7.6) III 160K chain - yeast (Saccharomyces cerevisiae) >gi 4400 emb CAA26905 (X03129) RNA polymerase III largest
                    subunit [Saccharomyces cerevisiae]
                    >gi_1050828_emb_CAA62123_ (X90518) ORF 03254 [Saccharomyces
                    cerevisiae] >gi_1164961_emb_CAA64036_ (X94335) YOR3254c
                    [Saccharomyces cerevisiae] >gi 1420309 emb CAA99314
                    (Z75024) ORF YOR116c [Saccharomyces cerevisiae]
                    135904
Seq. No.
                    123274 1.R1010
Contig ID
                    g2048831
5'-most EST
                    BLASTN
Method
NCBI GI
                    q3869070
                    327
BLAST score
                    0.0e + 00
E value
                    395
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                    MGO3, complete sequence [Arabidopsis thaliana]
```

135905 Seq. No.

123277 1.R1010 Contig ID jC-atXP9C94E17T7d1 5'-most EST

Method BLASTX NCBI GI g2618729

Match length

% identity

300 96

```
BLAST score
                  4.0e-17
E value
                  84
Match length
% identity
                  56
NCBI Description (U49076) IAA20 [Arabidopsis thaliana]
                  135906
Seq. No.
                  123280 1.R1010
Contig ID
                  jC-atX\overline{P}9C94F11T7d1
5'-most EST
                  BLASTX
Method
                  g4263779
NCBI GI
                   139
BLAST score
                   3.0e-37
E value
                   96
Match length
% identity
                   92
                   (AC006068) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   135907
                   123282 1.R1010
Contig ID
                   jC-atXP9C94F4T7d1
5'-most EST
Method
                   BLASTX
                   g2129562
NCBI GI
BLAST score
                   114
                   8.0e-13
E value
Match length
                   64
% identity
                   58
                   class III ADH, glutathione-dependent formaldehyde
NCBI Description
                   dehydrogenase. - Arabidopsis thaliana
                   >gi 1143388 emb CAA57973_ (X82647) class III ADH,
                   glutathione-dependent formaldehyde dehydrogenase.
                   [Arabidopsis thaliana]
                   135908
Seq. No.
                   123287 1.R1010
Contig ID
                   g2048840
5'-most EST
                   135909
Seq. No.
                   123290 1.R1010
Contig ID
                   jC-atXP9C94I21T7s1
5'-most EST
                   BLASTN
Method
                   g3461834
NCBI GI
                   206
BLAST score
                   1.0e-112
E value
                   326
Match length
                   93
% identity
                   Arabidopsis thaliana chromosome II BAC T9I4 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   135910
Seq. No.
Contig ID
                   123292 1.R1010
5'-most EST
                   q2048843
                   BLASTN
Method
                   q4589122
NCBI GI
BLAST score
                   261
                   1.0e-145
E value
```



```
NCBI Description Arabidopsis thaliana At14a protein mRNA, complete cds
                  135911
Seq. No.
                  123293_1.R1010
Contig ID
                  g1158838
5'-most EST
                  BLASTX
Method
                  q2244762
NCBI GI
BLAST score
                  419
                   3.0e-41
E value
Match length
                  100
                  78
% identity
                  (Z97335) major latex protein [Arabidopsis thaliana]
NCBI Description
                  135912
Seq. No.
Contig ID
                  123297 1.R1010
                   jC-atXP9C94J10T7s1
5'-most EST
                   BLASTX
Method
                   q3819697
NCBI GI
                   365
BLAST score
                   7.0e-35
E value
Match length
                   83
                   88
% identity
                  (AJ009608) BnMAP4K alpha1 [Brassica napus]
NCBI Description
                   135913
Seq. No.
                   123302 1.R1010
Contig ID
                   jC-atXP9C94L4T7d1
5'-most EST
Method
                   BLASTX
                   g3461847
NCBI GI
BLAST score
                   98
                   3.0e-32
E value
                   75
Match length
                   99
% identity
                   (AC005315) putative ubiquitin [Arabidopsis thaliana]
NCBI Description
                   135914
Seq. No.
                   123371_1.R1010
Contig ID
                   jC-atXmonuni10Ah04a1
5'-most EST
                   BLASTN
Method
                   g4159707
NCBI GI
BLAST score
                   339
                   0.0e + 00
E value
Match length
                   451
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MJK13, complete sequence
```

135915 Seq. No.

123393 1.R1010 Contig ID

q2062928 5'-most EST Method BLASTN q3449329 NCBI GI BLAST score 216 E value 1.0e-118 Match length 437 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

NCBI GI

E value

BLAST score

g4263694 210

1.0e-114



MDH9, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  135916
                  123536_1.R1010
Contig ID
                  jC-atXmonuni10Da06a1
5'-most EST
                  BLASTN
Method
                  g3128142
NCBI GI
BLAST score
                  341
                  0.0e + 00
E value
                  431
Match length
                  96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQN23, complete sequence [Arabidopsis thaliana]
                  135917
Seq. No.
                  124090 1.R1010
Contig ID
                  jC-atXmonuni25Da05b1
5'-most EST
                  BLASTN
Method
NCBI GI
                  q3327388
                  258
BLAST score
                  1.0e-143
E value
                   451
Match length
% identity
                   6
                  Arabidopsis thaliana chromosome II BAC T12J2 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   135918
Seq. No.
                   124156 1.R1010
Contig ID
                   jC-atX\overline{P}22C122C14T7055a1
5'-most EST
Method
                   BLASTN
                   g4589950
NCBI GI
                   393
BLAST score
                   0.0e+00
E value
Match length
                   421
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T28P16 genomic
                   sequence, complete sequence
                   135919
Seq. No.
                   124212 1.R1010
Contig ID
                   jC-atXP24C123M15T7063d1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g4580454
BLAST score
                   48
                   1.0e-17
E value
Match length
                   141
% identity
                   Arabidopsis thaliana chromosome II BAC T2G17 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   135920
                   124276 1.R1010
Contig ID
                   jC-atXmonuni26Ad04a1
5'-most EST
                   BLASTN
Method
```



Match length 418 % identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135921

Contig ID 124317_1.R1010

5'-most EST jC-atXmonuni26Af06a1

Method BLASTX
NCBI GI g4262180
BLAST score 301
E value 2.0e-27
Match length 63
% identity 90

NCBI Description (AC005508) 29621 [Arabidopsis thaliana]

Seq. No. 135922

Contig ID 124330_1.R1010 5'-most EST jC-atXP5C90E1T7088a1

Method BLASTN
NCBI GI g3869065
BLAST score 360
E value 0.0e+00
Match length 693
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K24M7, complete sequence [Arabidopsis thaliana]

Seq. No. 135923

Contig ID 124367_1.R1010 5'-most EST jC-atXmonuni26Ba05a1

Method BLASTX
NCBI GI g4646203
BLAST score 389
E value 2.0e-37
Match length 153
% identity 48

NCBI Description (AC007230) Belongs to PF_00026 Eukaryotic aspartyl protease

family. [Arabidopsis thaliana]

Seq. No. 135924

Contig ID 124381_1.R1010 5'-most EST jC-atXmonuni26Cc05a1

Method BLASTN
NCBI GI g3869071
BLAST score 449
E value 0.0e+00
Match length 453
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MIL23, complete sequence [Arabidopsis thaliana]

Seq. No. 135925

Contig ID 124396_1.R1010

5'-most EST g3449566
Method BLASTN
NCBI GI g4678315



```
BLAST score 323
E value 0.0e+00
Match length 435
% identity 97
NCBI Description Arabidops
```

NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15 (ESSA project)

Seq. No. 135926

Contig ID 124429_1.R1010

5'-most EST $g27494\overline{77}$

Seq. No. 135927

Contig ID 124442_1.R1010

5'-most EST jC-atXmonuni26Be02a1

Method BLASTN
NCBI GI g4096078
BLAST score 40
E value 4.0e-13
Match length 64
% identity 91

NCBI Description Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135928

Contig ID 124948_1.R1010 5'-most EST jC-atXmonuni27Ag06a1

Method BLASTX
NCBI GI g2341032
BLAST score 561
E value 1.0e-57
Match length 116
% identity 94

NCBI Description (AC000104) EST gb_ATTS0956 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 135929

Contig ID 125229_1.R1010

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBB18, complete sequence [Arabidopsis thaliana]

Seq. No. 135930

Contig ID 125409 1.R1010 5'-most EST jC-atXP20728r2

Method BLASTX
NCBI GI 94581109
BLAST score 499
E value 3.0e-50
Match length 147
% identity 65

NCBI Description (AC005825) unknown protein [Arabidopsis thaliana]



```
135931
Seq. No.
                  125410 1.R1010
Contig ID
                  jC-atXP20725r2
5'-most EST
                  BLASTX
Method
                  g4416307
NCBI GI
                   429
BLAST score
                  2.0e-46
E value
                  131
Match length
                  78
% identity
NCBI Description (AF105716) hypothetical protein [Zea mays]
                   135932
Seq. No.
                   125411 1.R1010
Contig ID
                   jC-atXP20608r2
5'-most EST
                   BLASTN
Method
                   g413796
NCBI GI
                   46
BLAST score
                   2.0e-16
E value
                   46
Match length
                   100
% identity
NCBI Description Cloning vector pMAMneoBlue, complete sequence
                   135933
Seq. No.
                   125412 1.R1010
Contig ID
                   jC-atXP20581r2
5'-most EST
                   BLASTN
Method
                   g2147
NCBI GI
BLAST score
                   42
                   5.0e-14
E value
                   42
Match length
                   100
% identity
NCBI Description S.scrofa UABP-2 gene exon
                   135934
Seq. No.
                   125413_1.R1010
Contig ID
                   jC-atXP20075r2
5'-most EST
                   BLASTX
Method
                   g2982285
NCBI GI
                   327
BLAST score
                   9.0e-30
E value
                   63
Match length
                   78
% identity
                   (AF051227) GASA5-like protein [Picea mariana]
NCBI Description
Seq. No.
                   135935
                   125430 1.R1010
Contig ID
                   jC-atX\overline{P}117C141024T7a1
5'-most EST
                   BLASTX
Method
                   g3445210
NCBI GI
BLAST score
                   307
                   1.0e-34
E value
                   166
Match length
                    55
% identity
                    (AC004786) putative flavonol 3-o-glucosyltransferase
NCBI Description
```

[Arabidopsis thaliana]



```
135936
Seq. No.
                   125488 1.R1010
Contig ID
                   jC-atX\overline{P}117C140C21T7a1
5'-most EST
                   135937
Seq. No.
                   125507 1.R1010
Contig ID
                   jC-atX\overline{P}112C130P5T7d2
5'-most EST
                   BLASTX
Method
                   g3834323
NCBI GI
                   324
BLAST score
                   1.0e-29
E value
                   243
Match length
% identity
NCBI Description (AC005679) F9K20.25 [Arabidopsis thaliana]
                   135938
Seq. No.
                   125508 1.R1010
Contig ID
                   jC-atXP112C130023T7d2
5'-most EST
                   BLASTN
Method
                   g2582640
NCBI GI
BLAST score
                   39
                   3.0e-12
E value
                   39
Match length
                   100
% identity
                   Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   135939
Seq. No.
                   125509 1.R1010
Contig ID
                   jC-atX\overline{P}112C130014T7d2
5'-most EST
                   BLASTX
Method
                   g2244765
NCBI GI
                    192
BLAST score
                    3.0e-14
E value
                    110
Match length
% identity
                    39
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]
                    135940
Seq. No.
                    125520 1.R1010
Contig ID
                    jC-atX\overline{P}71C222P11T7030d1
5'-most EST
Method
                    BLASTN
NCBI GI
                    g1785673
                    319
BLAST score
                    1.0e-179
E value
                    395
Match length
                    95
% identity
NCBI Description A.thaliana mitochondrial genome, part A
                    135941
Seq. No.
                    125530 1.R1010
Contig ID
                    jC-atXP112C129F3T7d2
5'-most EST
                    BLASTX
Method
                    g4587587
NCBI GI
BLAST score
                    286
E value
                    3.0e-25
```

16187

186

Match length



% identity 38 NCBI Description (AC007232) unknown protein [Arabidopsis thaliana]

Seq. No. 135942

Contig ID 125541_1.R1010

5'-most EST jC-atXP112C129A21T7d2

Method BLASTX
NCBI GI g2702365
BLAST score 178
E value 1.0e-12
Match length 116
% identity 40

NCBI Description (AF036706) similar to S. cerevisiae Lpg15p (GB:U43281)

[Caenorhabditis elegans]

Seq. No. 135943

Contig ID 125542_1.R1010

5'-most EST jC-atXP112C128I19T7d2

Method BLASTX
NCBI GI g133321
BLAST score 184
E value 3.0e-13
Match length 93
% identity 31

NCBI Description DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)

>gi_279534_pir__JDMU1_DNA-directed_RNA polymerase (EC

2.7.7.6) II largest chain (version 1) - Arabidopsis

thaliana >gi_16505_emb_CAA37130_ (X52954) RNA polymerase II

[Arabidopsis thaliana]

Seq. No. 135944

Contig ID 125548 1.R1010

5'-most EST jC-atXP112C127P7T7d2

Method BLASTX
NCBI GI g3201628
BLAST score 833
E value 1.0e-103
Match length 245
% identity 76

NCBI Description (AC004669) unknown protein [Arabidopsis thaliana]

Seq. No. 135945

Contig ID 125564 1.R1010

5'-most EST jC-atXP112C127A21T7d2

Method BLASTN
NCBI GI g4263762
BLAST score 81
E value 3.0e-37
Match length 164
% identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC F17L24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135946

Contig ID 125567_1.R1010

5'-most EST jC-atXP112C126O20T7d2

Method BLASTX

Contig ID



```
q3021274
NCBI GI
                   1089
BLAST score
                   1.0e-119
E value
                   216
Match length
                   73
% identity
                  (AL022347) serine/threonine kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   135947
Seq. No.
                   125569 1.R1010
Contig ID
                   jC-atX\overline{P}112C125P3T7a1
5'-most EST
                   BLASTN
Method
                   g2832639
NCBI GI
BLAST score
                   479
                   0.0e + 00
E value
                   543
Match length
                   97
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12
                   (ESSAII project)
                   135948
Seq. No.
                   125576_1.R1010
Contig ID
                   jC-atXN611170r2
5'-most EST
                   BLASTX
Method
                   g4455155
NCBI GI
                   166
BLAST score
                   4.0e-11
E value
                    43
Match length
                   74
% identity
                   (AL022023) EF-1 alpha-like protein (fragment) [Arabidopsis
NCBI Description
                    thaliana]
                    135949
Seq. No.
                    125578 1.R1010
Contig ID
                    jC-atx\overline{N}606176r2
5'-most EST
                    BLASTN
Method
                    q1944204
NCBI GI
BLAST score
                    44
                    3.0e-15
E value
                    96
Match length
                    94
 % identity
                    Oryza sativa mRNA for RicMT, complete cds
NCBI Description
                    135950
Seq. No.
                    125579 2.R1010
Contig ID
                    jC-atX\overline{N}605212r2
 5'-most EST
                    BLASTX
Method
                    q3551954
NCBI GI
 BLAST score
                    237
 E value
                    3.0e-19
Match length
                    132
                    39
 % identity
                    (AF082030) senescence-associated protein 5 [Hemerocallis
 NCBI Description
                    hybrid cultivar]
                    135951
 Seq. No.
```

16189

125580 1.R1010



```
jC-atXN594206r2
5'-most EST
                  BLASTN
Method
                  g902585
NCBI GI
                  45
BLAST score
                  1.0e-15
E value
                  77
Match length
                  90
% identity
                 Zea mays clone MubG9 ubiquitin gene, complete cds
NCBI Description
                  135952
Seq. No.
                  125581 1.R1010
Contig ID
                  jC-atXN585214r2
5'-most EST
                  135953
Seq. No.
                  125582 1.R1010
Contig ID
                  jC-atXN579208r2
5'-most EST
                  135954
Seq. No.
                  125583 2.R1010
Contig ID
                  jC-atXN563193d2
5'-most EST
Method
                  BLASTX
                  g3941500
NCBI GI
                  184
BLAST score
                   3.0e-13
E value
                   64
Match length
% identity
                   61
                  (AF062904) putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   135955
Seq. No.
                   125584 2.R1010
Contig ID
                   jC-atXN560189r2
5'-most EST
                   BLASTN
Method
                   g209241
NCBI GI
BLAST score
                   34
                   4.0e-09
E value
                   53
Match length
% identity
                   100
NCBI Description R6K synthetic cosmid vector
                   135956
Seq. No.
                   125585 1.R1010
Contig ID
                   jC-atXN458168d2
 5'-most EST
                   BLASTX
Method
                   g2160144
NCBI GI
BLAST score
                   299
                   1.0e-26
E value
                   236
Match length
                   42
 % identity
                   (AC000375) Strong similarity to Arabidopsis oligopeptide
 NCBI Description
                   transporter (gb X77503). [Arabidopsis thaliana]
                   135957
 Seq. No.
```

Contig ID 125586_1.R1010 5'-most EST jC-atXN457160r2 Method BLASTN

Method BLASTN NCBI GI g58124



```
BLAST score
                   1.0e-09
E value
                   55
Match length
                   100
% identity
NCBI Description Cloning vector pGEM3 (pJMSP-0) polylinker sequence (SP6
                   polymerase transcription vector)
                   135958
Seq. No.
                   125587 1.R1010
Contig ID
                   jC-atXN455156r2
5'-most EST
                   135959
Seq. No.
                   125588 1.R1010
Contig ID
                   jC-atX\overline{N}451155a2
5'-most EST
                   BLASTN
Method
                   g22246
NCBI GI
                   367
BLAST score
                   0.0e + 00
E value
                   373
Match length
                   99
% identity
NCBI Description Z. mays, cultivar COTX amplified 451 region DNA
                   135960
Seq. No.
                   125589 1.R1010
Contig ID
                   jC-atX\overline{N}449157a2
5'-most EST
                   BLASTN
Method
                   g209392
NCBI GI
                   44
BLAST score
                   3.0e-15
E value
                   148
Match length
                   89
% identity
NCBI Description Cloning vector PSU2719 DNA
                   135961
Seq. No.
                   125590 1.R1010
Contig ID
5'-most EST
                   jC-atXN447163r2
                   135962
Seq. No.
Contig ID
                   125591 1.R1010
5'-most EST
                   jC-atXN445148d2
                    135963
Seq. No.
                    125592 1.R1010
Contig ID
 5'-most EST
                    jC-atXN444151r2
                    135964
Seq. No.
                    125593 1.R1010
 Contig ID
 5'-most EST
                    jC-atXN443152r2
```

135965 Seq. No.

125594 2.R1010 Contig ID jC-atXN442143r1 5'-most EST

135966 Seq. No.

125595 1.R1010 Contig ID jC-atXN439146d2 5'-most EST



```
135967
Seq. No.
                   125596 1.R1010
Contig ID
                   jC-atXN438161r2
5'-most EST
                   135968
Seq. No.
                   125597 1.R1010
Contig ID
                    jC-atX\overline{N}414104d2
5'-most EST
                    BLASTX
Method
                    g3420052
NCBI GI
                    420
BLAST score
                    7.0e-41
E value
                    143
Match length
% identity
                   (AC004680) putative ubiqinone reductase [Arabidopsis
NCBI Description
                    thaliana]
                    135969
Seq. No.
                    125598 1.R1010
Contig ID
                    jC-atXN40990a2
5'-most EST
                    BLASTN
Method
                    g493617
NCBI GI
BLAST score
                    41
                    2.0e-13
E value
Match length
                    80
% identity
NCBI Description Synthetic plasimd pHSG399 DNA
                    135970
Seq. No.
                    125599 1.R1010
Contig ID
                    jC-atXN29949r1
5'-most EST
                    BLASTN
Method
                    g209101
NCBI GI
                    34
BLAST score
                    3.0e-09
E value
                    34
Match length
                    100
% identity
                    Shuttle vector consisting of DNA from E.coli and yeast.
NCBI Description
                    >gi 345214_emb_A01519.1_A01519 Nucleotide sequence of
                    multilinker (modified from pUC18)
                    >gi_1250059_gb_I15151_I15151 Sequence 22 from patent US
5460941 >gi_3409283_gb_I89343_I89343 Sequence 4 from patent
                     135971
 Seq. No.
                     125600 1.R1010
 Contig ID
                     jC-atX\overline{N}29084d1
 5'-most EST
                     BLASTN
 Method
                     g3819625
 NCBI GI
                     60
 BLAST score
                     9.0e-25
 E value
                     99
 Match length
```

96 % identity

NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG2217

135972 Seq. No.

125601 1.R1010 Contig ID jC-atXN25759a15'-most EST



```
135973
Seq. No.
                   125602 1.R1010
Contig ID
                   jC-atX\overline{N}32830d1
5'-most EST
                   135974
Seq. No.
                   125604 1.R1010
Contig ID
                   jC-atXN303164r1
5'-most EST
                   BLASTX
Method
                   g2956717
NCBI GI
                   90
BLAST score
                   5.4e-02
E value
                   95
Match length
                   75
% identity
NCBI Description (Y09722) beta-carotene hydroxylase 2 [Capsicum annuum]
                   135975
Seq. No.
                   125606 1.R1010
Contig ID
                   jC-atXN29582r1
5'-most EST
                   BLASTN
Method
                   g4538840
NCBI GI
                   36
BLAST score
                   3.0e-10
E value
                   56
Match length
                   100
% identity
NCBI Description Sus scrofa V-ATPase gene, exon
                   135976
Seq. No.
                   125607 1.R1010
Contig ID
                   jC-atX\overline{N}29241a1
5'-most EST
                   BLASTN
Method
                   g1333680
NCBI GI
                   49
BLAST score
                   4.0e-18
E value
                   61
Match length
                   95
% identity
NCBI Description Cloning vector pKF19k DNA, complete sequence
                    135977
Seq. No.
Contig ID
                    125608 1.R1010
                    jC-atXN288113r1
5'-most EST
                    135978
Seq. No.
                    125609 2.R1010
Contig ID
5'-most EST
                    jC-atXN28761r1
                    135979
Seq. No.
Contig ID
                    125610 2.R1010
                    jC-atX\overline{N}28680f1
 5'-most EST
                    BLASTN
Method
NCBI GI
                    q209392
                    38
BLAST score
                    1.0e-11
E value
                    129
Match length
                    95
 % identity
 NCBI Description Cloning vector PSU2719 DNA
```



Seq. No. 135980

Contig ID 125611_1.R1010 5'-most EST jC-atXN28593r1

Method BLASTN
NCBI GI g58124
BLAST score 36
E value 3.0e-10
Match length 55
% identity 100

NCBI Description Cloning vector pGEM3 (pJMSP-0) polylinker sequence (SP6

polymerase transcription vector)

Seq. No. 135981

Contig ID 125612_1.R1010 5'-most EST jC-atXN27742r1

Method BLASTX
NCBI GI g2130082
BLAST score 230
E value 1.0e-18
Match length 212
% identity 6

NCBI Description protein kinase Xa21 (EC 2.7.1.-) - rice >gi_1122443

(U37133) receptor kinase-like protein [Oryza sativa] >gi 2586085 (U72723) receptor kinase-like protein [Oryza

longistaminata] >gi_1586408_prf__2203451A receptor

kinase-like protein [Oryza sativa]

Seq. No. 135982

Contig ID 125613_1.R1010 5'-most EST jC-atXN26870a1

Seq. No. 135983

Contig ID 125615_1.R1010 5'-most EST jC-atXN264100r2

Seq. No. 135984

Contig ID 125617_1.R1010 5'-most EST jC-atXN25277a1

Seq. No. 135985

Contig ID 125618_1.R1010 5'-most EST jC-atXN24756f2

Seq. No. 135986

Contig ID 125619_1.R1010 5'-most EST jC-atXN23948r2

Method BLASTX
NCBI GI g3056586
BLAST score 270
E value 3.0e-23
Match length 130
% identity 42

NCBI Description (AC004255) T1F9.7 [Arabidopsis thaliana]

Seq. No. 135987

Contig ID 125620_2.R1010 5'-most EST jC-atXN23846r2



Seq. No. Contig ID 5'-most EST	135988 125621_1.R1010 jC-atXN23744r2
Seq. No. Contig ID 5'-most EST	135989 125622_1.R1010 jC-atXN23439r2
Seq. No. Contig ID 5'-most EST	135990 125623_1.R1010 jC-atXN223219d2
Seq. No. Contig ID 5'-most EST	135991 125624_1.R1010 jC-atXN21233d1
Seq. No.	135992
Contig ID	125625_2.R1010
5'-most EST	jC-atXN211218d2
Seq. No.	135993
Contig ID	125626_1.R1010
5'-most EST	jC-atXN120232r2
Seq. No.	135994
Contig ID	125627_1.R1010
5'-most EST	jC-atXN114228r2
Seq. No.	135995
Contig ID	125628_1.R1010
5'-most EST	jC-atXN110229d2
Seq. No.	135996
Contig ID	125629_1.R1010
5'-most EST	jC-atXN107234r1
Seq. No.	135997
Contig ID	125631_1.R1010
5'-most EST	jC-atXN10134d1
Seq. No.	135998

Seq. No. Contig ID 125632 1.R1010 5'-most EST $jC-atX\overline{B}944r2$ 135999 Seq. No.

125634_1.R1010 Contig ID 5'-most EST jC-atXB833r2

Seq. No. 136000 125635 1.R1010 Contig ID 5'-most EST $jC-atX\overline{B}823r2$

136001 Seq. No. 125636_1.R1010 jC-atXB815d2 Contig ID 5'-most EST



 Seq. No.
 136002

 Contig ID
 125637_1.R1010

 5'-most EST
 jC-atXB810r2

Seq. No. 136003

Contig ID 125638_1.R1010 5'-most EST jC-atXB805r2

Seq. No. 136004

Contig ID 125640_1.R1010 5'-most EST jC-atXB761r2

Seq. No. 136005

Contig ID 125641_1.R1010 5'-most EST jC-atXB743d2

Seq. No. 136006

Contig ID 125642_1.R1010 5'-most EST jC-atXB708d2

Seq. No. 136007

Contig ID 125643_1.R1010 5'-most EST jC-atXB632r2

Method BLASTN
NCBI GI g22103
BLAST score 42
E value 5.0e-14
Match length 214
% identity 83

NCBI Description Zea mays A2 gene

Seq. No. 136008

Contig ID 125645_1.R1010 5'-most EST jC-atXB304r2

Seq. No. 136009

Contig ID 125646_1.R1010
5'-most EST jC-atXA34r2
Method BLASTX
NCBI GI g2895866

NCBI GI GZ89380 BLAST score 137 E value 1.0e-07 Match length 95 % identity 83

NCBI Description (AF045770) methylmalonate semi-aldehyde dehydrogenase

[Oryza sativa]

Seq. No. 136010

Contig ID 125647_1.R1010
5'-most EST jC-atXA12f2
Method BLASTN
NCBI GI g58275

BLAST score 54 E value 3.0e-21 Match length 128 % identity 95

NCBI Description Plasmid vector pSU



```
136011
Seq. No.
                  125652 1.R1010
Contig ID
                  jC-atXP86CG9H6T7d2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4512715
                  744
BLAST score
                  6.0e-79
E value
                  191
Match length
                  77
% identity
NCBI Description (AC006569) unknown protein [Arabidopsis thaliana]
                   136012
Seq. No.
                   125656 2.R1010
Contig ID
                   jC-atXP86CG9H4T7d2
5'-most EST
                   BLASTN
Method
NCBI GI
                   q4220641
BLAST score
                   672
                   0.0e + 00
E value
                   924
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUL3, complete sequence [Arabidopsis thaliana]
                   136013
Seq. No.
                   125682 1.R1010
Contig ID
                   jC-atXP86CG9F8T7d2
5'-most EST
                   BLASTX
Method
                   q3643604
NCBI GI
BLAST score
                   203
                   1.0e-135
E value
                   267
Match length
% identity
                   (ACO05395) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   136014
Seq. No.
                   125761 1.R1010
Contig ID
                   jC-atXP86CG4H3T7d2
 5'-most EST
                   BLASTX
Method
                   q584794
NCBI GI
                   363
 BLAST score
                   2.0e-90
 E value
                   235
Match length
                   78
 % identity
                   PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
 NCBI Description
                   >gi_282953_pir__A41779 H+-transporting ATPase (EC 3.6.1.35)
                   - curled-leaved tobacco >gi_170289 (M80489) plasma membrane
                   H+ ATPase [Nicotiana plumbaginifolia]
                   136015
 Seq. No.
```

Contig ID 125771_1.R1010 5'-most EST jC-atXP86CG4G1T7d2

Method BLASTX
NCBI GI g2827630
BLAST score 68
E value 7.0e-86



```
Match length 219
% identity 79
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]
```

 Seq. No.
 136016

 Contig ID
 125784_1.R1010

 5'-most EST
 jC-atXP86CG10D4T7d2

 Method
 BLASTN

 NCBI GI
 g4467358

NCBI GI g4467358
BLAST score 44
E value 3.0e-15
Match length 44
% identity 100

NCBI Description Arabidopsis thaliana mRNA for Phosphatidylinositol 4-Kinase

 Seq. No.
 136017

 Contig ID
 125840_1.R1010

 5'-most EST
 jC-atXP34C153A23T7a1

 Method
 BLASTN

NCBI GI g3941523 BLAST score 45 E value 8.0e-16 Match length 49 % identity 98

NCBI Description Arabidopsis thaliana putative transcription factor (MYB92)

mRNA, complete cds

Seq. No. 136018

Contig ID 125848_1.R1010 5'-most EST jC-atXP34C150P21T7a1

Method BLASTX
NCBI GI g2462834
BLAST score 145
E value 4.0e-12
Match length 92
% identity 47

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 136019

Contig ID 125929 1.R1010

5'-most EST jC-atXP71C222O9T7061d1

Method BLASTX
NCBI GI g2077943
BLAST score 393
E value 9.0e-38
Match length 158
% identity 49

NCBI Description (D88672) phospholipase D [Rattus norvegicus]

Seq. No. 136020

Contig ID 125937_1.R1010 5'-most EST jC-atXP32C147L2T7d2

Method BLASTX
NCBI GI g4432857
BLAST score 317
E value 7.0e-29
Match length 151



% identity 41
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 136021

Contig ID 125943_1.R1010 5'-most EST jC-atXP32C147K8T7d2

Seq. No. 136022

Contig ID 125944_1.R1010

5'-most EST jC-atXP32C147H10T7d2

Method BLASTN
NCBI GI g2342717
BLAST score 66
E value 2.0e-28
Match length 78
% identity 10

NCBI Description Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136023

Contig ID 125951_1.R1010 5'-most EST jC-atXP32C147J9T7d2

Method BLASTN
NCBI GI g1946354
BLAST score 288
E value 1.0e-161
Match length 654
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC T06B20 genomic

sequence, complete sequence

Seq. No. 136024

Contig ID 125966_1.R1010 5'-most EST jC-atXP32C147F21T7d2

Method BLASTN
NCBI GI g4589421
BLAST score 167
E value 1.0e-88
Match length 606
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K5K13, complete sequence

Seq. No. 136025

Contig ID 126017_1.R1010 5'-most EST jC-atXP31C146J10T7d2

Method BLASTN
NCBI GI g2656032
BLAST score 33
E value 9.0e-09
Match length 104
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MZF18

Seq. No. 136026

Contig ID 126040_1.R1010

NCBI Description

MXC20



```
jC-atXP31C14504T7d2
5'-most EST
                   BLASTN
Method
                   q3510347
NCBI GI
BLAST score
                   332
                   0.0e + 00
E value
Match length
                   533
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MSJ11, complete sequence [Arabidopsis thaliana]
                   136027
Seq. No.
Contig ID
                   126078 1.R1010
                   jC-atX\overline{P}31C144G24T7d2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3912921
                   187
BLAST score
                   9.0e-14
E value
                   154
Match length
                   37
% identity
                   (AF001308) G/T DNA mismatch repair enzyme [Arabidopsis
NCBI Description
                   thaliana]
                   136028
Seq. No.
Contig ID
                   126158 1.R1010
                   jC-atX\overline{P}29C135M10T7005d1
5'-most EST
Method
                   BLASTX
                   q4455363
NCBI GI
                   468
BLAST score
                   2.0e-68
E value
                   188
Match length
                   78
% identity
                   (AL035524) Medicago nodulin N21-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   136029
Seq. No.
Contig ID
                   126168 1.R1010
                   jC-atXP29C135J16T7065d1
5'-most EST
                   BLASTX
Method
                   q2443883
NCBI GI
BLAST score
                   625
                   5.0e-65
E value
                   184
Match length
% identity
                   73
                   (AC002294) Similar to RPS-2 disease resistance protein
NCBI Description
                    [Arabidopsis thaliana]
                   136030
Seq. No.
Contig ID
                   126250 2.R1010
5'-most EST
                   g2597732
Method
                   BLASTN
                   q2656031
NCBI GI
BLAST score
                   239
                   1.0e-132
E value
Match length
                   382
 % identity
                   95
```

16200

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



Seq. No. 136031

Contig ID 126268 1.R1010

jC-atXP112C130023T7a1 5'-most EST

12

Method BLASTX NCBI GI g3150404 BLAST score 97 5.0e-03 E value Match length 95

% identity NCBI Description (AC004165) putative mitochondrial carrier protein

[Arabidopsis thaliana]

Seq. No. 136032

Contig ID 126278 1.R1010

5'-most EST jC-atXP112C129022T7a1

Seq. No. 136033

Contig ID 126288 1.R1010

jC-atXP112C129G21T7a1 5'-most EST

Method BLASTN NCBI GI q2689438 BLAST score 569 E value 0.0e + 00Match length 593 % identity 94

NCBI Description Arabidopsis thaliana BAC F2401 chromosome 1, complete

sequence [Arabidopsis thaliana]

Seq. No. 136034

Contig ID 126342 1.R1010 jC-atXP98CH8D1T7b1 5'-most EST

Method BLASTX NCBI GI g2244973 BLAST score 543 2.0e-55 E value Match length 169 % identity 72

NCBI Description (Z97340) similarity to extensin class 1 protein

[Arabidopsis thaliana]

Seq. No. 136035

126438 1.R1010 Contig ID

5'-most EST jC-atXP46C174G2T7032a1

Method BLASTX NCBI GI g3047096 BLAST score 842 2.0e-90 E value 187 Match length % identity 89

(AF058826) similar to eukaryotic protein kinase domains NCBI Description

(Pfam: pkinase.hmm, score: 189.74) [Arabidopsis thaliana]

136036 Seq. No.

126552 1.R1010 Contig ID

5'-most EST jC-atXP18C115D23T7029a1

Method BLASTN



NCBI GI q2760316 BLAST score 305 1.0e-171 E value Match length 404 % identity 97 NCBI Description The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana] Seq. No. 136037 Contig ID 126554 1.R1010 5'-most EST g2739541

Seq. No. 136038

126561 1.R1010 Contig ID

5'-most EST iC-atXP18C113P14T7004a1

Method BLASTN NCBI GI g2583106 BLAST score 288 E value 1.0e-161 Match length 347 % identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F4L23 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136039

Contig ID 126565 1.R1010

5'-most EST jC-atXP18C113M5T7026a1

Method BLASTX NCBI GI g3114901 BLAST score 135 3.0e-19 E value Match length 91 % identity 55

NCBI Description (AJ005804) pcbere [Populus balsamifera subsp. trichocarpa]

>gi 3114905 emb CAA06709.1 (AJ005806) pceberh [Populus

balsamifera subsp. trichocarpa]

Seq. No. 136040

126576 1.R1010 Contig ID

5'-most EST jC-atXP18C111E10T7064a1

Method BLASTN NCBI GI g598848 BLAST score 40 5.0e-13 E value Match length 44 98 % identity

NCBI Description Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No. 136041

126591 1.R1010 Contig ID

5'-most EST jC-atXP18C108017T7022a1

Method BLASTN NCBI GI g2462264 BLAST score 51 1.0e-19 E value Match length 51 % identity 100



NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 136042

Contig ID 126595 1.R1010

Method BLASTN
NCBI GI g2264317
BLAST score 213
E value 1.0e-116
Match length 288
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUG13, complete sequence [Arabidopsis thaliana]

Seq. No. 136043

Contig ID 126602_1.R1010 5'-most EST jC-atXP104CE8A3T7b1

Method BLASTN
NCBI GI g4680765
BLAST score 407
E value 0.0e+00
Match length 446
% identity 98

NCBI Description Arabidopsis thaliana BAC F14I23 from chromosome V near 69

cM, complete sequence

Seq. No. 136044

Contig ID 126613_1.R1010 5'-most EST jC-atXP104CE7B7T7b1

Method BLASTX
NCBI GI g4678920
BLAST score 767
E value 1.0e-81
Match length 158
% identity 98

NCBI Description (AL049711) putative heat shock transcription factor

[Arabidopsis thaliana]

Seq. No. 136045

Contig ID 126653_1.R1010 5'-most EST jC-atXP104CE10C2T7b1

Method BLASTN
NCBI GI g4165340
BLAST score 536
E value 0.0e+00
Match length 626
% identity 96

NCBI Description Arabidopsis thaliana chromosome I BAC F11M15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136046

Contig ID 126676_1.R1010

5'-most EST jC-atXP102CE6A2T7035d1

Method BLASTX
NCBI GI g4572681
BLAST score 235
E value 4.0e-19



Match length 67 % identity 66

NCBI Description (AC006954) putative ubiquitin carboxyl terminal hydrolase [Arabidopsis thaliana]

[indotedpoid cir

Seq. No. 136047 Contig ID 126683

Contig ID 126683_1.R1010 5'-most EST jC-atXP102CE5F3T7b1

Method BLASTX
NCBI GI g3650032
BLAST score 497
E value 4.0e-50
Match length 85
% identity 100

NCBI Description (AC005396) gibberellin-regulated protein GAST1-like

[Arabidopsis thaliana]

Seq. No. 136048

Contig ID 126684 1.R1010

5'-most EST jC-atXP102CE5F2T7016d1

Method BLASTX
NCBI GI g2702376
BLAST score 201
E value 3.0e-15
Match length 49
% identity 80

NCBI Description (AF038605) Similar to acyl-CoA dehydrogenase; coded for by

C. elegans cDNA yk58h2.3; coded for by C. elegans cDNA yk466c12.3; coded for by C. elegans cDNA yk258d6.3; coded for by C. elegans cDNA yk158e10.3; coded for by C. elegans

cDNA yk427... >gi 4455127 gb AAD21088 (AF127558)

isovaleryl-CoA dehydrogenase precursor [Caenorhabditis

elegans]

Seq. No. 136049

Contig ID 126690 1.R1010

5'-most EST jC-atXP102CE5E3T7055d1

Method BLASTX
NCBI GI g3047123
BLAST score 407
E value 2.0e-39
Match length 116
% identity 63

NCBI Description (AF058919) similar to the family of glycosyl hydrolases

[Arabidopsis thaliana]

Seq. No. 136050

Contig ID 126693 1.R1010 5'-most EST jC-atXP102CE5D5T7b1

Method BLASTX
NCBI GI g1651965
BLAST score 189
E value 6.0e-14
Match length 107
% identity 39

NCBI Description (D90901) hypothetical protein [Synechocystis sp.]



```
Seq. No.
Contig ID
                   126698 1.R1010
5'-most EST
                   jC-atXP102CE5C7T7054d1
Method
                   BLASTX
NCBI GI
                   q82200
BLAST score
                   319
E value
                   3.0e-29
Match length
                   96
% identity
                   60
NCBI Description hypothetical protein 1244 - common tobacco chloroplast
Seq. No.
                  136052
                  126718 1.R1010
Contig ID
5'-most EST
                   jC-atX\overline{P}102CE3H4T7091d1
Method
                  BLASTN
NCBI GI
                   q4589950
BLAST score
                   238
E value
                  1.0e-131
Match length
                   273
% identity
                  97
                  Arabidopsis thaliana chromosome II BAC T28P16 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  136053
                  126876_1.R1010
Contig ID
5'-most EST
                   jC-atXP96C249K4T7b1
Method
                  BLASTX
NCBI GI
                  q1619962
BLAST score
                   287
E value
                   6.0e-69
Match length
                  192
                   67
% identity
NCBI Description (U72068) catalase isozyme [Pseudomonas fluorescens]
Seq. No.
                   136054
                   126940 1.R1010
Contig ID
5'-most EST
                  jC-atXP92C249E2T7006d1
Seq. No.
                   136055
                  126958 1.R1010
Contig ID
5'-most EST
                   jC-atXP92C247P6T7035d1
Method
                  BLASTX
NCBI GI
                  g4006829
BLAST score
                   448
E value
                  2.0e-44
                  212
Match length
% identity
NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  136056
                  126967 1.R1010
Contig ID
```

5'-most EST jC-atXP92C247N11T7066d1

Method BLASTX
NCBI GI g2347199
BLAST score 423
E value 1.0e-46
Match length 176

Method NCBI GI



```
% identity
                  (AC002338) protein kinase isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  136057
                  126982 1.R1010
Contig ID
5'-most EST
                  jC-atXP92C246N12T7026d1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  51
E value
                  2.0e-19
Match length
                  59
% identity
                  97
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  136058
Seq. No.
                  126986 3.R1010
Contig ID
5'-most EST
                  q958192
Method
                  BLASTX
NCBI GI
                  q3928099
BLAST score
                  284
                  1.0e-28
E value
Match length
                  149
% identity
                  24
NCBI Description
                  (AC005770) unknown protein [Arabidopsis thaliana]
Seq. No.
                  136059
                  127023 1.R1010
Contig ID
5'-most EST
                  jC-atXP4C88F5T7052a1
Method
                  BLASTX
NCBI GI
                  g407938
BLAST score
                  229
E value
                  4.0e-38
Match length
                  154
% identity
                  53
NCBI Description
                  (U02494) epoxide hydrolase [Solanum tuberosum]
                  136060
Seq. No.
                  127026 1.R1010
Contig ID
5'-most EST
                  jC-atXP123C117E8T7052a1
Seq. No.
                  136061
                  127035 1.R1010
Contig ID
5'-most EST
                  jC-atXP4C88D9T7044a1
Method
                  BLASTX
NCBI GI
                  g421924
BLAST score
                  237
                  8.0e-25
E value
Match length
                  145
                  48
% identity
                  peroxidase (EC 1.11.1.7) - tomato >gi 296910 emb CAA50597
NCBI Description
                   (X71593) peroxidase [Lycopersicon esculentum]
Seq. No.
                  136062
Contig ID
                  127139 1.R1010
5'-most EST
                  jC-atXP46C172I6T7029a1
                  BLASTX
```

16206

g4510388



BLAST score 8.0e-94 E value Match length 165 % identity 100 NCBI Description (AC007017) unknown protein [Arabidopsis thaliana] Seq. No. 136063 127150 1.R1010 Contig ID 5'-most EST jC-atXP46C172G2T7028a1 Method BLASTX NCBI GI g282430

NCBI GI g282430
BLAST score 435
E value 2.0e-42
Match length 234
% identity 40

NCBI Description leucine--tRNA ligase (EC 6.1.1.4) - Bacillus subtilis >qi 143148 (M88581) transfer RNA-Leu synthetase [Bacillus

subtilis]

Seq. No. 136064

Contig ID 127156 1.R1010

5'-most EST jC-atXP46C172F20T7020a1

Seq. No. 136065

Contig ID 127190 1.R1010

5'-most EST jC-atXP44C170K19T7046a1

Method BLASTX
NCBI GI g3548808
BLAST score 242
E value 5.0e-30
Match length 158
% identity 48

NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 136066

Contig ID 127210 1.R1010

5'-most EST jC-atXP44C170H11T7028a1

Method BLASTN
NCBI GI g3860242
BLAST score 589
E value 0.0e+00
Match length 673
% identity 97

NCBI Description Arabidopsis thaliana chromosome I BAC T13M11 genomic

sequence, complete sequence

Seq. No. 136067

Contig ID 127213 1.R1010

5'-most EST jC-atXP44C169M4T7089a1

Method BLASTN
NCBI GI 94580732
BLAST score 195
E value 1.0e-105
Match length 331
% identity 96

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F5J5,

complete sequence



```
Seq. No.
                  136068
                  127219 1.R1010
Contig ID
5'-most EST
                  jC-atXP44C169L24T7081a1
                  BLASTX
Method
NCBI GI
                  q4314391
BLAST score
                  597
E value
                  2.0e-76
Match length
                  179
% identity
                  88
NCBI Description
                  (AC006232) unknown protein [Arabidopsis thaliana]
Seq. No.
                  136069
                  127237 1.R1010
Contig ID
                  jC-atXP44C168J10T7082a1
5'-most EST
Method
                  BLASTX
                  q3142300
NCBI GI
BLAST score
                  43
                  2.0e-47
E value
Match length
                  144
% identity
                  67
                  (AC002411) Contains similarity to pre-mRNA processing
NCBI Description
                  protein PRP39 gb L29224 from S. cerevisiae. ESTs gb_R64908
                  and gb_T88158, gb_N38703 and gb_AA651043 come from this
                  gene. [Arabidopsis thaliana]
                  136070
Seq. No.
                  127250 1.R1010
Contig ID
                  jC-atXP37C159B1T7d2
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3738309
BLAST score
                  593
E value
                  7.0e-87
Match length
                  283
% identity
                  65
NCBI Description
                  (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                  136071
Contig ID
                  127300 1.R1010
5'-most EST
                  jC-atXP37C157I19T7d2
                  BLASTN
Method
                  g2462264
NCBI GI
BLAST score
                  47
                  5.0e-17
E value
                  51
Match length
% identity
                  98
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  136072
Seq. No.
                  127331 1.R1010
Contig ID
```

5'-most EST jC-atXP2C79D5T7092a1

Method BLASTN g2462264 NCBI GI BLAST score 54 3.0e-21E value Match length 54 100 % identity



NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Method BLASIN

NCBI GI g2864607

BLAST score 519

E value 0.0e+00

Match length 547

% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6

(ESSAII project)

Seq. No. 136074

Contig ID 127358 1.R1010

5'-most EST jC-atXP2C77G12T7067a1

Method BLASTX
NCBI GI g2827143
BLAST score 712
E value 3.0e-75
Match length 167
% identity 79

NCBI Description (AF027174) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 136075

Contig ID 127383 1.R1010

5'-most EST jC-atXP2C75H9T7035a1

Method BLASTX
NCBI GI g4651204
BLAST score 165
E value 4.0e-11
Match length 58
% identity 50

NCBI Description (AB026262) ring finger protein [Cicer arietinum]

Seq. No. 136076

Contig ID 127385 2.R1010

5'-most EST g2413857
Method BLASTN
NCBI GI g4185128
BLAST score 384
E value 0.0e+00
Match length 414
% identity 98

NCBI Description Arabidopsis thaliana chromosome II P1 MSF3 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136077

Contig ID 127408 1.R1010

5'-most EST jC-atXP2C73H10T7012a1

Method BLASTN NCBI GI g2462264 BLAST score 42

E value 6.0e-14
Match length 42



% identity 100
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 136078

Contig ID 127417_1.R1010

5'-most EST jC-atXP26C128L4T7071a1

Method BLASTN
NCBI GI g2980787
BLAST score 551
E value 0.0e+00
Match length 669
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2

(ESSAII project)

Seq. No. 136079

Contig ID 127421 1.R1010

5'-most EST jC-atXP26C128L1T7055a1

Method BLASTN
NCBI GI g3241925
BLAST score 249
E value 1.0e-137
Match length 635
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOK9, complete sequence [Arabidopsis thaliana]

Seq. No. 136080

Contig ID 127517 1.R1010

5'-most EST jC-atX\overline{P}24C123N7T7008a1

Method BLASTN
NCBI GI g2462264
BLAST score 54
E value 3.0e-21
Match length 54
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 136081

Contig ID 127535_1.R1010

5'-most EST jC-atXP24C123M22T7087a1

Seq. No. 136082

Contig ID 127565 1.R1010

5'-most EST jC-atXP24C123J23T7038a1

Method BLASTN
NCBI GI g4757414
BLAST score 489
E value 0.0e+00
Match length 588
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYF24, complete sequence

Seq. No. 136083

Contig ID 127566 1.R1010

5'-most EST jC-atXP24C123J17T7030d1



Method BLASTN
NCBI GI g2656028
BLAST score 273
E value 1.0e-152
Match length 690
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNF13

Seq. No. 136084

Contig ID 127573 1.R1010

5'-most EST jC-atXP24C123I21T7066d1

Method BLASTN
NCBI GI g2564051
BLAST score 247
E value 1.0e-136
Match length 689
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWD9, complete sequence [Arabidopsis thaliana]

Seq. No. 136085

Contig ID 127575_1.R1010

5'-most EST jC-atXP24C123I19T7058a1

Method BLASTX
NCBI GI g3924596
BLAST score 410
E value 7.0e-40
Match length 102
% identity 80

NCBI Description (AF069442) putative phospho-ser/thr phosphatase

[Arabidopsis thaliana]

Seq. No. 136086

Contig ID 127577_1.R1010

5'-most EST jC-atXP24C123I18T7050a1

Method BLASTX
NCBI GI g1532175
BLAST score 411
E value 8.0e-40
Match length 124
% identity 76

NCBI Description (U63815) similar to protein disulfide isomerase

[Arabidopsis thaliana]

Seq. No. 136087

Contig ID 127585_1.R1010

5'-most EST jC-atXP24C123F9T7060a1

Method BLASTX
NCBI GI g2335101
BLAST score 562
E value 3.0e-89
Match length 166
% identity 95

NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

Seq. No. 136088

127590 1.R1010 Contig ID 5'-most EST iC-atXP24C123E1T7020d1 BLASTX Method g3738310 NCBI GI 428 BLAST score 4.0e-96 E value Match length 207 % identity 89 (AC005309) putative nuclear protein [Arabidopsis thaliana] NCBI Description 136089 Seq. No. Contig ID 127591_1.R1010 5'-most EST jC-atXP24C123E1T7020a1 Method BLASTN NCBI GI q2462264 BLAST score 57 6.0e-23 E value Match length 57 % identity 100 NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 136090 Seq. No. 127595 1.R1010 Contig ID jC-atXP24C123D13T7083a1 5'-most EST Method BLASTN NCBI GI q4757395 BLAST score 538 E value 0.0e+00Match length 566 % identity 99 NCBI Description K21L13, complete sequence Seq. No. 136091 127604 1.R1010 Contig ID

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

jC-atXP24C123D15T7091a1 5'-most EST

Method BLASTX NCBI GI q3559805 BLAST score 150 E value 4.0e-29 Match length 123 % identity 56

(AJ006787) putative phytochelatin synthetase [Arabidopsis NCBI Description

thaliana]

Seq. No. 136092

127607 1.R1010 Contig ID

5'-most EST jC-atXP24C123D12T7075d1

Method BLASTX NCBI GI q4646199 BLAST score 536 E value 1.0e-114 224 Match length 32 % identity

(AC007230) EST gb T22166 comes from this gene. [Arabidopsis NCBI Description

thaliana]

% identity



```
Seq. No.
Contig ID
                  127616 1.R1010
5'-most EST
                  jC-atXP24C123C19T7035a1
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  44
                  3.0e-15
E value
Match length
                  52
% identity
                  96
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  136094
Seq. No.
Contig ID
                  127619 1.R1010
5'-most EST
                  jC-atXP24C123C10T7019a1
Method
                  BLASTN
NCBI GI
                  q3449327
BLAST score
                  328
E value
                  0.0e + 00
Match length
                   600
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MCA23, complete sequence [Arabidopsis thaliana]
Seq. No.
                  136095
Contig ID
                  127629 1.R1010
5'-most EST
                  jC-atXP24C122L18T7093a1
Method
                  BLASTN
NCBI GI
                  g2244788
BLAST score
                   372
E value
                  0.0e + 00
                  792
Match length
                  97
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
Seq. No.
                   136096
Contig ID
                   127630 1.R1010
5'-most EST
                   jC-atXP24C122L17T7085a1
Method
                  BLASTX
NCBI GI
                  q3914449
BLAST score
                  385
E value
                   6.0e-37
Match length
                  83
% identity
                  89
                  26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                  7) >gi 3172331 (AF041258) 26S proteasome subunit 7 [Prunus
                  persica]
                  136097
Seq. No.
                  127643 1.R1010
Contig ID
5'-most EST
                  jC-atXP24C120P14T7089a1
Method
                  BLASTN
NCBI GI
                  g2290120
BLAST score
                  38
                  1.0e-11
E value
                  65
Match length
```



NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No. 136098

Contig ID 127673 1.R1010

5'-most EST jC-atXP24C120014T7033a1

Seq. No. 136099

Contig ID 127704_1.R1010

5'-most EST jC-atXP22C119D7T7023a1

Method BLASTN
NCBI GI g4165340
BLAST score 411
E value 0.0e+00
Match length 535
% identity 88

NCBI Description Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136100

Contig ID 127705 1.R1010

5'-most EST jC-atXP22C119D6T7015a1

Method BLASTN
NCBI GI g2244950
BLAST score 356
E value 0.0e+00
Match length 524
% identity 93

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 136101

Contig ID 127709 1.R1010

5'-most EST jC-atXP22C119C8T7054a1

Method BLASTX
NCBI GI g2493482
BLAST score 259
E value 4.0e-22
Match length 135
% identity 46

NCBI Description GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE)

(GLYCEROKINASE) (GK) >gi_1399490 (U49666) glycerol kinase

[Pseudomonas aeruginosa]

Seq. No. 136102

Contig ID 127713 1.R1010

Method BLASTN
NCBI GI g3859658
BLAST score 46
E value 2.0e-16
Match length 104
% identity 88

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1

(ESSAII project)

Seq. No. 136103

E value Match length



```
127714 1.R1010
Contig ID
                   jC-atX\overline{P}22C119C10T7070a1
5'-most EST
Method
                   BLASTX
                   q3046695
NCBI GI
BLAST score
                   146
                   4.0e-13
E value
Match length
                   68
% identity
                   66
NCBI Description
                  (AL022224) putative protein [Arabidopsis thaliana]
                   136104
Seq. No.
Contig ID
                   127716 1.R1010
5'-most EST
                   g3449441
Method
                   BLASTX
NCBI GI
                   g4587610
BLAST score
                   60
                   9.0e-18
E value
Match length
                   69
% identity
                   72
                  (AC006951) putative indole-3-glycerol phosphate synthase
NCBI Description
                   precursor [Arabidopsis thaliana]
                   136105
Seq. No.
Contig ID
                   127724 1.R1010
5'-most EST
                   jC-atXP22C116L16T7077a1
Method
                   BLASTX
NCBI GI
                   g3128168
BLAST score
                   287
                   2.0e-25
E value
Match length
                   86
% identity
                   58
NCBI Description
                   (AC004521) putative carboxyl-terminal peptidase
                   [Arabidopsis thaliana]
Seq. No.
                   136106
                   127735 1.R1010
Contig ID
5'-most EST
                   jC-atXP22C116I7T7017a1
Seq. No.
                   136107
Contig ID
                   127738 1.R1010
5'-most EST
                   jC-atXP22C116H22T7001a1
Method
                   BLASTX
NCBI GI
                   g2244779
BLAST score
                   356
E value
                   1.0e-33
Match length
                   75
% identity
                   92
NCBI Description
                   (Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   136108
                   127758 1.R1010
Contig ID
5'-most EST
                   jC-atXP22C114O10T7066a1
                   BLASTX
Method
NCBI GI
                   g2098713
BLAST score
                   188
```

16215

9.0e-27



```
% identity
NCBI Description
                  (U82977) pectinesterase [Citrus sinensis]
                  136109
Seq. No.
                  127791 1.R1010
Contig ID
                  jC-atXP19C111N8T7083a1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g598848
BLAST score
                  40
                  8.0e-13
E value
Match length
                  64
                  92
% identity
NCBI Description Human HepG2 3' region MboI cDNA, clone hmd4h12m3
                  136110
Seq. No.
                  127796 1.R1010
Contig ID
                  jC-atXP19C111M8T7043a1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2462264
                  52
BLAST score
E value
                  6.0e-20
Match length
                  56
                  98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  136111
                  127809 1.R1010
Contig ID
5'-most EST
                  jC-atXP19C111I7T7026a1
Method
                  BLASTN
NCBI GI
                  q531828
BLAST score
                  35
                  8.0e-10
E value
                  70
Match length
% identity
                  90
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  136112
Contig ID
                  127837 1.R1010
5'-most EST
                  jC-atXP19C109M16T7086a1
Method
                  BLASTN
NCBI GI
                  g2245126
BLAST score
                  230
E value
                  1.0e-126
Match length
                  419
% identity
                  98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  136113
Contig ID
                  127838 1.R1010
5'-most EST
                  q550218
Method -
                  BLASTN
NCBI GI
                  q2760167
BLAST score
                  299
E value
                  1.0e-167
Match length
                  684
% identity
                  96
```



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No. 136114

Contig ID 127850 1.R1010

5'-most EST jC-atXP19C109K10T7077a1

Method BLASTX
NCBI GI g1495366
BLAST score 339
E value 1.0e-49
Match length 167
% identity 60

NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

Seq. No. 136115

Contig ID 127867 1.R1010

5'-most EST jC-atXP13C104N16T7086a1

Method BLASTX
NCBI GI g3386604
BLAST score 299
E value 8.0e-27
Match length 56
% identity 100

NCBI Description (AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No. 136116

Contig ID 127906_1.R1010

5'-most EST jC-atXP13C104B13T7039a1

Method BLASTN
NCBI GI g3241927
BLAST score 296
E value 1.0e-165
Match length 471
% identity 91

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

MTE17, complete sequence [Arabidopsis thaliana]

Seq. No. 136117

Contig ID 127925 1.R1010

Method BLASTX
NCBI GI g2275196
BLAST score 702
E value 6.0e-74
Match length 219
% identity 51

NCBI Description (AC002337) water stress-induced protein, WSI76 isolog

[Arabidopsis thaliana] >gi 4630746 gb AAD26596.1 AC007236 1

(AC007236) water stress-induced protein [Arabidopsis

thaliana]

Seq. No. 136118

Contig ID 127928_1.R1010

5'-most EST jC-atXP12C99P16T7037a1

Method BLASTN NCBI GI g2462264

BLAST score 50



E value 7.0e-19 Match length 54

% identity 98

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 136119

Contig ID 127952 1.R1010

5'-most EST jC-atXP12C99F4T7006a1

Method BLASTN
NCBI GI 94580745
BLAST score 333
E value 0.0e+00
Match length 599
% identity 98

NCBI Description Arabidopsis thaliana chromosome 1 BAC F1003 sequence,

complete sequence

Seq. No. 136120

Contig ID 127957 1.R1010

5'-most EST jC-atXP12C99D14T7001a1

Method BLASTN
NCBI GI g4510338
BLAST score 350
E value 0.0e+00
Match length 594
% identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC F2H17 genomic

sequence, complete sequence

Seq. No. 136121

Contig ID 127976 1.R1010

5'-most EST jC-atXP12C103J22T7078a1

Method BLASTN
NCBI GI g4586241
BLAST score 186
E value 1.0e-100
Match length 578
% identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18

(ESSA project)

Seg. No. 136122

Contig ID 127986 1.R1010

5'-most EST jC-atXP12C103G15T7072a1

Method BLASTN
NCBI GI g3402695
BLAST score 528
E value 0.0e+00
Match length 592
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T3K9 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136123

Contig ID 128000_1.R1010

5'-most EST jC-atXP12C103C6T7051a1

Method BLASTX



NCBI GI g2129698 BLAST score 423 E value 2.0e-55 Match length 153 % identity 74

NCBI Description protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana

>gi_1054633_emb_CAA63387_ (X92728) protein kinase

[Arabidopsis thaliana]

Seq. No. 136124

Contig ID 128004 1.R1010

5'-most EST jC-atXP12C103B5T7046a1

Method BLASTN
NCBI GI g4757404
BLAST score 307
E value 1.0e-172
Match length 597
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MLJ15, complete sequence

Seq. No. 136125

Contig ID 128019_1.R1010

5'-most EST jC-atXP123C117P11T7032d1

Method BLASTX
NCBI GI g2506277
BLAST score 548
E value 6.0e-56
Match length 143
% identity 74

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60

KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi 806808

(U21139) chaperonin precursor [Pisum sativum]

Seq. No. 136126

Contig ID 128081 1.R1010

Method BLASTN
NCBI GI g3860242
BLAST score 306
E value 1.0e-171
Match length 602
% identity 98

NCBI Description Arabidopsis thaliana chromosome I BAC T13M11 genomic

sequence, complete sequence

Seq. No. 136127

Contig ID 128084_1.R1010

5'-most EST jC-atXP125C135G9T7053a1

Method BLASTN
NCBI GI g2462264
BLAST score 56
E value 2.0e-22
Match length 56
% identity 100

NCBI Description Cucumis sativus mRNA for patatin-like protein, partial



```
Seq. No.
                  136128
                  128119 1.R1010
Contig ID
5'-most EST
                  jC-atXP123C119N23T7058a1
                  BLASTX
Method
                  g4220454
NCBI GI
BLAST score
                  90
E value
                  4.0e-36
Match length
                  184
% identity
                  39
NCBI Description
                  (AC006216) Similar to gi 3413714 T19L18.21 putative
                  myrosinase-binding protein from Arabidopsis thaliana BAC
                  gb AC004747. ESTs gb 65870 and gb T20812 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  136129
Contig ID
                  128126 1.R1010
5'-most EST
                  jC-atXP123C118M7T7007a1
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  48
E value
                  1.0e-17
Match length
                  111
% identity
                  93
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  136130
                  128139 2.R1010
Contig ID
5'-most EST
                  q2048438
Method
                  BLASTX
NCBI GI
                  g2252854
BLAST score
                  433
E value
                  1.0e-42
Match length
                  80
                  97
% identity
NCBI Description
                  (AF013294) similar to auxin-induced protein [Arabidopsis
                  thaliana]
Seq. No.
                  136131
                  128161 1.R1010
Contig ID
5'-most EST
                  jC-atXP123C117F2T7076a1
Method
                  BLASTN
NCBI GI
                  g3785992
BLAST score
                  400
E value
                  0.0e+00
Match length
                  565
% identity
                  96
                  Arabidopsis thaliana chromosome II BAC T6A23 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
```

Seq. No. 136132

128181 1.R1010 Contig ID 5'-most EST jC-atXP122C159H21T7032a1

Method BLASTX NCBI GI g1351747 BLAST score 752 E value 9.0e-80 Match length 219



Seg. No. 136133

Contig ID 128187 1.R1010

5'-most EST jC-atXP122C159B8T7063a1

Method BLASTN
NCBI GI g4510408
BLAST score 359
E value 0.0e+00
Match length 687
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T1E2 genomic

sequence, complete sequence

Seq. No. 136134

Contig ID 128201 1.R1010

5'-most EST jC-atXP122C156L23T7030a1

Method BLASTX
NCBI GI g2829896
BLAST score 152
E value 3.0e-24
Match length 227
% identity 42

NCBI Description (AC002311) highly similar to auxin-regulated protein GH3,

gp X60033 18591 [Arabidopsis thaliana]

Seq. No. 136135

Contig ID 128219_1.R1010

5'-most EST jC-atXP122C120G1T7076a1

Method BLASTX
NCBI GI g3980380
BLAST score 424
E value 2.0e-41
Match length 103
% identity 85

NCBI Description (AC004561) putative enolase [Arabidopsis thaliana]

Seq. No. 136136

Contig ID 128225 1.R1010

5'-most EST jC-at \overline{XP} 122C118I9T7035a1

Seq. No. 136137

Contig ID 128252_1.R1010

5'-most EST jC-atXP122C117J13T7020a1

Method BLASTX
NCBI GI g2194126
BLAST score 300
E value 5.0e-34
Match length 112
% identity 73

NCBI Description (AC002062) EST gb T43335 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 136138

Contig ID 128323_1.R1010



```
jC-atXP121C118B4T7038d1
5'-most EST
Method
                  BLASTX
                  q4587680
NCBI GI
BLAST score
                  561
                  1.0e-57
E value
Match length
                  116
% identity
                  90
                 (AC007197) putative cytochrome p450 [Arabidopsis thaliana]
NCBI Description
                  136139
Seq. No.
Contig ID
                  128346 1.R1010
5'-most EST
                  jC-atXP119C209I19T7063a1
Method
                  BLASTN
NCBI GI
                  q531828
BLAST score
                  52
                  5.0e-20
E value
Match length
                  64
% identity
                  95
NCBI Description Cloning vector pSport1, complete cds
                  136140
Seq. No.
                  128373 1.R1010
Contig ID
5'-most EST
                  jC-atXP119C193023T7060a1
Method
                  BLASTX
NCBI GI
                  g2832677
BLAST score
                  112
E value
                  4.0e-27
Match length
                  198
% identity
                  44
NCBI Description (AL021712) hypothetical protein [Arabidopsis thaliana]
                  136141
Seq. No.
                  128405 1.R1010
Contig ID
5'-most EST
                  jC-atXP119C156J1T7081a1
Seq. No.
                  136142
                  128405 2.R1010
Contig ID
5'-most EST
                  jC-atXP119C155P21T7041a1
                  BLASTN
Method
NCBI GI
                  q2462264
BLAST score
                  33
E value
                  8.0e-09
Match length
                  41
                  95
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  136143
                  128441 1.R1010
Contig ID
                  jC-atXP100CE3E11T7b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4467145
BLAST score
                  804
                  5.0e-86
E value
Match length
                  153
% identity
                  100
                   (AL035540) farnesylated protein (ATFP6) [Arabidopsis
NCBI Description
```

16222

thaliana]



```
136144
Seq. No.
Contig ID
                  128507 1.R1010
5'-most EST
                   jC-atXN593177r1
Method
                  BLASTX
NCBI GI
                   g2738996
BLAST score
                   231
                  1.0e-18
E value
Match length
                   140
% identity
                  75
NCBI Description (AF022457) CYP97B2p [Glycine max]
Seq. No.
                   136145
Contig ID
                   128511 1.R1010
5'-most EST
                   jC-atXN567190a1
Method
                  BLASTN
NCBI GI
                   q2739021
BLAST score
                   33
E value
                   1.0e-08
Match length
                   37
                   97
% identity
NCBI Description
                  Rhododendron metternichii var. hondoense CT repeats,
                  genomic sequence
                   136146
Seq. No.
Contig ID
                   128527 1.R1010
5'-most EST
                   jC-atXN43264d1
Method
                  BLASTN
NCBI GI
                   q432601
BLAST score
                   37
                   8.0e-11
E value
Match length
                   37
% identity
                   100
                  MLC1c/1s=cardiac/slow skeletal alkali myosin light-chain
NCBI Description
                   {5' region} [chickens, liver, Genomic, 607 nt]
Seq. No.
                   136147
                   128533 1.R1010
Contig ID
5'-most EST
                   jC-atXN40185d1
Seq. No.
                   136148
                   128538 1.R1010
Contig ID
5'-most EST
                   jC-atXN392166a1
Method
                   BLASTX
NCBI GI
                   g4741187
BLAST score
                   406
                   3.0e - 39
E value
Match length
                   186
% identity
                   46
                  (AL049746) putative protein [Arabidopsis thaliana]
NCBI Description
                   136149
Seq. No.
Contig ID
                   128540 1.R1010
5'-most EST
                   jC-atXN38694d1
```

Seq. No. 136150

Contig ID 128542 1.R1010



```
5'-most EST
                  jC-atXN373140d1
                  136151
Seq. No.
Contig ID
                  128557 1.R1010
5'-most EST
                  jC-atXN28071r1
Method
                  BLASTN
NCBI GI
                  q432601
BLAST score
                  36
                  3.0e-10
E value
Match length
                  36
% identity
                  100
NCBI Description
                  MLC1c/1s=cardiac/slow skeletal alkali myosin light-chain
                  {5' region} [chickens, liver, Genomic, 607 nt]
Seq. No.
                  136152
Contig ID
                  128560 1.R1010
5'-most EST
                  jC-atXN272114r1
Method
                  BLASTX
NCBI GI
                  q1167955
BLAST score
                  111
E value
                  9.0e-18
Match length
                  147
% identity
                  39
NCBI Description
                  (U43497) putative 32.7 kDa jasmonate-induced protein
                  [Hordeum vulgare] >gi_2465428 (AF021257) 32 kDa protein
                  [Hordeum vulgare]
Seq. No.
                  136153
Contig ID
                  128574 1.R1010
5'-most EST
                  jC-atXN209221d1
Seq. No.
                  136154
Contig ID
                  128598 1.R1010
5'-most EST
                  jC-atXWAXYa1
Method
                  BLASTX
NCBI GI
                  g136757
BLAST score
                  293
E value
                  3.0e-62
Match length
                  186
% identity
                  76
                  GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR
NCBI Description
                  >gi 100881 pir S07314 UDPglucose--starch
                  glucosyltransferase (EC 2.4.1.11) precursor - maize
                  >gi 168653 (M24258) amyloplast-specific transit protein
                  [Zea mays] >gi_1644339_emb_CAA27574_ (X03935) glucosyl
                  transferase [Zea mays]
Seq. No.
                  136155
                  128600 1.R1010
Contig ID
5'-most EST
                  jC-atXU93r1
Method
                  BLASTX
NCBI GI
                  q3641836
BLAST score
                  382
E value
                  2.0e-47
Match length
                  136
% identity
                  68
NCBI Description (AL023094) putative serine/threonine protein kinase
```

Contig ID

Method

NCBI GI

5'-most EST



[Arabidopsis thaliana]

```
Seq. No.
                   136156
Contig ID
                   128602 1.R1010
5'-most EST
                   jC-atXU90r1
Seq. No.
                   136157
                   128604 1.R1010
Contig ID
5'-most EST
                   jC-atX\overline{U}84d1
Method
                   BLASTN
NCBI GI
                   g1419369
BLAST score
                   64
E value
                   5.0e-27
Match length
                   64
% identity
                   100
                  Z.mays ZmABP3 mRNA for actin depolymerizing factor
NCBI Description
                   136158
Seq. No.
                   128606 1.R1010
Contig ID
                   jC-atXU66r1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4335731
BLAST score
                   190
E value
                   3.0e-29
Match length
                   197
% identity
                   43
NCBI Description (AC006248) putative polyprotein [Arabidopsis thaliana]
                   136159
Seq. No.
                   128609 1.R1010
Contig ID
5'-most EST
                   jC-atXU63r1
Method
                   BLASTX
                   q4415924
NCBI GI
BLAST score
                   216
                   6.0e-17
E value
Match length
                   114
% identity
                   42
NCBI Description
                   (AC006282) putative glucosyl transferase [Arabidopsis
                   thalianal
Seq. No.
                   136160
Contig ID
                   128611 1.R1010
5'-most EST
                   jC-atXU60r1
Method
                   BLASTX
NCBI GI
                   q3785977
BLAST score
                   268
E value
                   7.0e-23
Match length
                   223
% identity
NCBI Description
                   (AC005560) putative growth regulator protein [Arabidopsis
                   thaliana]
                   136161
Seq. No.
                   128613 1.R1010
```

16225

jC-atXU54r1

BLASTX

g2979554



```
BLAST score
E value
                   9.0e-15
Match length
                  107
                   46
% identity
NCBI Description
                  (AC003680) CDC4 like protein [Arabidopsis thaliana]
Seq. No.
                  136162
                  128615 1.R1010
Contig ID
5'-most EST
                  jC-atXU52r1
Seq. No.
                  136163
Contig ID
                  128617 1.R1010
5'-most EST
                  iC-atXU48d1
Method
                  BLASTX
NCBI GI
                  q1184075
BLAST score
                   447
E value
                   4.0e-44
Match length
                  278
% identity
                   (U42444) Cf-2.1 [Lycopersicon pimpinellifolium]
NCBI Description
                  >gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon
                  esculentum]
Seq. No.
                  136164
                  128621 1.R1010
Contig ID
5'-most EST
                  jC-atXU358r1
Seq. No.
                  136165
Contig ID
                  128623 1.R1010
5'-most EST
                  jC-atXU34r1
Seq. No.
                   136166
Contig ID
                   128625 1.R1010
5'-most EST
                   jC-atXU330r1
Method
                  BLASTX
NCBI GI
                   q4580468
BLAST score
                   670
                   5.0e-70
E value
Match length
                   254
                   50
% identity
                   (AC006081) putative protein kinase; similar to human PKX1
NCBI Description
                   and Drosophila DC2 [Arabidopsis thaliana]
Seq. No.
                   136167
                   128627 1.R1010
Contig ID
5'-most EST
                   jC-atXU32r1
Method
                   BLASTN
                   g432601
NCBI GI
BLAST score
                   36
                   3.0e-10
E value
                   36
Match length
                  100
% identity
```

Seq. No. 136168

NCBI Description

Contig ID ____ 128629_1.R1010

{5' region} [chickens, liver, Genomic, 607 nt]

MLC1c/1s=cardiac/slow skeletal alkali myosin light-chain

NCBI GI

E value

BLAST score

Match length

g209392

3.0e-18 56



```
5'-most EST
                   jC-atXU313r1
Method
                   BLASTX
NCBI GI
                   q100506
BLAST score
                   1109
E value
                   1.0e-121
Match length
                   225
% identity
NCBI Description
                  Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)
                   (EC 1.1.1.40) - Flaveria trinervia (fragment)
Seq. No.
                   136169
Contig ID
                   128631 1.R1010
5'-most EST
                   jC-atXU27r1
Method
                  BLASTN
NCBI GI
                  q468055
BLAST score
                   40
E value
                   9.0e-13
Match length
                   44
% identity
                   98
NCBI Description
                  Zea mays B73 QM protein mRNA, complete cds
Seq. No.
                   136170
Contig ID
                   128633 1.R1010
                   jC-atXU254r1
5'-most EST
Method
                   BLASTN
NCBI GI
                   a22430
BLAST score
                   27
E value
                   6.0e-05
Match length
                   88
% identity
                   93
NCBI Description
                  Maize pseudo-Gpa2 pseudogene for glyceraldehyde-3-phosphate
                   dehydrogenase subunit A
Seq. No.
                   136171
                   128635 1.R1010
Contig ID
5'-most EST
                   jC-atXU19a1
Method
                   BLASTN
NCBI GI
                   g53723
BLAST score
                   50
E value
                   9.0e-19
Match length
                   75
                   100
% identity
NCBI Description
                  M.musculus extrachromosomal DNA for V kappa and J kappa
                   coding joint (clone pKDE 34)
                   136172
Seq. No.
                   128636 1.R1010
Contig ID
5'-most EST
                   jC-atXU168r1
Seq. No.
                  136173
                   128638 1.R1010
Contig ID
5'-most EST
                   jC-atXU161r1
Method
                  BLASTN
```



```
% identity
NCBI Description Cloning vector PSU2719 DNA
                   136174
Seq. No.
                   128640 1.R1010
Contig ID
5'-most EST
                   jC-atXU109r1
Seq. No.
                   136175
                   128642 1.R1010
Contig ID
5'-most EST
                   jC-atXU104r1
Method
                   BLASTX
NCBI GI
                   g3928084
BLAST score
                   348
E value
                   2.0e-32
Match length
                   177
% identity
                   46
                  (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   136176
                   128644 1.R1010
Contig ID
5'-most EST
                   jC-atXU102r1
Seq. No.
                   136177
Contig ID
                   128732 1.R1010
5'-most EST
                   jC-atXP92CH3H5T7031d1
Method
                   BLASTX
NCBI GI
                   q2826900
BLAST score
                   396
E value
                   3.0e-64
Match length
                   193
                   72
% identity
NCBI Description
                   (AB004461) DNA polymerase alpha catalytic subunit [Oryza
                   sativa]
                   136178
Seq. No.
                   128735 1.R1010
Contig ID
5'-most EST
                   jC-atXP92CH3H12T7079d1
Method
                   BLASTN
                   q4263642
NCBI GI
BLAST score
                   138
E value
                   2.0e-71
                   538
Match length
% identity
                   92
                  Arabidopsis thaliana chromosome II BAC T13H18 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136179
                   128759 1.R1010
Contig ID
5'-most EST
                   jC-atXP46C174E15T7016d1
Method
                   BLASTX
NCBI GI
                   g3927836
BLAST score
                   555
E value
                   7.0e-62
                  156
Match length
                   77
% identity
```

16228

NCBI Description (AC005727) unknown protein [Arabidopsis thaliana]



Seq. No. 136180

Contig ID 128762 1.R1010

5'-most EST $jC-atX\overline{P}46C174C20T7071d1$

Method BLASTX
NCBI GI g4056482
BLAST score 481
E value 1.0e-73
Match length 213
% identity 63

NCBI Description (AC005896) putative ABC transporter [Arabidopsis thaliana]

Seq. No. 136181

Contig ID 128772_1.R1010

Method BLASTX
NCBI GI g2194127
BLAST score 508
E value 2.0e-80
Match length 210
% identity 74

NCBI Description (AC002062) Strong similarity to Arabidopsis receptor-like

protein kinase (gb_ATLECGENE) and F20P5.16. [Arabidopsis

thaliana]

Seq. No. 136182

Contig ID 128796 1.R1010

5'-most EST jC-atXP46C173E14T7010d1

Method BLASTN
NCBI GI g3702732
BLAST score 155
E value 2.0e-81
Match length 698
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGF10, complete sequence [Arabidopsis thaliana]

Seq. No. 136183

Contig ID 128822 1.R1010

Method BLASTX
NCBI GI 9465898
BLAST score 268
E value 4.0e-23
Match length 209
% identity 38

NCBI Description HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III

>gi_630692_pir__S44849 K12H4.8 protein - Caenorhabditis elegans >gi_289703 (L14331) homology with eukaryotic initiation factor-4A (eIF-4A) and E. coli Ribonuclease III;

coded for by C. elegans cDNA GenBank: T02268; putative

[Caenorhabditis elegans]

Seq. No. 136184

Contig ID 128829_1.R1010

5'-most EST jC-at $\overline{XP25C12509T7080a1}$

Method BLASTX

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A Constitution of the Cons
```

```
NCBI GI
                   q4490334
BLAST score
                   365
E value
                  1.0e-34
Match length
                  73
                  100
% identity
NCBI Description
                  (AL035656) putative protein [Arabidopsis thaliana]
Seq. No.
                  136185
                  128845 1.R1010
Contig ID
5'-most EST
                  jC-atXP25C125K20T7071a1
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  57
E value
                  4.0e-23
Match length
                  57
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  136186
Seq. No.
Contig ID
                  128875 1.R1010
5'-most EST
                  jC-atXP25C125C21T7037a1
Method
                  BLASTN
NCBI GI
                  q2104523
BLAST score
                  488
E value
                  0.0e + 00
Match length
                  528
% identity
                  98
                  Arabidopsis thaliana BAC T10M13 from chromosome IV, from
NCBI Description
                  10.8 cM to 11.6 cM, complete sequence
Seq. No.
                  136187
                  128879 1.R1010
Contig ID
5'-most EST
                  jC-atXP25C125B10T7044a1
Method
                  BLASTX
NCBI GI
                  g3128210
BLAST score
                  384
E value
                  7.0e-37
Match length
                  70
% identity
                  100
                   (AC004077) putative cytochrome P450 protein [Arabidopsis
NCBI Description
                  thaliana] >gi 3337378 (AC004481) putative cytochrome P450
                  protein [Arabidopsis thaliana]
Seq. No.
                  136188
                  128890 2.R1010
Contig ID
                  g572594
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2829918
BLAST score
                  180
E value
                  3.0e-13
Match length
                  38
% identity
                  84
                  (AC002291) similar to "tub" protein gp U82468 2072162
NCBI Description
```

[Arabidopsis thaliana]

Seq. No.

136189

Contig ID 128898 1.R1010



```
jC-atXP25C123O17T7025a1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q3738275
BLAST score
                  474
                  0.0e + 00
E value
Match length
                  538
                  97
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F17A22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  136190
Seq. No.
                  128903 1.R1010
Contig ID
5'-most EST
                  jC-atXP25C123H20T7067a1
Method
                  BLASTN
NCBI GI
                  g4589411
BLAST score
                  277
E value
                  1.0e-154
Match length
                   620
                  93
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  F5H8, complete sequence
                  136191
Seq. No.
Contig ID
                  128926 1.R1010
5'-most EST
                  jC-atXP123C159K15T7025d1
Method
                  BLASTN
NCBI GI
                  g298035
BLAST score
                  330
                  0.0e + 00
E value
Match length
                  338
                  99
% identity
NCBI Description A.thaliana Lhcb4 gene
                  136192
Seq. No.
Contig ID
                  128933_1.R1010
                   jC-atX\overline{P}123C119P7T7019d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1351869
BLAST score
                   308
E value
                   8.0e-28
Match length
                  153
                   44
% identity
                  ACTIN >gi 508701 (U10867) actin [Filobasidiella neoformans]
NCBI Description
Seq. No.
                   136193
                   129009 1.R1010
Contig ID
5'-most EST
                   jC-atXP110CG7F6T7014a1
Method
                  BLASTN
NCBI GI
                  q4580386
BLAST score
                   140
E value
                   2.0e-72
Match length
                   421
% identity
```

Seq. No. 136194

NCBI Description

16231

sequence, complete sequence

Arabidopsis thaliana chromosome II BAC T8018 genomic



Contig ID 129014 1.R1010

5'-most EST jC-atXP110CG7E12T7077a1

Method BLASTX
NCBI GI g3152587
BLAST score 704
E value 3.0e-74
Match length 214
% identity 63

NCBI Description (AC002986) Similar to CREB-binding protein homolog

gb_U88570 from D. melanogaster and contains similarity to callus-associated protein gb_U01961 from Nicotiana tabacum. EST gb W43427 comes from this gene. [Arabidopsis thaliana]

Seq. No. 136195

Contig ID 129038 1.R1010

5'-most EST jC-atXP110CG3H12T7078a1

Method BLASTX
NCBI GI g3540219
BLAST score 378
E value 2.0e-49
Match length 170
% identity 61

NCBI Description (D87686) KIAA0017 protein [Homo sapiens]

Seq. No. 136196

Contig ID 129048 1.R1010

5'-most EST jC-atXP110C84G7T7079a1

Method BLASTX
NCBI GI g4467110
BLAST score 585
E value 2.0e-60
Match length 167
% identity 71

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 136197

Contig ID 129068 1.R1010

Method BLASTN
NCBI GI 94757395
BLAST score 331
E value 0.0e+00
Match length 705
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21L13, complete sequence

Seq. No. 136198

Contig ID 129117 1.R1010

5'-most EST jC-atXP108C170C12T7068d1

Method BLASTX
NCBI GI g4115916
BLAST score 365
E value 2.0e-34
Match length 180
% identity 56

NCBI Description (AF118222) F3H7.9 gene product [Arabidopsis thaliana]



>gi 4539441 emb CAB40029.1 (AL049523) putative protein [Arabidopsis thaliana]

136199 Seq. No. 129179 1.R1010 Contig ID jC-atXP3C83E7T7065a1 5'-most EST BLASTN Method g4539378 NCBI GI BLAST score 162 1.0e-85 E value Match length 540 98 % identity (ESSA project)

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21

129181 1.R1010 Contig ID $jC-atX\overline{P}3C83D2T7062a1$ 5'-most EST Method BLASTX NCBI GI g4522012 BLAST score 313

136200

E value 2.0e-28 137 Match length 58 % identity

Seq. No.

NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 136201

Contig ID 129212 1.R1010 5'-most EST jC-atXP3C81E5T7033a1

Method BLASTN NCBI GI q4337186 BLAST score 283 1.0e-158 E value Match length 572 % identity 97

Arabidopsis thaliana chromosome II BAC T28I24 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

136202 Seq. No. Contig ID

129218 1.R1010 5'-most EST iC-atXP3C81B4T7023a1

Method BLASTX NCBI GI g4539440 BLAST score 319 E value 3.0e-29 Match length 140 % identity

NCBI Description (AL049523) putative protein [Arabidopsis thaliana]

Seq. No. 136203

129234 1.R1010 Contig ID

jC-atXP3C80D11T7006a1 5'-most EST

Method BLASTX NCBI GI g3036806 BLAST score 421 E value 5.0e-59 Match length 141



% identity (AL022373) glycine-rich protein [Arabidopsis thaliana] NCBI Description 136204 Seq. No. 129239 1.R1010 Contig ID jC-atXP74C226B4T7096d1 5'-most EST Method BLASTX q1421741 NCBI GI 533 BLAST score 4.0e-54 E value Match length 157 % identity 66 (U54770) cytochrome P450 homolog [Lycopersicon esculentum] NCBI Description 136205 Seq. No. 129239 2.R1010 Contig ID 5'-most EST jC-atXP74C224H11T7081d1 Method BLASTX g1421741 NCBI GI BLAST score 213 7.0e-83 E value Match length 195 75 % identity (U54770) cytochrome P450 homolog [Lycopersicon esculentum] NCBI Description 136206 Seq. No. 129266 1.R1010 Contig ID jC-atXP74C225B10T7029d1 5'-most EST Method BLASTX q4586117 NCBI GI 328 BLAST score 3.0e-30 E value 237 Match length % identity 41 NCBI Description (AL049638) putative protein [Arabidopsis thaliana] Seq. No. 136207 129307 1.R1010 Contig ID jC-atXP74C223N21T7036d1 5'-most EST Method BLASTX NCBI GI q3548802 BLAST score 266 E value 1.0e-48 Match length 228 % identity 47 (AC005313) axi 1-like protein [Arabidopsis thaliana] NCBI Description >gi 4335769 gb AAD17446 (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana] Seq. No. 136208 129416 1.R1010 Contig ID jC-atXP69C219M19T7055d1 5'-most EST Method BLASTN

Method BLASTN
NCBI GI g2582640
BLAST score 39
E value 3.0e-12
Match length 39



% identity 100
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 136209

Contig ID 129437 1.R1010

5'-most EST jC-atXP69C219B15T7022d1

Method BLASTN
NCBI GI g3941523
BLAST score 40
E value 8.0e-13
Match length 40
% identity 100

NCBI Description Arabidopsis thaliana putative transcription factor (MYB92)

mRNA, complete cds

Seq. No. 136210

Contig ID 129462 1.R1010

5'-most EST jC-atXP69C217J14T7051d1

Method BLASTX
NCBI GI g3386600
BLAST score 582
E value 6.0e-60
Match length 167
% identity 71

NCBI Description (AC004665) putative glycoprotein [Arabidopsis thaliana]

Seq. No. 136211

Contig ID 129474 1.R1010

5'-most EST jC-atXP69C217C23T7001d1

Method BLASTX
NCBI GI g3928102
BLAST score 366
E value 1.0e-34
Match length 182
% identity 56

NCBI Description (AC005770) putative protein kinase [Arabidopsis thaliana]

Seq. No. 136212

Contig ID 129481_1.R1010

5'-most EST jC-atXP65C208L10T7032d1

Method BLASTN
NCBI GI g2582640
BLAST score 40
E value 7.0e-13
Match length 40
% identity 100

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No. 136213

Contig ID 129486_1.R1010

5'-most EST jC-atXP65C206N17T7018d1

Method BLASTX
NCBI GI g3128176
BLAST score 723
E value 2.0e-76



Match length 201 % identity 72

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 136214

Contig ID 129514 1.R1010

5'-most EST jC-atXP65C207P23T7092d1

Method BLASTN
NCBI GI g3941523
BLAST score 38
E value 1.0e-11
Match length 38
% identity 100

NCBI Description Arabidopsis thaliana putative transcription factor (MYB92)

mRNA, complete cds

Seq. No. 136215

Contig ID 129517 1.R1010

5'-most EST jC-atXP65C208B22T7061d1

Method BLASTN
NCBI GI g3549651
BLAST score 349
E value 0.0e+00
Match length 603
% identity 97

NCBI Description Arabidopsis thaliana MAP3K epsilon gene

Seq. No. 136216

Contig ID 129520 1.R1010

5'-most EST jC-atXP65C208A7T7013d1

Method BLASTN
NCBI GI g2832689
BLAST score 277
E value 1.0e-154
Match length 586
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21

(ESSAII project)

Seq. No. 136217

Contig ID 129522 1.R1010

5'-most EST jC-atXP65C208A11T7021d1

Method BLASTN
NCBI GI g3746057
BLAST score 559
E value 0.0e+00
Match length 603
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T16B12 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136218

Contig ID 129524_1.R1010

5'-most EST jC-atXP65C207P24T7005d1

Method BLASTX
NCBI GI g2244841
BLAST score 773



2.0e-82 E value Match length 206 % identity 75

(Z97337) hypothetical protein [Arabidopsis thaliana] NCBI Description

136219 Seq. No.

129529 1.R1010 Contig ID

jC-atXP65C207M8T7083d1 5'-most EST

Method BLASTN NCBI GI g2582640 38 BLAST score 1.0e-11 E value Match length 38 % identity 100

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

136220 Seq. No.

129539 1.R1010 Contig ID

5'-most EST jC-atXP65C207K24T7059d1

BLASTX Method g3928099 NCBI GI BLAST score 347 E value 2.0e-32 Match length 181 22 % identity

NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

136221 Seq. No.

Contig ID 129624 1.R1010

5'-most EST jC-atXP5C89E10T7032a1

136222 Seq. No.

Contig ID 129632 1.R1010

jC-atXP5C89B18T7024a1 5'-most EST

Seq. No. 136223

129652 1.R1010 Contig ID

jC-atXP43C170E23T7076d1 5'-most EST

Method BLASTX a4337175 NCBI GI 290 BLAST score 9.0e-26 E value Match length 114 % identity 51

(AC006416) ESTs gb_T20589, gb T04648, gb AA597906, NCBI Description

gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 136224

Contig ID 129684 1.R1010

5'-most EST jC-atXP43C169I3T7041d1

Seq. No. 136225

129700 1.R1010 Contig ID

5'-most EST jC-atXP43C169B3T7032d1



Method BLASTX
NCBI GI g3914467
BLAST score 699
E value 1.0e-73
Match length 215
% identity 70
NCBI Description 26S PROT
>gi_1864

26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)

>gi 1864003 dbj BAA19252 (AB001422) 21D7 [Nicotiana

tabacum]

Seq. No. 136226

Contig ID 129713 1.R1010

5'-most EST jC-atXP43C168E4T7090d1

Method BLASTN
NCBI GI g3860243
BLAST score 334
E value 0.0e+00
Match length 410
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC F15K20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136227

Contig ID 129727 1.R1010

5'-most EST jC-atXP40C164D24T7072a1

Method BLASTX
NCBI GI g3445204
BLAST score 464
E value 4.0e-46
Match length 184
% identity 52

NCBI Description (AC004786) putative GTP-binding protein [Arabidopsis

thaliana]

Seq. No. 136228

Contig ID 129762_1.R1010

5'-most EST g2749228
Method BLASTN
NCBI GI g3046847
BLAST score 183
E value 2.0e-98
Match length 291
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:

K11J9, complete sequence [Arabidopsis thaliana]

Seq. No. 136229

Contig ID 129785 1.R1010

5'-most EST jC-atXP40C161L14T7066a1

Method BLASTX
NCBI GI g3914002
BLAST score 378
E value 1.0e-64
Match length 142
% identity 94

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279

(AF033862) Lon protease [Arabidopsis thaliana]



```
Seq. No.
                  136230
                  129788 1.R1010
Contig ID
5'-most EST
                  jC-atXP40C161K20T7042a1
Method
                  BLASTX
NCBI GI
                  q3643085
BLAST score
                  201
E value
                  3.0e-40
Match length
                  148
% identity
                  61
NCBI Description
                  (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum
                  crystallinum]
Seq. No.
                  136231
Contig ID
                  129795 1.R1010
5'-most EST
                  jC-atXP40C161J17T7057a1
Seq. No.
                  136232
Contig ID
                  129856 1.R1010
                  jC-atXP20C114B21T7044a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3885331
BLAST score
                  286
E value
                  5.0e-38
Match length
                  148
                  55
% identity
NCBI Description
                  (AC005623) putative cytochrome p450 protein [Arabidopsis
                  thaliana]
Seq. No.
                  136233
                  129881 1.R1010
Contig ID
5'-most EST
                  jC-atXP20C113E2T7081a1
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  37
E value
                  5.0e-11
Match length
                  37
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  136234
Seq. No.
Contig ID
                  129896 1.R1010
5'-most EST
                  jC-atXP15C108F1T7093a1
Method
                  BLASTX
NCBI GI
                  g3955021
BLAST score
                  171
                  2.0e-12
E value
Match length
                  112
% identity
                  45
                  (AJ010811) HB2 homeodomain protein [Populus tremula x
NCBI Description
                  Populus tremuloides]
```

Seq. No. 136235

Contig ID 129921 1.R1010

5'-most EST jC-atXP15C107M23T7068a1

Method BLASTN NCBI GI g2252639



```
BLAST score 334
E value 0.0e+00
Match length 693
% identity 99
```

NCBI Description Genomic sequence of Arabidopsis BAC F8A5, complete sequence

[Arabidopsis thaliana]

Seq. No. 136236

Contig ID 129928 1.R1010

5'-most EST jC-atXP15C107J6T7058a1

Method BLASTX
NCBI GI g3212610
BLAST score 145
E value 2.0e-18
Match length 103
% identity 50

NCBI Description Chain A, Sulfite Oxidase From Chicken Liver

>gi 3212611 pdb 1SOX_B Chain B, Sulfite Oxidase From

Chicken Liver

Seq. No. 136237

Contig ID 129983_1.R1010 5'-most EST jC-atXP20728f2

Method BLASTX
NCBI GI g4581109
BLAST score 608
E value 5.0e-63
Match length 149
% identity 73

NCBI Description (AC005825) unknown protein [Arabidopsis thaliana]

Seq. No. 136238

Contig ID 129987_1.R1010 5'-most EST jC-atXP20608f2

Method BLASTN
NCBI GI g619522
BLAST score 45
E value 8.0e-16
Match length 53
% identity 98

NCBI Description Synechococcus PCC 6301 genomic DNA (clone PJRSY01)

Seq. No. 136239

Contig ID 129989_1.R1010 5'-most EST jC-atXP20581f2 Method BLASTN

NCBI GI g4314333 BLAST score 45 E value 8.0e-16 Match length 53 % identity 96

NCBI Description Homo sapiens chromosome 10 clone CIT987SK-1161G12 map

10q25, complete sequence [Homo sapiens]

Seq. No. 136240

Contig ID 130005_1.R1010 5'-most EST jC-atXN579208a2



cds

136249

Seq. No.

```
Seq. No.
                  136241
                  130074 1.R1010
Contig ID
5'-most EST
                  jC-atXN25473f1
Method
                  BLASTX
NCBI GI
                  q4512263
BLAST score
                  190
E value
                  5.0e-14
Match length
                  58
                   69
% identity
NCBI Description
                  (AB018526) H+/Ca2+ exchanger 2 [Ipomoea nil]
Seq. No.
                   136242
                   130099 1.R1010
Contig ID
5'-most EST
                   jC-atXN110229f2
Seq. No.
                   136243
                   130107 1.R1010
Contig ID
5'-most EST
                   jC-atXB944a2
                   136244
Seq. No.
Contig ID
                   130113 1.R1010
5'-most EST
                   jC-atXB823a2
                   136245
Seq. No.
                   130115 1.R1010
Contig ID
5'-most EST
                   jC-atXB815a2
Seq. No.
                   136246
                   130119 1.R1010
Contig ID
5'-most EST
                   jC-atXB805f2
Seq. No.
                   136247
                   130123 1.R1010
Contig ID
5'-most EST
                   jC-atXB761f2
Method
                   BLASTX
                   q3550436
NCBI GI
BLAST score
                   228
                   2.0e-18
E value
                   69
Match length
% identity
                   68
                   (AJ001317) putative transcription repressor HOTR [Hordeum
NCBI Description
                   vulgare]
                   136248
Seq. No.
Contig ID
                   130129 1.R1010
                   jC-atXB632a2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g507770
BLAST score
                   33
                   1.0e-08
E value
                   65
Match length
                   89
% identity
                   Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete
NCBI Description
```

Method NCBI GI



```
Contig ID
                   130132 1.R1010
5'-most EST
                   jC-atXB304a2
                   136250
Seq. No.
                   130240_1.R1010
Contig ID
5'-most EST
                   g17426
Method
                   BLASTX
NCBI GI
                   g3172538
BLAST score
                   179
E value
                   9.0e-13
Match length
                   113
% identity
                   46
NCBI Description
                  (AF067789) tSNARE AtTLG2p [Arabidopsis thaliana]
                   136251
Seq. No.
                   130243 1.R1010
Contig ID
5'-most EST
                   q935450
Method
                   BLASTX
NCBI GI
                   g4510376
BLAST score
                  - 242
                   2.0e-20
E value
Match length
                   83
% identity
                   54
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
                   136252
Seq. No.
                   130267 1.R1010
Contig ID
5'-most EST
                   g396890
                   136253
Seq. No.
                   130298 1.R1010
Contig ID
5'-most EST
                   g17298
Method
                   BLASTN
NCBI GI
                   g4455321
BLAST score
                   217
E value
                   1.0e-118
Match length
                   529
% identity
                   45
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10
                   (ESSAII project)
Seq. No.
                   136254
Contig ID
                   130308 1.R1010
5'-most EST
                   g17273
Method
                   BLASTX
NCBI GI
                   q1651689
BLAST score
                   202
E value
                   8.0e-16
                   99
Match length
% identity
                   44
NCBI Description
                  (D90899) hypothetical protein [Synechocystis sp.]
                   136255
Seq. No.
                   130312 1.R1010
Contig ID
5'-most EST
                   g12159\overline{3}9
```

16242

BLASTN

g4454004



```
BLAST score
E value
                   1.0e-164
Match length
                   395
                   99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6
NCBI Description
                   (ESSAII project)
Seq. No.
                   136256
                   130315 1.R1010
Contig ID
                   g2748118
5'-most EST
Method
                  BLASTX
NCBI GI
                   g479413
BLAST score
                   728
E value
                   6.0e-77
                   229
Match length
                   69
% identity
NCBI Description myosin-like protein - Arabidopsis thaliana
                   136257
Seq. No.
                   130371 1.R1010
Contig ID
5'-most EST
                   g16753
Method
                   BLASTN
NCBI GI
                   g4757403
BLAST score
                   321
                   0.0e + 00
E value
Match length
                   371
% identity
                   97
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MJL12, complete sequence
                   136258
Seq. No.
Contig ID
                   130374 1.R1010
5'-most EST
                   g27497\overline{1}3
                   136259
Seq. No.
                   130391 1.R1010
Contig ID
5'-most EST
                   g2749235
Method
                   BLASTN
NCBI GI
                   q2864607
BLAST score
                   259
E value
                   1.0e-143
Match length
                   428
% identity
                   99
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
                   (ESSAII project)
Seq. No.
                   136260
Contig ID
                   130392 1.R1010
5'-most EST
                   g16804
Method
                   BLASTN
NCBI GI
                   q4757399
                   302
BLAST score
E value
                   1.0e-169
Match length
                   318
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

MEE13, complete sequence



```
Seq. No.
                  136261
                  130435_1.R1010
Contig ID
                  q16850°
5'-most EST
Method
                  BLASTN
                  g4531433
NCBI GI
BLAST score
                  366
                  0.0e+00
E value
Match length
                  416
% identity
                  Arabidopsis thaliana chromosome II P1 MFL8 genomic
NCBI Description
                  sequence, complete sequence
                  136262
Seq. No.
                  130477 1.R1010
Contig ID
5'-most EST
                  g2580825
Method
                  BLASTN
                  g3228389
NCBI GI
BLAST score
                  409
                  0.0e+00
E value
                  517
Match length
% identity
                  98
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F17L21,
                  complete sequence [Arabidopsis thaliana]
                  136263
Seq. No.
                  130491_1.R1010
Contig ID
5'-most EST
                  g2756764
Method
                  BLASTN
NCBI GI
                  g2618677
                  272
BLAST score
                  1.0e-151
E value
                   474
Match length
% identity
                  Arabidopsis thaliana BAC F21B7 chromosome 1, complete
NCBI Description
                   sequence [Arabidopsis thaliana]
Seq. No.
                   136264
                   130527 1.R1010
Contig ID
5'-most EST
                   q2723103
Method
                  BLASTN
NCBI GI
                   g3236234
BLAST score
                   216
E value
                   1.0e-118
                   468
Match length
                   95
% identity
                  Arabidopsis thaliana chromosome II BAC F13M22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136265
                   130553 1.R1010
Contig ID
5'-most EST
                   g2722809
                   BLASTX
Method
                   g3152585
NCBI GI
```

329

121

2.0e-30

BLAST score

E value Match length



Method BLASTN
NCBI GI g2244901
BLAST score 186
E value 1.0e-100
Match length 380
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 136267

Contig ID 130693 1.R1010

5'-most EST g17134
Method BLASTN
NCBI GI g3738313
BLAST score 282
E value 1.0e-157
Match length 453
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC T29E15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136268

Contig ID 130702_1.R1010

5'-most EST g17146

Method BLASTN

NCBI GI g3128137

BLAST score 311

E value 1.0e-175

Match length 360

% identity 77

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9I9, complete sequence [Arabidopsis thaliana]

Seq. No. 136269

Contig ID 130789_1.R1010

5'-most EST g906739
Method BLASTX
NCBI GI g1841357
BLAST score 291
E value 5.0e-26
Match length 128
% identity 50

NCBI Description (D85382) mitochondrial ribosomal protein S11 (nuclear

encoded) [Oryza sativa]

Seq. No. 136270

Contig ID 130806 1.R1010

5'-most EST g506521 Method BLASTN

```
N 20 41
```

```
q4734003
NCBI GI
BLAST score
                  54
E value
                  1.0e-21
Match length
                  62
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC F3L12 genomic
NCBI Description
                  sequence, complete sequence
                  136271
Seq. No.
Contig ID
                  130811_1.R1010
5'-most EST
                  g16667
                  BLASTX
Method
NCBI GI
                  g4689108
BLAST score
                  422
                  2.0e-41
E value
                  113
Match length
% identity
                  63
                  (AF077030) hypothetical 43.2 kDa protein [Homo sapiens]
NCBI Description
                  136272
Seq. No.
                  130825 1.R1010
Contig ID
5'-most EST
                  g394887
Method
                  BLASTX
NCBI GI
                  g2827637
BLAST score
                  250
E value
                  2.0e-21
Match length
                  64
                  72
% identity
                  (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
                  136273
Seq. No.
                  130910_1.R1010
Contig ID
5'-most EST
                  g16655
Method
                  BLASTX
                  g543565
NCBI GI
BLAST score
                  226
E value
                  2.0e-18
Match length
                  94
                  49
% identity
NCBI Description
                  hypothetical 10.0K protein - Zinnia elegans
                  >gi 493721 dbj BAA06462 (D30802) TED4 [Zinnia elegans]
                  >qi 641903 (U19266) putative nonspecific lipid transfer;
                  auxin induced gene [Zinnia elegans]
Seq. No.
                  136274
Contig ID
                  130938 1.R1010
5'-most EST
                  g17599
Method
                  BLASTN
NCBI GI
                  g4235150
BLAST score
                  149
E value
                  3.0e-78
Match length
                  306
                  97
% identity
                  Arabidopsis thaliana chromosome I BAC T25B24 genomic
NCBI Description
```

Seq. No. 136275

sequence, complete sequence

I

H L



Contig ID 130993 1.R1010

5'-most EST g17573 Method BLASTN NCBI GI g2213606 BLAST score 194 E value 1.0e-105 Match length 395 % identity 98

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F21J9,

complete sequence [Arabidopsis thaliana]

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Seq. No. 136276

Contig ID 131015_1.R1010

5'-most EST g2393174

Method BLASTN

NCBI GI g2924653

BLAST score 200

E value 1.0e-108

Match length 412

% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDA7, complete sequence [Arabidopsis thaliana]

Seq. No. 136277

Contig ID 131074_1.R1010

5'-most EST g315162

Seq. No. 136278

Contig ID 131075_1.R1010

5'-most EST g315175
Method BLASTX
NCBI GI g2979549
BLAST score 285
E value 2.0e-51
Match length 130
% identity 88

NCBI Description (AC003680) putative 7-ethoxycoumarin O-deethylase

[Arabidopsis thaliana]

Seq. No. 136279

Contig ID 131077 1.R1010

5'-most EST g1223592
Method BLASTN
NCBI GI g4309747
BLAST score 334
E value 0.0e+00
Match length 448
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC T13E11 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136280

Contig ID 131080_1.R1010

5'-most EST $g31521\overline{3}$ Method BLASTX NCBI GI g1946365 BLAST score 108



```
2.0e-36
E value
Match length
                  93
% identity
                  85
                  (U93215) glutaredoxin isolog [Arabidopsis thaliana]
NCBI Description
                  136281
Seq. No.
Contig ID
                  131083 1.R1010
                  g315217
5'-most EST
                  136282
Seq. No.
                  131169 1.R1010
Contig ID
5'-most EST
                  g315386
Seq. No.
                  136283
                  131175 1.R1010
Contig ID
                  g315392
5'-most EST
                  BLASTX
Method
                  g3882203
NCBI GI
BLAST score
                  298
                  2.0e-33
E value
Match length
                  150
                  51
% identity
NCBI Description (AB018284) KIAA0741 protein [Homo sapiens]
Seq. No.
                  136284
                  131180_1.R1010
Contig ID
5'-most EST
                  g2756818
Method
                  BLASTX
NCBI GI
                  g1621268
BLAST score
                   197
E value
                   4.0e-15
Match length
                  120
% identity
                   41
NCBI Description
                  (Z81012) unknown [Ricinus communis]
Seq. No.
                   136285
                   131198 1.R1010
Contig ID
5'-most EST
                   q2757313
Method
                  BLASTX
NCBI GI
                   q4753655
BLAST score
                   449
E value
                   1.0e-44
Match length
                   93
% identity
                   84
                   (AL049751) pectate lyase like protein [Arabidopsis
NCBI Description
                   thaliana]
                   136286
Seq. No.
                   131208 1.R1010
Contig ID
5'-most EST
                   g315428
                   BLASTX
Method
                   g4678943
NCBI GI
BLAST score
                   446
E value
                   6.0e-66
                   156
Match length
                   74
% identity
NCBI Description (ALO49711) putative protein [Arabidopsis thaliana]
```



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136287
Seq. No.
                   131223_1.R1010
Contig ID
5'-most EST
                   g315444
Method
                   BLASTN
                   q4580386
NCBI GI
BLAST score
                   438
                   0.0e + 00
E value
                   530
Match length
% identity
                   98
                   Arabidopsis thaliana chromosome II BAC T8018 genomic
NCBI Description
                   sequence, complete sequence
                   136288
Seq. No.
Contig ID
                   131236 1.R1010
                   g315643
5'-most EST
                   BLASTN
Method
                   g4220510
NCBI GI
BLAST score
                   142
                   5.0e-74
E value
Match length
                   403
                   98
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
NCBI Description
                   (ESSAII project)
Seq. No.
                   136289
                   131246_1.R1010
Contig ID
5'-most EST
                   g315476
                   136290
Seq. No.
                   131311 1.R1010
Contig ID
5'-most EST
                   g315547
                   136291
Seq. No.
Contig ID
                   131318_1.R1010
                   g27633<del>0</del>3
5'-most EST
Method
                   BLASTX
                   g3618320
NCBI GI
                   249
BLAST score
                   3.0e-21
E value
Match length
                   93
% identity
                   48
                   (AB001888) zinc finger protein [Oryza sativa]
NCBI Description
                   136292
Seq. No.
                   131335_1.R1010
Contig ID
5'-most EST
                   g315576
                   BLASTX
Method
NCBI GI
                   q3892701
BLAST score
                   211
E value
                   7.0e-17
Match length
                   93
% identity
                   46
                   (AL033545) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

16249

136293

131417 1.R1010

Seq. No.

Contig ID



```
5'-most EST
                  q958178
Method
                  BLASTN
NCBI GI
                  a3510345
BLAST score
                  90
                  6.0e-43
E value
                  391
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNJ8, complete sequence [Arabidopsis thaliana]
                  136294
Seq. No.
Contig ID
                  131476_1.R1010
5'-most EST
                  g2758438
Method
                  BLASTX
NCBI GI
                  g3482919
BLAST score
                  403
E value
                  8.0e-40
Match length
                  102
% identity
                  82
                  (AC003970) Putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  136295
Seq. No.
Contig ID
                  131480_1.R1010
5'-most EST
                  g2393412
Method
                  BLASTX
NCBI GI
                  g4567304
BLAST score
                   561
                  1.0e-57
E value
Match length
                  129
                   89
% identity
                  (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
                   136296
Seq. No.
Contig ID
                   131498 1.R1010
5'-most EST
                   q2758078
Method
                   BLASTX
NCBI GI
                   q2494041
BLAST score
                   245
E value
                   1.0e-20
Match length
                   164
% identity
                   DIAMINOPIMELATE EPIMERASE >gi 1653875 dbj BAA18785
NCBI Description
                   (D90917) diaminopimelate epimerase [Synechocystis sp.]
Seq. No.
                   136297
                   131560 1.R1010
Contig ID
5'-most EST
                   g2763468
Method
                   BLASTX
                   g2160166
NCBI GI
BLAST score
                   82
                   2.0e-15
E value
                   186
Match length
% identity
                   (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   136298
Seq. No.
                   131644_1.R1010
Contig ID
```

E value



```
5'-most EST
                   q2762822
Method
                  BLASTN
                   q4678291
NCBI GI
BLAST score
                   277
                   1.0e-154
E value
                   330
Match length
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10
NCBI Description
                   (ESSA project)
                   136299
Seq. No.
                   131653 1.R1010
Contig ID
5'-most EST
                   g315976
Method
                   BLASTX
NCBI GI
                   g1706714
BLAST score
                   297
                   8.0e-27
E value
Match length
                   92
% identity
                   63
                   ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF)
NCBI Description
                   (ELECTRON TRANSFER FLAVOPROTEIN SMALL SUBUNIT) (ETFSS)
                   >qi 1209054 (U32230) EtfS [Bradyrhizobium japonicum]
                   136300
Seq. No.
Contig ID
                   131702 1.R1010
5'-most EST
                   g2047618
                   136301
Seq. No.
                   131748_1.R1010
Contig ID
5'-most EST
                   q394894
Method
                   BLASTX
NCBI GI
                   q4512667
BLAST score
                   330
                   5.0e-52
E value
Match length
                   116
% identity
                   84
                  (AC006931) putative MAP kinase [Arabidopsis thaliana]
NCBI Description
                   136302
Seq. No.
Contig ID
                   131755 1.R1010
5'-most EST
                   g396604
Method
                   BLASTN
                   g4586098
NCBI GI
BLAST score
                   339
E value
                   0.0e + 00
                   383
Match length
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13
NCBI Description
                   (ESSA project)
Seq. No.
                   136303
Contia ID
                   131795 1.R1010
5'-most EST
                   q396867
Method
                   BLASTX
NCBI GI
                   g99771
                   279
BLAST score
```

7.0e-25



Match length % identity

ubiquitin 81-aa extension protein 1 - Arabidopsis thaliana NCBI Description >gi 166934 (J05539) ubiquitin extension protein (UBQ5)

[Arabidopsis thaliana]

136304 Seq. No.

131800 1.R1010 Contig ID

g396873 5'-most EST Method BLASTN g4159699 NCBI GI BLAST score 447 0.0e+00E value 459 Match length % identity 99

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K16E1, complete sequence

136305 Seq. No.

131803_1.R1010 Contig ID

5'-most EST g396891

Seq. No.

136306

131837 1.R1010 Contig ID

g397188 5'-most EST Method BLASTX g3128200 NCBI GI BLAST score 247 6.0e-21 E value Match length 84 % identity 62

(AC004521) unknown protein [Arabidopsis thaliana] NCBI Description

136307 Seq. No.

131839 1.R1010 Contig ID

g397190 5'-most EST BLASTX Method NCBI GI g4490297 BLAST score 554 7.0e-57 E value Match length 184 % identity 62

(AL035678) putative protein [Arabidopsis thaliana] NCBI Description

136308 Seq. No.

131906_1.R1010 Contig ID

5'-most EST g397266 BLASTN Method NCBI GI g2244991 BLAST score 261 E value 1.0e-145 328 Match length % identity

Arabidopsis thaliana DNA chromosome 4, ESSA I contig NCBI Description

fragment No

Seq. No. 136309

BLAST score

E value

343 0.0e+00



```
131941 1.R1010
Contig ID
                   g397310
5'-most EST
                   BLASTX
Method
                   g4220474
NCBI GI
                   497
BLAST score
                   6.0e-50
E value
                   156
Match length
                   72
% identity
                  (AC006069) putative myosin heavy chain [Arabidopsis
NCBI Description
                   thaliana]
                   136310
Seq. No.
                   131980 1.R1010
Contig ID
5'-most EST
                   g2576801
                   136311
Seq. No.
                   132104 1.R1010
Contig ID
5'-most EST
                   q406618
Method
                   BLASTN
NCBI GI
                   q3080430
                   427
BLAST score
                   0.0e+00
E value
                   590
Match length
                   96
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19
NCBI Description
                   (ESSAII project)
                   136312
Seq. No.
                   132107 1.R1010
Contig ID
                   g2722678
5'-most EST
                   BLASTX
Method
                   g4589974
NCBI GI
BLAST score
                   559
                   2.0e-57
E value
Match length
                   118
                   92
% identity
                  (AC007195) unknown protein [Arabidopsis thaliana]
NCBI Description
                   136313
Seq. No.
Contig ID
                   132169 1.R1010
5'-most EST
                   g2048503
Method
                   BLASTN
NCBI GI
                   g3449326
BLAST score
                   375
E value
                   0.0e + 00
Match length
                   429
% identity
                   97
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K19M22, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136314
Contig ID
                   132179 1.R1010
5'-most EST
                   q2749492
Method
                   BLASTN
NCBI GI
                   g3869074
```



```
Match length
% identity
                   96
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MMI9, complete sequence [Arabidopsis thaliana]
                   136315
Seq. No.
Contig ID
                   132186 1.R1010
                   g398883
5'-most EST
                   BLASTN
Method
NCBI GI
                   q2828180
BLAST score
                   366
E value
                   0.0e + 00
Match length
                   442
                   100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MDK4, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136316
Contig ID
                   132229 1.R1010
                   g435205
5'-most EST
Method
                   BLASTN
                   g4558656
NCBI GI
BLAST score
                   323
E value
                   0.0e + 00
Match length
                   387
% identity
                   96
                  Arabidopsis thaliana chromosome II BAC T10F5 genomic
NCBI Description
                   sequence, complete sequence
                   136317
Seq. No.
                   132312 1.R1010
Contig ID
5'-most EST
                   q40294\overline{5}
Method
                   BLASTN
NCBI GI
                   q3046856
BLAST score
                   301
E value
                   1.0e-169
Match length
                   381
                   100
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MXI22, complete sequence [Arabidopsis thaliana]
                   136318
Seq. No.
                   132375 1.R1010
Contig ID
5'-most EST
                   g2708350
                   136319
Seq. No.
                   132394 1.R1010
Contig ID
5'-most EST
                   g2580949
                   BLASTX
Method
NCBI GI
                   q2811048
```

BLAST score 174 E value 2.0e-12 Match length 80 50 % identity

DEVB PROTEIN HOMOLOG >gi 2131051 emb_CAB09261_ (Z95844) NCBI Description

devB [Mycobacterium tuberculosis]



Seq. No. 136320 132488 1.R1010 Contig ID 5'-most EST q406691 Method BLASTN NCBI GI g3046854 BLAST score 448 E value 0.0e + 00Match length 509 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MRG7, complete sequence [Arabidopsis thaliana] Seq. No. 136321 Contig ID 132499 1.R1010 5'-most EST q2048229 BLASTX Method q4586576 NCBI GI BLAST score 239 5.0e-20 E value 65 Match length 69 % identity (AB024992) multidrug resistance protein [Cicer arietinum] NCBI Description Seq. No. 136322 132537 1.R1010 Contig ID $q40681\overline{1}$ 5'-most EST Method BLASTN q1785729 NCBI GI BLAST score 353 0.0e + 00E value 391 Match length 98 % identity NCBI Description A.thaliana mitochondrial genome, part B 136323 Seq. No. 132591 1.R1010 Contiq ID 5'-most EST q410350 Method BLASTN NCBI GI q4220631 BLAST score 328 0.0e + 00E value Match length 368 % identity 99 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K5J14, complete sequence [Arabidopsis thaliana] Seq. No. 136324

132603 1.R1010 Contig ID

5'-most EST g410365

136325 Seq. No.

132608 1.R1010 Contig ID

5'-most EST g410372

136326 Seq. No.

132628 1.R1010 Contig ID

5'-most EST q410397

NCBI Description



```
BLASTN
Method
NCBI GI
                   q3128140
                   218
BLAST score
                   1.0e-119
E value
                   226
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MJE4, complete sequence [Arabidopsis thaliana]
                   136327
Seq. No.
                   132646 1.R1010
Contig ID
5'-most EST
                   q41643\overline{4}
Method
                   BLASTX
                   g3335336
NCBI GI
                   612
BLAST score
                   7.0e-64
E value
                   127
Match length
% identity
                   (AC004512) Contains similarity to DnaJ gene YM8520.10
NCBI Description
                   gb 825566 from from S. cerevisiae cosmid gb Z49705. ESTs
                   gb_Z47720 and gb_Z29879 come from this gene. [Arabidopsis
                   thaliana]
                   136328
Seq. No.
                   132667_1.R1010
Contig ID
5'-most EST
                   g3450623
                   BLASTN
Method
                   g3047060
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
Match length
                   83
                   87
% identity
                   Arabidopsis thaliana BAC F7N22
NCBI Description
                   136329
Seq. No.
                   132668 1.R1010
Contig ID
5'-most EST
                   q416463
                   BLASTN
Method
                   q1785673
NCBI GI
BLAST score
                   549
                   0.0e + 00
E value
                   572
Match length
% identity
                   A.thaliana mitochondrial genome, part A
NCBI Description
                   136330
Seq. No.
                   132695 1.R1010
Contig ID
5'-most EST
                   q2413491
Method
                   BLASTN
NCBI GI
                   g3894179
BLAST score
                   304
E value
                   1.0e-170
Match length
                   357
% identity
                   38
```

Arabidopsis thaliana chromosome II BAC F13H10 genomic

sequence, complete sequence [Arabidopsis thaliana]

NCBI GI

E value

BLAST score



```
Seq. No.
                   136331
                   132713 1.R1010
Contig ID
                   q63522\overline{4}
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3241925
BLAST score
                   176
E value
                   4.0e-94
Match length
                   387
                   98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MOK9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136332
                   132722 1.R1010
Contig ID
5'-most EST
                   q27642\overline{5}5
Seq. No.
                   136333
Contig ID
                   132750 1.R1010
                   g634171
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3212846
BLAST score
                   281
E value
                   1.0e-157
Match length
                   309
% identity
                   Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   136334
Seq. No.
Contig ID
                   132752 1.R1010
5'-most EST
                   g2062883
                   BLASTN
Method
NCBI GI
                   g1050427
BLAST score
                   345
                   0.0e + 00
E value
Match length
                   400
% identity
                   98
NCBI Description A.thaliana mRNA for an exon from SNAP25A protein
                   136335
Seq. No.
                   132790 1.R1010
Contig ID
5'-most EST
                   q2759858
Method
                   BLASTN
NCBI GI
                   g2098816
BLAST score
                   243
E value
                   1.0e-134
Match length
                   361
                   96
% identity
NCBI Description Arabidopsis thaliana BAC F19G10, complete sequence
                   136336
Seq. No.
                   132798 1.R1010
Contig ID
                   g435234
5'-most EST
                   BLASTX
Method
```

g2244926

1.0e-23



```
Match length
                   87
% identity
                  (Z97339) glutaredoxin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   136337
Contig ID
                  132799 1.R1010
5'-most EST
                  q435235
Method
                  BLASTX
NCBI GI
                  q3377841
BLAST score
                  201
E value
                   5.0e-35
Match length
                   90
% identity
                   (AF075598) contains similarity to phosphofructokinases
NCBI Description
                   (Pfam; PFK.hmm, score; 36.60) [Arabidopsis thaliana]
                   136338
Seq. No.
Contig ID
                   132885 1.R1010
5'-most EST
                   g906333
                  BLASTX
Method
                   q1620898
NCBI GI
BLAST score
                   192
E value
                   2.0e-14
Match length
                   73
% identity
                   (D87957) protein involved in sexual development [Homo
NCBI Description
                   sapiens]
Seq. No.
                   136339
                   132951 1.R1010
Contig ID
5'-most EST
                   g2749660
Method
                   BLASTN
NCBI GI
                   g4220643
BLAST score
                   212
E value
                   1.0e-115
Match length
                   409
                   97
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MWD22, complete sequence [Arabidopsis thaliana]
                   136340
Seq. No.
                   132969 1.R1010
Contig ID
                   q453739
5'-most EST
Method
                   BLASTN
                   g3873174
NCBI GI
BLAST score
                   301
E value
                   1.0e-169
Match length
                   305
                   79
% identity
                   Genomic sequence for Arabidopsis thaliana BAC F14N23,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
```

Seq. No. 136341

Contig ID 132996_1.R1010
5'-most EST g453766

No. 136341

PLACENTAL PROPERTY OF THE PROPERTY

Method BLASTN NCBI GI g2264315

NCBI GI BLAST score

E value



```
BLAST score
                   1.0e-180
E value
Match length
                   383
% identity
                   97
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MRN17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136342
                   132997 1.R1010
Contig ID
                   q24459\overline{2}4
5'-most EST
Method
                   BLASTN
NCBI GI
                   q2264315
BLAST score
                   238
E value
                   1.0e-131
                   367
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MRN17, complete sequence [Arabidopsis thaliana]
                   136343
Seq. No.
                   133004 1.R1010
Contig ID
5'-most EST
                   q936377
Seq. No.
                   136344
                   133086_1.R1010
Contig ID
                   q45387\overline{5}
5'-most EST
Method
                   BLASTX
                   q3935151
NCBI GI
BLAST score
                   312
                   1.0e-28
E value
                   68
Match length
                   90
% identity
NCBI Description
                   (AC005106) T25N20.15 [Arabidopsis thaliana]
                   136345
Seq. No.
                   133110 1.R1010
Contig ID
5'-most EST
                   q3450014
Seq. No.
                   136346
                   133152 1.R1010
Contig ID
5'-most EST
                   g454213
Method
                   BLASTX
                   g4567279
NCBI GI
BLAST score
                   565
                   2.0e-62
E value
Match length
                   156
% identity
                   74
                   (AC006841) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   136347
Seq. No.
                   133170 1.R1010
Contig ID
5'-most EST
                   g458747
                   BLASTN
Method
```

16259

g3128166

364 0.0e+00

Contig ID

Method NCBI GI

5'-most EST

g496461

g2497913

BLASTX



Match length 98 % identity Arabidopsis thaliana chromosome II BAC F4I1 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 136348 133196 1.R1010 Contig ID 5'-most EST g2393161 Method BLASTX NCBI GI g4559380 BLAST score 581 E value 6.0e-60 Match length 110 100 % identity (AC006526) putative auxin-responsive GH3 protein NCBI Description [Arabidopsis thaliana] Seq. No. 136349 133218 1.R1010 Contig ID 5'-most EST q458795 BLASTN Method NCBI GI g2618677 BLAST score 219 E value 1.0e-120 299 Match length 95 % identity Arabidopsis thaliana BAC F21B7 chromosome 1, complete NCBI Description sequence [Arabidopsis thaliana] 136350 Seq. No. 133355 1.R1010 Contig ID $g46047\overline{4}$ 5'-most EST 136351 Seq. No. 133357 1.R1010 Contig ID 5'-most EST q2596380 BLASTX Method q3980379 NCBI GI BLAST score 460 6.0e-46 E value 92 Match length 99 % identity (AC004561) putative cyclin, PCNA [Arabidopsis thaliana] NCBI Description 136352 Seq. No. 133359 1.R1010 Contig ID 5'-most EST g460478 136353 Seq. No. 133459 1.R1010 Contig ID 5'-most EST q496460 136354 Seq. No. 133460 1.R1010



```
BLAST score
                  1.0e-50
E value
                  82
Match length
% identity
                  99
NCBI Description EC PROTEIN HOMOLOG
                  136355
Seq. No.
                  133467 1.R1010
Contig ID
5'-most EST
                  g473296
                  BLASTX
Method
NCBI GI
                  q3738325
BLAST score
                   331
E value
                   7.0e - 31
                   90
Match length
% identity
                   (AC005170) putative CaMB-channel protein [Arabidopsis
NCBI Description
                   thaliana]
                   136356
Seq. No.
                   133473 1.R1010
Contig ID
5'-most EST
                   q49646\overline{3}
                   BLASTN
Method
NCBI GI
                   g3128137
BLAST score
                   281
                   1.0e-157
E value
                   494
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K9I9, complete sequence [Arabidopsis thaliana]
                   136357
Seq. No.
                   133492 1.R1010
Contig ID
5'-most EST
                   q2048883
Method
                   BLASTN
NCBI GI
                   q4678291
BLAST score
                   294
E value
                   1.0e-164
Match length
                   411
                   95
% identity
                   Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10
NCBI Description
                   (ESSA project)
                   136358
Seq. No.
                   133497 1.R1010
Contig ID
5'-most EST
                   g2393352
Seq. No.
                   136359
Contig ID
                   133510 1.R1010
                   g473347
5'-most EST
Method
                   BLASTN
```

5'-most EST g473347
Method BLASTN
NCBI GI g1785729
BLAST score 488
E value 0.0e+00
Match length 513
% identity 99

NCBI Description A.thaliana mitochondrial genome, part B

E value

Match length



```
Seq. No.
                   136360
                   133526 1.R1010
Contig ID
5'-most EST
                   q493266
Method
                  BLASTX
NCBI GI
                   g4063733
BLAST score
                   964
E value
                   1.0e-105
Match length
                   203
% identity
NCBI Description
                  (AC006259) putative P450 [Arabidopsis thaliana]
Seq. No.
                   136361
                   133529 1.R1010
Contig ID
5'-most EST
                   g493310
                   136362
Seq. No.
                   133546 1.R1010
Contig ID
5'-most EST
                   g2413968
                   BLASTX
Method
NCBI GI
                   q4582436
BLAST score
                   233
                   3.0e-19
E value
Match length
                   90
% identity
                   56
                  (AC007196) unknown protein [Arabidopsis thaliana]
NCBI Description
                   136363
Seq. No.
                   133554 1.R1010
Contig ID
5'-most EST
                   q1328262
                   BLASTN
Method
                   g2351067
NCBI GI
BLAST score
                   361
E value
                   0.0e + 00
Match length
                   396
                   97
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MPO12, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136364
                   133559 1.R1010
Contig ID
                   q24141\overline{4}6
5'-most EST
Method
                   BLASTX
                   g1220453
NCBI GI
BLAST score
                   408
                   1.0e-39
E value
Match length
                   124
% identity
                   (M79328) alpha-amylase [Solanum tuberosum]
NCBI Description
                   136365
Seq. No.
                   133571 1.R1010
Contig ID
                   q493312
5'-most EST
Method
                   BLASTN
NCBI GI
                   g940179
BLAST score
                   224
```

16262

1.0e-123



% identity NCBI Description Arabidopsis thaliana floral homeotic (AP3) gene, promoter region and partial cds 136366 Seq. No. 133572 1.R1010 Contig ID 5'-most EST g2393354 Method BLASTN g4580386 NCBI GI 278 BLAST score 1.0e-155 E value 383 Match length % identity 96 Arabidopsis thaliana chromosome II BAC T8018 genomic NCBI Description sequence, complete sequence 136367 Seq. No. 133677 1.R1010 Contig ID 5'-most EST $q50709\overline{4}$ 136368 Seq. No. 133723_1.R1010 Contig ID 5'-most EST g496401 Method BLASTX NCBI GI g2583129 BLAST score 303 1.0e-27 E value Match length 56 98 % identity (AC002387) putative methionine aminopeptidase [Arabidopsis NCBI Description thaliana] 136369 Seq. No. Contig ID 133760 1.R1010 $q49643\overline{9}$ 5'-most EST Method BLASTX NCBI GI g3164138 144 BLAST score 1.0e-13 E value Match length 102 % identity 43 (D78604) cytochrome p450 monooxygenase [Arabidopsis NCBI Description thaliana] >gi_4115378 (AC005967) cytochrome p450 monooxygenase [Arabidopsis thaliana] 136370 Seq. No. 133761_1.R1010 Contig ID q5069485'-most EST Method BLASTN NCBI GI g2351063 BLAST score 104 E value 2.0e-51

Match length 224 % identity 93

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MCL19, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                   136371
Contig ID
                   133772 1.R1010
                   g623727
5'-most EST
                   136372
Seq. No.
                   133881 1.R1010
Contig ID
5'-most EST
                   q20477\overline{5}9
Method
                   BLASTN
                   g2280508
NCBI GI
                   284
BLAST score
                   1.0e-158
E value
Match length
                   388
% identity
NCBI Description Arabidopsis thaliana tRNA-Glu gene
                   136373
Seq. No.
                   133887 1.R1010
Contig ID
5'-most EST
                   g1158841
Method
                   BLASTN
                   g3355463
NCBI GI
BLAST score
                   233
                   1.0e-128
E value
                   436
Match length
% identity
                   100
NCBI Description Arabidopsis thaliana chromosome II BAC F12L6 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   136374
Seq. No.
Contig ID
                   133900 1.R1010
5'-most EST
                   g498476
Seq. No.
                   136375
                   133906 1.R1010
Contig ID
5'-most EST
                   q49848\overline{2}
                   BLASTN
Method
NCBI GI
                   q4519197
BLAST score
                   44
E value
                   1.0e-15
Match length
                   135
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MTC11, complete sequence
Seq. No.
                   136376
                   133939 1.R1010
Contig ID
5'-most EST
                   g498515
Method
                   BLASTX
NCBI GI
                   g4567304
BLAST score
                   462
E value
                   1.0e-122
                   233
Match length
                   93
% identity
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]
```

Seq. No. 136377 Contig ID 134082 1.R1010 5'-most EST g2747650

```
BLASTX
Method
NCBI GI
                  q3413703
                  471
BLAST score
                  4.0e-47
E value
                  148
Match length
                  70
% identity
NCBI Description (AC004747) unknown protein [Arabidopsis thaliana]
                  136378
Seq. No.
                  134095_1.R1010
Contig ID
5'-most EST
                  g957900
                  BLASTX
Method
                  g4646206
NCBI GI
BLAST score
                   617
                  3.0e-64
E value
Match length
                  172
                  72
% identity
                   (AC007230) Contains similarity to gb_D13630 KIAA0005 gene
NCBI Description
                   from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360,
                   gb_T20468, gb_T45191 and gb_AI100459 come from this gene.
                   [Arabidopsis thaliana]
                   136379
Seq. No.
                   134128_1.R1010
Contig ID
5'-most EST
                   g2733521
                  BLASTX
Method
                   g4309681
NCBI GI
                   331
BLAST score
                   1.0e-30
E value
Match length
                   120
% identity
                   51
                  (AC006930) R33423_1 [Homo sapiens]
NCBI Description
                   136380
Seq. No.
                   134131 1.R1010
Contig ID
5'-most EST
                   q2757674
Method
                   BLASTX
                   g2213600
NCBI GI
BLAST score
                   430
E value
                   3.0e-42
Match length
                   161
                   58
% identity
                  (AC000348) T7N9.20 [Arabidopsis thaliana]
NCBI Description
                   136381
Seq. No.
                   134132 1.R1010
Contig ID
5'-most EST
                   g2733523
Method
                   BLASTN
                   g3873174
NCBI GI
BLAST score
                   363
                   0.0e + 00
E value
Match length
                   410
```

% identity 98

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14N23,

complete sequence [Arabidopsis thaliana]

Seq. No. 136382

NCBI Description



```
134189 1.R1010
Contig ID
5'-most EST
                   g3450386
Method
                   BLASTX
NCBI GI
                   q4689473
                   522
BLAST score
                   4.0e-53
E value
                   139
Match length
                   73
% identity
                   (AC007213) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   136383
Seq. No.
                   134276 1.R1010
Contig ID
5'-most EST
                   g1217058
Method
                   BLASTX
                   g2062155
NCBI GI
                   390
BLAST score
                   2.0e-37
E value
Match length
                   200
% identity
                   38
                  (AC001645) mitochondrial processing peptidase alpha subunit
NCBI Description
                   precusor isolog [Arabidopsis thaliana]
                   136384
Seq. No.
Contig ID
                   134280 1.R1010
                   q50214\overline{4}
5'-most EST
Method
                   BLASTN
                   g3985957
NCBI GI
BLAST score
                   513
E value
                   0.0e + 00
                   547
Match length
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MYN8, complete sequence [Arabidopsis thaliana]
                   136385
Seq. No.
                   134318_1.R1010
Contig ID
                   g502195
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1617274
BLAST score
                   441
E value
                   3.0e-44
Match length
                   233
                   55
% identity
NCBI Description
                   (Z72152) AMP-binding protein [Brassica napus]
                   136386
Seq. No.
Contig ID
                   134347 1.R1010
5'-most EST
                   q1217184
Method
                   BLASTN
                   q4580386
NCBI GI
BLAST score
                   126
                   2.0e-64
E value
                   403
Match length
% identity
                   98
                   Arabidopsis thaliana chromosome II BAC T8018 genomic
```

16266

sequence, complete sequence



136387 Seq. No. 134377_1.R1010 Contig ID g557621 5'-most EST BLASTN Method NCBI GI g2564046 BLAST score 172 E value 7.0e-92 408 Match length 99 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MGI19, complete sequence [Arabidopsis thaliana] Seq. No. 136388 134431 1.R1010 Contig ID 5'-most EST $g24461\overline{3}9$ 136389 Seq. No. 134494 1.R1010 Contig ID 5'-most EST q506591 Method BLASTN g2191126 NCBI GI 93 BLAST score 1.0e-44 E value Match length 149 97 % identity NCBI Description Arabidopsis thaliana BAC IG002N01 136390 Seq. No. 134543 1.R1010 Contig ID 5'-most EST g1517266 BLASTX Method g4580391 NCBI GI BLAST score 162 6.0e-11 E value Match length 75 49 % identity (AC007171) unknown protein [Arabidopsis thaliana] NCBI Description 136391 Seq. No. Contig ID 134546 1.R1010 5'-most EST g506934 Method BLASTN g3201608 NCBI GI BLAST score 211 1.0e-115 E value Match length 495 % identity 96 NCBI Description Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana] 136392 Seq. No.

Contig ID 134554 1.R1010

 5'-most EST
 g509100

 Method
 BLASTX

 NCBI GI
 g4539337

 BLAST score
 165



```
E value
                   1.0e-12
Match length
                   43
% identity
                   78
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                  136393
Seq. No.
                  134559 1.R1010
Contig ID
                  g506952
5'-most EST
                  BLASTX
Method
                  g1903357
NCBI GI
BLAST score
                   249
                   3.0e-21
E value
Match length
                   73
% identity
                   66
                   (AC000104) Strong similarity to Arabidopsis 2A6
NCBI Description
                   (gb X83096). [Arabidopsis thaliana]
                   136394
Seq. No.
                   134568 1.R1010
Contig ID
5'-most EST
                   q506963
                   BLASTX
Method
NCBI GI
                   g2979549
                   472
BLAST score
                   2.0e-47
E value
Match length
                   89
                   99
% identity
                   (AC003680) putative 7-ethoxycoumarin O-deethylase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   136395
                   134626 1.R1010
Contig ID
5'-most EST
                   q957935
                   136396
Seq. No.
                   134655_1.R1010
Contig ID
5'-most EST
                   q507104
Method
                   BLASTN
                   q3241924
NCBI GI
BLAST score
                   102
E value
                   4.0e-50
                   359
Match length
                   95
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MNC6, complete sequence [Arabidopsis thaliana]
                   136397
Seq. No.
Contig ID
                   134820 1.R1010
5'-most EST
                   g937858
Method
                   BLASTX
NCBI GI
                   g3548808
BLAST score
                   220
E value
                   4.0e-20
```

Match length 128 % identity 45

NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

136398 Seq. No.



134864 1.R1010 Contig ID q511167 5'-most EST BLASTX Method g3024666 NCBI GI 341 BLAST score 5.0e-32 E value 81 Match length 75 % identity STRICTOSIDINE SYNTHASE 1/2 PRECURSOR >gi_1754983 (U43713) NCBI Description strictosidine synthase [Arabidopsis thaliana] >gi 1754985 (U43945) strictosidine synthase [Arabidopsis thaliana] 136399 Seq. No. 134866_1.R1010 Contig ID 5'-most EST q511169 Method BLASTX q4263715 NCBI GI BLAST score 669 2.0e-70 E value Match length 130 100 % identity (AC006223) putative alanine acetyl transferase [Arabidopsis NCBI Description thaliana] 136400 Seq. No. 134881 1.R1010 Contig ID 5'-most EST q511184 BLASTN Method g3046848 NCBI GI BLAST score 489 0.0e + 00E value 569 Match length % identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K18C1, complete sequence [Arabidopsis thaliana] 136401 Seq. No. 134932_1.R1010 Contig ID $q51543\overline{3}$ 5'-most EST Method BLASTN q3980263 NCBI GI 42 BLAST score 3.0e-14 E value Match length 42 % identity 100 Cicer arietinum mRNA for 20S proteasome beta subunit NCBI Description 136402 Seq. No. 134971 1.R1010 Contig ID 5'-most EST g2763682 136403 Seq. No.

135056 1.R1010 Contig ID

5'-most EST g550167 Method BLASTX g4539601 NCBI GI BLAST score 146



E value 4.0e-09 Match length 108 % identity 35

NCBI Description (AL049522) serine/threonine-protein kinase

[Schizosaccharomyces pombe]

Seq. No. 136404

Contig ID 135072 1.R1010

5'-most EST g550184

Method BLASTN

NCBI GI g4584531

BLAST score 317

E value 1.0e-178

Match length 329

% identity 82

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8

(ESSA project)

Seq. No. 136405

Contig ID 135092 1.R1010

5'-most EST g550204

Seq. No. 136406

Contig ID 135097_1.R1010

5'-most EST g2722958

Seq. No. 136407

Contig ID 135136_1.R1010

5'-most EST g550248
Method BLASTX
NCBI GI g4506399
BLAST score 142
E value 1.0e-08
Match length 87
% identity 40

NCBI Description homolog of yeast Rael (Bharathi) mRNA-associated protein of

41 kDa (Kraemer) >gi_3122666_sp_P78406_RA1L_HUMAN MRNA-ASSOCIATED PROTEIN MRNP41 (RAE1 PROTEIN HOMOLOG) >gi_1903456 (U84720) mRNA export protein [Homo sapiens]

Seq. No. 136408

Contig ID 135137_1.R1010

5'-most EST g935677
Method BLASTX
NCBI GI g3122671
BLAST score 470
E value 2.0e-59
Match length 125
% identity 91

NCBI Description HYPOTHETICAL RAE1-LIKE PROTEIN >gi_2129676_pir__S71241

probable export protein - Arabidopsis thaliana >gi_1297188 (U53501) Theoretical protein with similarity to Swiss-Prot

Accession Number P41838 poly A+ RNA export protein

[Arabidopsis thaliana]

Seq. No. 136409

Contig ID 135138_1.R1010



```
5'-most EST
                   a550250
Method
                  BLASTX
                  q4741927
NCBI GI
                   409
BLAST score
                  5.0e-40
E value
                   82
Match length
% identity
                   96
                   (AF130252) calcium dependent protein kinase CP4
NCBI Description
                   [Arabidopsis thaliana]
                  136410
Seq. No.
Contig ID
                  135199_1.R1010
                  g572552
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2828185
BLAST score
                   519
E value
                  0.0e+00
Match length
                   527
% identity
                   100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUD21, complete sequence [Arabidopsis thaliana]
                   136411
Seq. No.
Contig ID
                   135208_1.R1010
5'-most EST
                   g557631
Method
                   BLASTN
NCBI GI
                   q2924651
                   406
BLAST score
E value
                   0.0e+00
                   446
Match length
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K2A18, complete sequence [Arabidopsis thaliana]
                   136412
Seq. No.
Contig ID
                   135288 1.R1010
5'-most EST
                   q2393345
                   BLASTN
Method
NCBI GI
                   g3859658
BLAST score
                   305
E value
                   1.0e-171
Match length
                   412
                   99
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1
                   (ESSAII project)
Seq. No.
                   136413
Contig ID
                   135327 1.R1010
5'-most EST
                   q572590
Seq. No.
                   136414
                   135342 1.R1010
Contig ID
5'-most EST
                   g2062800
                   BLASTN
Method
                   g4097544
NCBI GI
```

249

1.0e-138

BLAST score

E value



Match length 369 % identity 94

NCBI Description Arabidopsis thaliana farnesylated protein ATFP2 mRNA,

partial cds

Seq. No. 136415

Contig ID 135411_1.R1010

5'-most EST g586964

Method BLASTN

NCBI GI g4580514

BLAST score 407

E value 0.0e+00

Match length 431

% identity 99

NCBI Description Arabidopsis thaliana scarecrow-like 3 (SCL3) mRNA, partial

cds

Seq. No. 136416

Contig ID 135420 1.R1010

5'-most EST g586973
Method BLASTX
NCBI GI g4510406
BLAST score 275
E value 3.0e-24
Match length 66
% identity 77

NCBI Description (AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No. 136417

Contig ID 135468_1.R1010

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21L13, complete sequence

Seq. No. 136418

Contig ID 135469_1.R1010

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21L13, complete sequence

Seq. No. 136419

Contig ID 135481 1.R1010

5'-most EST g587042

Seq. No. 136420



```
Contig ID
                   135528 1.R1010
5'-most EST
                  g623005
                   136421
Seq. No.
                  135698 1.R1010
Contig ID
                  g634190
5'-most EST
Method
                  BLASTN
                  g2656024
NCBI GI
                   350
BLAST score
                  0.0e+00
E value
Match length
                   406
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K15E6
                   136422
Seq. No.
                   135702 1.R1010
Contig ID
5'-most EST
                   q634242
Method
                   BLASTN
                   g3869074
NCBI GI
BLAST score
                   273
                   1.0e-152
E value
                   305
Match length
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MMI9, complete sequence [Arabidopsis thaliana]
                   136423
Seq. No.
                   135726 1.R1010
Contig ID
5'-most EST
                   g634434
                   BLASTX
Method
NCBI GI
                   g4115934
BLAST score
                   587
E value
                   1.0e-60
                   139
Match length
% identity
                   69
                   (AF118223) contains similarity to Methanobacterium
NCBI Description
                   thermoautotrophicum transcriptional regulator (GB:AE000850)
                   [Arabidopsis thaliana]
                   136424
Seq. No.
Contig ID
                   135805 1.R1010
5'-most EST
                   q634781
                   BLASTX
Method
NCBI GI
                   g3047127
BLAST score
                   256
E value
                   6.0e-22
Match length
                   110
% identity
                   (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
                   136425
Seq. No.
```

Contig ID 135837 1.R1010

5'-most EST g634880

Seq. No. 136426

Contig ID 135926 1.R1010



```
5'-most EST
                    g671760
                   136427
Seq. No.
                   135927_1.R1010
Contig ID
5'-most EST
                   g957936
                   BLASTX
Method
NCBI GI
                   g2702283
                   510
BLAST score
                   8.0e-52
E value
                    124
Match length
% identity
                    76
NCBI Description
                   (AC003033) unknown protein [Arabidopsis thaliana]
                    136428
Seq. No.
                   135963 1.R1010
Contig ID
                    q67180\overline{2}
5'-most EST
                    BLASTN
Method
                    g2618602
NCBI GI
BLAST score
                    51
E value
                    1.0e-19
Match length
                    143
% identity
                    84
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSJ1, complete sequence [Arabidopsis thaliana]
                    136429
Seq. No.
                    135986_1.R1010
Contig ID
5'-most EST
                    g683513
Seq. No.
                    136430
                    136066 1.R1010
Contig ID
                    g773438
5'-most EST
                    BLASTX
Method
NCBI GI
                    q1168530
BLAST score
                    304
E value
                    5.0e-39
Match length
                    99
                    90
% identity
                    SERINE/THREONINE-PROTEIN KINASE ASK2 >gi 99748 pir S24586
NCBI Description
                    probable serine/threonine-specific protein kinase (EC
                    2.7.1.-) (clone ASK2) - Arabidopsis thaliana >gi_16443_emb_CAA78106_ (Z12120) protein kinase
                    [Arabidopsis thaliana]
Seq. No.
                    136431
Contig ID
                    136100 1.R1010
5'-most EST
                    q11588\overline{9}7
Method
                    BLASTX
NCBI GI
                    g2275210
BLAST score
                    271
                    1.0e-23
E value
                    134
Match length
% identity
                    46
                    (AC002337) peptidyl-prolyl cis-trans isomerase isolog
NCBI Description
                    [Arabidopsis thaliana]
```

136432

Seq. No.

Seq. No.

Contig ID

136438

136332 1.R1010



```
Contig ID
                   136129 1.R1010
                   g2762996
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3080428
BLAST score
                   541
E value
                   2.0e-55
Match length
                   101
                   99
% identity
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   136433
Contig ID
                   136142 1.R1010
5'-most EST
                   q1216770
Method
                   BLASTN
NCBI GI
                   q2264312
BLAST score
                   360
E value
                   0.0e + 00
Match length
                   424
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MOK16, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136434
Contig ID
                   136156 1.R1010
5'-most EST
                   g2759115
Method
                   BLASTX
NCBI GI
                   q3738302
BLAST score
                   467
E value
                   9.0e-52
Match length
                   168
% identity
                   (AC005309) tubby-like protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4249398 (AC006072) putative tubby protein [Arabidopsis
                   thalianal
                   136435
Seq. No.
                   136199 1.R1010
Contig ID
5'-most EST
                   g757597
                   136436
Seq. No.
                   136211 1.R1010
Contig ID
5'-most EST
                   g757609
                   136437
Seq. No.
                   136297 1.R1010
Contig ID
5'-most EST
                   g1932914
                   {\tt BLASTN}
Method
NCBI GI
                   g3402671
BLAST score
                   304
                   1.0e-170
E value
                   339
Match length
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC T16B24 genomic
NCBI Description
```

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.

136445



```
5'-most EST
                   q773491
                   136439
Seq. No.
                   136369 1.R1010
Contig ID
5'-most EST
                   g1054483
Method
                  BLASTX
NCBI GI
                  g2642444
BLAST score
                   325
                   2.0e-39
E value
                   130
Match length
% identity
                   (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   136440
Seq. No.
                   136462 1.R1010
Contig ID
                   g860757
5'-most EST
                   BLASTN
Method
NCBI GI
                   q3128166
BLAST score
                   377
                   0.0e + 00
E value
Match length
                   498
                   90
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F4I1 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   136441
Seq. No.
                   136467 1.R1010
Contig ID
5'-most EST
                   q860763
                   136442
Seq. No.
                   136468 1.R1010
Contig ID
5'-most EST
                   g895730
Seq. No.
                   136443
Contig ID
                   136518 1.R1010
5'-most EST
                   g895726
Method
                   BLASTN
NCBI GI
                   g3927822
BLAST score
                   518
E value
                   0.0e + 00
Match length
                   595
                   97
% identity
                   Arabidopsis thaliana chromosome II BAC F8N16 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136444
                   136532_1.R1010
Contig ID
5'-most EST
                   g872008
                   BLASTX
Method
NCBI GI
                   q3738333
BLAST score
                   62
                   5.0e-49
E value
                   168
Match length
                   64
% identity
                   (AC005170) unknown protein [Arabidopsis thaliana]
NCBI Description
```



```
136538 1.R1010
Contig ID
5'-most EST
                  q872007
                  BLASTN
Method
                  g3738313
NCBI GI
                  294
BLAST score
E value
                  1.0e-164
Match length
                  356
% identity
                   98
                  Arabidopsis thaliana chromosome II BAC T29E15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  136446
Contig ID
                  136552_1.R1010
                  g935991
5'-most EST
                  BLASTX
Method
                   q2244984
NCBI GI
BLAST score
                   514
                   3.0e-52
E value
Match length
                   132
                   81
% identity
                  (Z97340) strong similarity to beta-1,3-glucanase class I
NCBI Description
                   precursor [Arabidopsis thaliana]
                   136447
Seq. No.
Contig ID
                   136574 1.R1010
5'-most EST
                   g895738
                   BLASTN
Method
                   g2337888
NCBI GI
BLAST score
                   336
E value
                   0.0e+00
Match length
                   455
% identity
                   Genomic sequence for Arabidopsis thaliana BAC F14J16,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   136448
                   136585 1.R1010
Contig ID
5'-most EST
                   q897686
Seq. No.
                   136449
                   136626 1.R1010
Contig ID
5'-most EST
                   g899190
                   BLASTN
Method
NCBI GI
                   g4733952
BLAST score
                   228
E value
                   1.0e-125
Match length
                   280
                   96
% identity
                   Arabidopsis thaliana chromosome I BAC F23H11 genomic
NCBI Description
                   sequence, complete sequence
                   136450
Seq. No.
```

136713 1.R1010 Contig ID

5'-most EST g1158562

136451 Seq. No.

136726 1.R1010 Contig ID



```
q905495
5'-most EST
Method
                  BLASTX
                  g4538901
NCBI GI
                  216
BLAST score
                  3.0e-17
E value
                  133
Match length
                  40
% identity
                   (AL049482) RNA-directed DNA polymerase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  136452
Seq. No.
                  136735_1.R1010
Contig ID
5'-most EST
                  g905505
Method
                  BLASTX
                  g4531434
NCBI GI
                   81
BLAST score
                   5.0e-41
E value
                   127
Match length
                   76
% identity
                   (AC006224) unknown protein [Arabidopsis thaliana]
NCBI Description
                   136453
Seq. No.
                   136754_1.R1010
Contig ID
5'-most EST
                   g905526
Method
                   BLASTN
                   g1707006
NCBI GI
BLAST score
                   366
                   0.0e+00
E value
                   472
Match length
% identity
                   Arabidopsis thaliana chromosome II BAC T1B8 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   136454
Seq. No.
                   136849 1.R1010
Contig ID
                   g905631
5'-most EST
Method
                   BLASTX
                   q2213594
NCBI GI
BLAST score
                   273
E value
                   5.0e-24
                   77
Match length
                   65
% identity
                   (AC000348) T7N9.14 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   136455
                   136882 1.R1010
Contig ID
5'-most EST
                   g2596326
                   136456
Seq. No.
                   136930 1.R1010
Contig ID
                   q930930
5'-most EST
                   BLASTN
Method
                   g3461810
NCBI GI
BLAST score
                   45
                   5.0e-16
E value
                   77
Match length
```

90

% identity



```
NCBI Description Arabidopsis thaliana chromosome II BAC T17M13 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   136457
Seq. No.
                   137008 1.R1010
Contig ID
                   g906898
5'-most EST
                   BLASTX
Method
                   q478809
NCBI GI
BLAST score
                   564
                   5.0e-61
E value
                   170
Match length
                    67
% identity
                   protein kinase 6 (EC 2.7.1.-) - soybean >gi_170047 (M67449)
protein kinase [Glycine max] >gi_444789_prf__1908223A
NCBI Description
                   protein kinase [Glycine max]
                   136458
Seq. No.
                   137217 1.R1010
Contig ID
                    q2758405
5'-most EST
                   BLASTN
Method
                    g3702734
NCBI GI
BLAST score
                    294
                    1.0e-164
E value
                    411
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MNB8, complete sequence [Arabidopsis thaliana]
                    136459
Seq. No.
                    137259 1.R1010
Contig ID
5'-most EST
                    q90611\overline{2}
                    BLASTN
Method
                    g2673901
NCBI GI
BLAST score
                    176
                    3.0e-94
E value
Match length
                    298
                    99
% identity
                    Arabidopsis thaliana chromosome II BAC T24P15 genomic
NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
                    136460
Seq. No.
                    137356 1.R1010
Contig ID
5'-most EST
                    g906215
                    BLASTX
Method
NCBI GI
                    q466022
BLAST score
                    183
                    2.0e-13
E value
                    162
Match length
```

% identity

HYPOTHETICAL 77.3 KD PROTEIN T05G5.8 IN CHROMOSOME III NCBI Description >qi 482214 pir S41008 hypothetical protein T05G5.8 -

Caenorhabditis elegans

Seq. No. 136461

137455 1.R1010 Contig ID

g906330 5'-most EST BLASTX Method

Contig ID 5'-most EST



```
g4262154
NCBI GI
                  282
BLAST score
                  4.0e-26
E value
                  125
Match length
                  58
% identity
                  (AC005275) putative protein phosphatase regulatory subunit
NCBI Description
                  [Arabidopsis thaliana]
                  136462
Seq. No.
                  137534_1.R1010
Contig ID
                  g906429
5'-most EST
                  BLASTN
Method
                  g2924733
NCBI GI
BLAST score
                  34
                  3.0e-09
E value
Match length
                  142
% identity
                  81
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUF9, complete sequence [Arabidopsis thaliana]
                  136463
Seq. No.
                  137592 1.R1010
Contig ID
                  g906494
5'-most EST
                  BLASTN
Method
NCBI GI
                  g3510340
                  118
BLAST score
                   1.0e-59
E value
Match length
                   396
% identity
                   93
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDN11, complete sequence [Arabidopsis thaliana]
                   136464
Seq. No.
                   137739_1.R1010
Contig ID
5'-most EST
                   g2596714
Method
                   BLASTX
NCBI GI
                   g4262234
BLAST score
                   683
                   8.0e-72
E value
                   195
Match length
% identity
                   55
                  (AC006200) unknown protein [Arabidopsis thaliana]
NCBI Description
                   136465
Seq. No.
Contig ID
                   137810 1.R1010
                   g2756677
5'-most EST
                   BLASTX
Method
                   q3582340
NCBI GI
BLAST score
                   160
                   9.0e-11
E value
Match length
                   58
                   53
% identity
                  (AC005496) unknown protein [Arabidopsis thaliana]
NCBI Description
                   136466
Seq. No.
```

16280

137872 1.R1010

g906815

```
BLASTN
Method
                  g2760168
NCBI GI
                  185
BLAST score
                  2.0e-99
E value
                  593
Match length
                  96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MEE6, complete sequence [Arabidopsis thaliana]
                  136467
Seq. No.
                  137929 1.R1010
Contig ID
                  g2747839
5'-most EST
                  136468
Seq. No.
                  137938_1.R1010
Contig ID
                  g957765
5'-most EST
                  136469
Seq. No.
                  137986 1.R1010
Contig ID
                  g906949
5'-most EST
Method
                  BLASTX
                  g4586039
NCBI GI
                   249
BLAST score
                   3.0e-21
E value
                  76
Match length
                   67
% identity
                  (AC007109) unknown protein [Arabidopsis thaliana]
NCBI Description
                   136470
Seq. No.
                   138035 1.R1010
Contig ID
5'-most EST
                   q907005
                   136471
Seq. No.
                   138096_1.R1010
Contig ID
5'-most EST
                   g937520
                   BLASTX
Method
                   g3176687
NCBI GI
                   558
BLAST score
                   1.0e-100
E value
Match length
                   198
% identity
                   92
                   (AC003671) Strong similarity to trehalose-6-phosphate
NCBI Description
                   synthase homolog from A. thaliana chromosome 4 contig
                   gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and
                   gb R64855 come from this gene. [Arabidopsis thaliana]
                   136472
Seq. No.
                   138132 1.R1010
Contig ID
```

5'-most EST q2758070 BLASTX Method NCBI GI g1903360 BLAST score 391 1.0e-37 E value Match length 160 % identity 49

(AC000104) Similar to Arabidopsis 2A6 (gb X83096). EST NCBI Description gb T76913 comes from this gene. [Arabidopsis thaliana]



```
136473
Seq. No.
                   138198 1.R1010
Contig ID
5'-most EST
                   g907192
Method
                   BLASTX
                   q4454044
NCBI GI
BLAST score
                   363
                   8.0e-35
E value
                   89
Match length
% identity
                   80
                   (AL035394) putative Ap2 domain protein [Arabidopsis
NCBI Description
                   thaliana]
                   136474
Seq. No.
                   138206_1.R1010
Contig ID
5'-most EST
                   g2759446
Method
                   BLASTX
                   g115783
NCBI GI
BLAST score
                   89
                   2.0e-48
E value
Match length
                   110
% identity
                   93
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
                   136475
Seq. No.
                   138287_1.R1010
Contig ID
                   q930373
5'-most EST
Method
                   BLASTX
                   g2129471
NCBI GI
                   394
BLAST score
                   3.0e-38
E value
                   101
Match length
                   79
% identity
                   glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
NCBI Description
                   precursor - Scotch pine >gi_1100223 (L32560)
                   glyceraldehyde-3-phosphate \overline{d}ehydrogenase [Pinus sylvestris]
                   136476
Seq. No.
                   138309 1.R1010
Contig ID
                   g930491
5'-most EST
                   136477
Seq. No.
                   138377_1.R1010
Contig ID
5'-most EST
                   g930645
                   BLASTX
Method
NCBI GI
                   g2190550
                   258
BLAST score
E value
                   2.0e-22
                   73
Match length
                    66
% identity
```

Seq. No. 136478

NCBI Description

16282

[Arabidopsis thaliana]

(AC001229) ESTs gb_T45673,gb_N37512 come from this gene.

E value Match length

```
138391 1.R1010
Contig ID
                  q930655
5'-most EST
                  BLASTX
Method
                  g3894191
NCBI GI
                  290
BLAST score
                  9.0e-26
E value
                  175
Match length
                  48
% identity
                  (AC005662) unknown protein [Arabidopsis thaliana]
NCBI Description
                  136479
Seq. No.
                  138391 2.R1010
Contig ID
5'-most EST
                  g2393408
Method
                  BLASTX
                  g3894191
NCBI GI
BLAST score
                  269
                   2.0e-23
E value
                   132
Match length
% identity
                   48
                  (AC005662) unknown protein [Arabidopsis thaliana]
NCBI Description
                   136480
Seq. No.
                   138435 1.R1010
Contig ID
5'-most EST
                   g23934<u>7</u>9
                   136481
Seq. No.
                   138438 1.R1010
Contig ID
                   g930720
5'-most EST
                   136482
Seq. No.
                   138445 1.R1010
Contig ID
5'-most EST
                   g930729
                   136483
Seq. No.
                   138494_1.R1010
Contig ID
5'-most EST
                   g930783
                   136484
Seq. No.
                   138613 1.R1010
Contig ID
                   g930941
5'-most EST
                   BLASTN
Method
                   q3641835
NCBI GI
BLAST score
                   204
                   1.0e-111
E value
Match length
                   400
                   98
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20
NCBI Description
                   (ESSAII project)
                   136485
Seq. No.
                   138696 1.R1010
Contig ID
                   g931047
5'-most EST
Method
                   BLASTX
                   g4587540
NCBI GI
BLAST score
                   546
```

16283

3.0e-56



% identity (AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase NCBI Description with GDSL-motif family. [Arabidopsis thaliana] Seq. No. 136486 138705 1.R1010 Contig ID q931059 5'-most EST 136487 Seq. No. 138706_1.R1010 Contig ID g931060 5'-most EST BLASTN Method g4027862 NCBI GI 232 BLAST score E value 1.0e-127 Match length 367 90 % identity Arabidopsis thaliana chromosome 1 BAC T7A14 sequence, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 136488 138860 1.R1010 Contig ID g2764066 5'-most EST Method BLASTN g3327922 NCBI GI BLAST score 335 0.0e+00E value Match length 343 % identity 100 Arabidopsis thaliana chromosome II BAC T31E10 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 136489 Seq. No. 138862 1.R1010 Contig ID 5'-most EST g931243 Method BLASTX g4468803 NCBI GI 351 BLAST score 2.0e-33 E value 107 Match length % identity (AL035601) cytochrome P450-like protein [Arabidopsis NCBI Description thaliana] 136490 Seq. No. Contig ID 138969 1.R1010

5'-most EST g1158777

136491 Seq. No.

139006 1.R1010 Contig ID

g931937 5'-most EST BLASTX Method NCBI GI q2827625 BLAST score 478 E value 6.0e-48 Match length 147 % identity 71



```
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]
                  136492
Seq. No.
                  139067 1.R1010
Contig ID
5'-most EST
                  q2048954
                  136493
Seq. No.
                  139077 1.R1010
Contig ID
5'-most EST
                  g931928
                  BLASTX
Method
                  g4220485
NCBI GI
                  556
BLAST score
                   4.0e-57
E value
Match length
                   155
% identity
                   (AC006069) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                   thaliana]
                   136494
Seq. No.
                   139209 1.R1010
Contig ID
5'-most EST
                   g933367
                   BLASTN
Method
                   g2696018
NCBI GI
                   519
BLAST score
                   0.0e + 00
E value
                   643
Match length
                   96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXC9, complete sequence [Arabidopsis thaliana]
                   136495
Seq. No.
                   139232 1.R1010
Contig ID
                   g93346<del>5</del>
5'-most EST
                   BLASTX
Method
                   g3746060
NCBI GI
BLAST score
                   322
                   5.0e-42
E value
Match length
                   134
% identity
                   65
                   (AC005311) unknown protein [Arabidopsis thaliana]
NCBI Description
                   136496
Seq. No.
                   139404 1.R1010
Contig ID
5'-most EST
                   g933694
Seq. No.
                   136497
                   139459 1.R1010
Contig ID
                   g935200
5'-most EST
Method
                   BLASTX
                   q629561
NCBI GI
BLAST score
                   449
E value
                   1.0e-44
Match length
                   142
                   63
% identity
NCBI Description
                   SRG1 protein - Arabidopsis thaliana
                   >gi 479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis
```

thaliana]

NCBI GI



```
Seq. No.
                   136498
                   139499 1.R1010
Contig ID
                   g1159576
5'-most EST
                   136499
Seq. No.
                   139594 1.R1010
Contig ID
5'-most EST
                   g2762216
                   BLASTX
Method
                   g2281088
NCBI GI
                   174
BLAST score
                   2.0e-12
E value
                   104
Match length
                   38
% identity
                   (AC002333) indole-3-acetate beta-glucosyltransferase isolog
NCBI Description
                   [Arabidopsis thaliana]
                   136500
Seq. No.
                   139605 1.R1010
Contig ID
5'-most EST
                   g1565873
                   BLASTX
Method
                   g2911059
NCBI GI
BLAST score
                   541
                   2.0e-55
E value
                   151
Match length
                   79
% identity
                   (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                   136501
Seq. No.
                   139804 1.R1010
Contig ID
5'-most EST
                   g2048118
                   136502
Seq. No.
                   139826 1.R1010
Contig ID
5'-most EST
                   g27633<del>9</del>8
                   BLASTX
Method
                   g3582341
NCBI GI
BLAST score
                   699
                   7.0e-74
E value
                   171
Match length
                   75
% identity
                   (AC005496) putative flavonol 3-o-glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   136503
Seq. No.
                   139830 1.R1010
Contig ID
5'-most EST
                   g935087
                   136504
Seq. No.
                   139889_1.R1010
Contig ID
5'-most EST
                   g935154
                   136505
Seq. No.
                   139933 1.R1010
Contig ID
                   q935210
5'-most EST
Method
                   BLASTX
```

16286

g3236247

NCBI Description

```
BLAST score
                  4.0e-51
E value
                  104
Match length
                  94
% identity
                  (AC004684) SCARECROW-like protein [Arabidopsis thaliana]
NCBI Description
                  136506
Seq. No.
                  140158 1.R1010
Contig ID
                  g935479
5'-most EST
                  BLASTX
Method
                  g4455033
NCBI GI
                  182
BLAST score
                  2.0e-13
E value
                  86
Match length
% identity
                  45
                  (AF116237) pseudouridine synthase 1 [Mus musculus]
NCBI Description
                  136507
Seq. No.
                  140230 1.R1010
Contig ID
5'-most EST
                  q935567
Method
                  BLASTN
                  g2656024
NCBI GI
BLAST score
                  143
                   1.0e-74
E value
Match length
                   312
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K15E6
                   136508
Seq. No.
                   140642 1.R1010
Contig ID
                   g936045
5'-most EST
                   136509
Seq. No.
                   140665_1.R1010
Contig ID
                   g936071
5'-most EST
Method
                   BLASTX
                   q4063752
NCBI GI
BLAST score
                   454
                   5.0e-45
E value
Match length
                   114
% identity
                   (AC005851) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4510410 gb AAD21496.1_ (AC006929) unknown protein
                   [Arabidopsis thaliana]
                   136510
Seq. No.
                   140722 1.R1010
Contig ID
5'-most EST
                   g2733339
                   BLASTN
Method
NCBI GI
                   q2815404
BLAST score
                   59
E value
                   4.0e-24
Match length
                   154
% identity
                   85
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

16287

MMG4, complete sequence [Arabidopsis thaliana]

Method

NCBI GI



```
136511
Seq. No.
                  140833 1.R1010
Contig ID
                  g2759079
5'-most EST
                  136512
Seq. No.
                  140946_1.R1010
Contig ID
                  g936416
5'-most EST
                  BLASTN
Method
                  g4733953
NCBI GI
BLAST score
                   90
                   7.0e-43
E value
Match length
                   393
% identity
                   97
                  Arabidopsis thaliana chromosome I BAC F13011 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   136513
                   141052 1.R1010
Contig ID
                   g2748467
5'-most EST
                   BLASTN
Method
                   g3212102
NCBI GI
                   114
BLAST score
                   4.0e-57
E value
Match length
                   477
                   97
% identity
                   Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   136514
Seq. No.
                   141143 1.R1010
Contig ID
                   g936645
5'-most EST
                   BLASTN
Method
NCBI GI
                   g1785729
                   261
BLAST score
E value
                   1.0e-145
Match length
                   299
                   96
% identity
NCBI Description A.thaliana mitochondrial genome, part B
                   136515
Seq. No.
Contig ID
                   141280 1.R1010
5'-most EST
                   g958000
                   BLASTN
Method
NCBI GI
                   g2564048
BLAST score
                   367
E value
                   0.0e + 00
Match length
                   452
% identity
                   49
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MKD15, complete sequence [Arabidopsis thaliana]
                   136516
Seq. No.
                   141318 1.R1010
Contig ID
                   g3228571
 5'-most EST
```

16288

BLASTN

g2656028



```
BLAST score
E value
                   0.0e + 00
                   699
Match length
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   136517
Seq. No.
                   141384 1.R1010
Contig ID
                   g936936
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4522009
BLAST score
                   852
                   1.0e-91
E value
                   169
Match length
                   99
% identity
                  (AC007069) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   136518
                   141471 1.R1010
Contig ID
                   g937041
5'-most EST
                   136519
Seq. No.
                   141649_1.R1010
Contig ID
5'-most EST
                   g2749255
                   136520
Seq. No.
                   141712 1.R1010
Contig ID
5'-most EST
                   g937327
                   136521
Seq. No.
                   141793 1.R1010
Contig ID
5'-most EST
                   g957634
Method
                   BLASTX
                   g2739382
NCBI GI
BLAST score
                   313
E value
                   1.0e-28
                   131
Match length
% identity
                   (AC002505) myosin heavy chain-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   136522
Seq. No.
Contig ID
                   141871 1.R1010
5'-most EST
                   g937526
                   BLASTN
Method
NCBI GI
                   g4467131
BLAST score
                   300
                   1.0e-168
E value
Match length
                   342
                   97
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13
NCBI Description
                   (ESSA project)
```

Seq. No. 136523 Contig ID 141945

141945_1.R1010

5'-most EST g2758876



```
136524
Seq. No.
                   142148 1.R1010
Contig ID
                   g937881
5'-most EST
                   BLASTX
Method
                   g4510406
NCBI GI
BLAST score
                   176
                   1.0e-12
E value
                   80
Match length
                   54
% identity
NCBI Description (AC006587) putative protein kinase [Arabidopsis thaliana]
                   136525
Seq. No.
                   142273 1.R1010
Contig ID
                   q928952
5'-most EST
                   136526
Seq. No.
                   142297 1.R1010
Contig ID
                   g10154\overline{3}2
5'-most EST
                   BLASTX
Method
                   g4406778
NCBI GI
                   358
BLAST score
                   1.0e-57
E value
Match length
                   130
% identity
                   86
                   (AC006532) putative brassinosteroid insensitive protein
NCBI Description
                   [Arabidopsis thaliana]
                   136527
Seq. No.
                   142373 1.R1010
Contig ID
5'-most EST
                   q2048111
Seq. No.
                   136528
                   142447 1.R1010
Contig ID
                   g949067
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3249105
                   210
BLAST score
                   2.0e-16
E value
Match length
                   128
% identity
                   40
                   (AC003114) Contains similarity to protein phosphatase 2C
NCBI Description
                    (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                   136529
Contig ID
                   142471 1.R1010
5'-most EST
                   g949304
Seq. No.
                   136530
                   142552 1.R1010
Contig ID
5'-most EST
                   q1217096
Method
                   BLASTN
                   g1785673
NCBI GI
BLAST score
                    433
E value
                   0.0e+00
```

544

95

Match length % identity

```
NCBI Description A.thaliana mitochondrial genome, part A
                  136531
Seq. No.
                  142658 1.R1010
Contig ID
                  q957585
5'-most EST
                  136532
Seq. No.
                  142680 1.R1010
Contig ID
                  q957612
5'-most EST
                  BLASTN
Method
NCBI GI
                  q3449334
BLAST score
                  326
E value
                  0.0e + 00
                  441
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYH9, complete sequence [Arabidopsis thaliana]
                  136533
Seq. No.
                  142749 1.R1010
Contig ID
                  g957698
5'-most EST
                  BLASTN
Method
NCBI GI
                  q4220638
BLAST score
                  220
                  1.0e-120
E value
                  374
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIF21, complete sequence [Arabidopsis thaliana]
                  136534
Seq. No.
                   142787 1.R1010
Contig ID
5'-most EST
                   g2759501
Method
                  BLASTN
NCBI GI
                   g4159712
BLAST score
                   259
E value
                   1.0e-143
Match length
                   470
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MWI23, complete sequence
                   136535
```

Seq. No.

Contig ID 142793 1.R1010 g957745 5'-most EST

BLASTN Method NCBI GI g2264310 240 BLAST score 1.0e-132 E value Match length 264 % identity 98

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MKP11, complete sequence [Arabidopsis thaliana]

136536 Seq. No.

142802 1.R1010 Contig ID 5'-most EST g2047435

```
Method
                   BLASTX
NCBI GI
                   g2244860
BLAST score
                   210
                   1.0e-16
E value
                   126
Match length
                   39
% identity
                   (Z97337) cucumisin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   136537
                   142912 1.R1010
Contig ID
5'-most EST
                   g2749692
Method
                   BLASTX
NCBI GI
                   q4558558
                   601
BLAST score
                   1.0e-62
E value
                   116
Match length
% identity
                   (AC007138) putative polygalacturonidase [Arabidopsis
NCBI Description
                   thaliana]
                   136538
Seq. No.
                   143072 1.R1010
Contig ID
5'-most EST
                   q95804\overline{9}
Method
                   BLASTN
                   g4589439
NCBI GI
                   338
BLAST score
                   0.0e + 00
E value
                   491
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MQM1, complete sequence
                   136539
Seq. No.
                   143139 1.R1010
Contig ID
5'-most EST
                   q958126
                   BLASTN
Method
NCBI GI
                   g4006885
BLAST score
                   161
E value
                   2.0e-85
Match length
                   300
                   99
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                   fragment No
                   136540
Seq. No.
                   143198 1.R1010
Contig ID
5'-most EST
                   g958191
Method
                   BLASTX
                   q3047104
NCBI GI
                   285
BLAST score
                   2.0e-25
E value
                   140
Match length
                    55
% identity
                   (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
```

136541

143209 1.R1010

Seq. No.

Contig ID



```
a3719146
5'-most EST
                  BLASTX
Method
                  q3386611
NCBI GI
                  253
BLAST score
                  5.0e-22
E value
                  90
Match length
                  50
% identity
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
                  136542
Seq. No.
                  143277 1.R1010
Contig ID
5'-most EST
                  g2749268
Seq. No.
                  136543
                  143305 1.R1010
Contig ID
                  g1328084
5'-most EST
                  136544
Seq. No.
                  143442 1.R1010
Contig ID
                  g1041270
5'-most EST
                  136545
Seq. No.
                  143511_1.R1010
Contig ID
5'-most EST
                  g2722388
Method
                  BLASTX
                   g3242723
NCBI GI
                   44
BLAST score
                   2.0e-39
E value
                   95
Match length
% identity
                   97
                  (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis
NCBI Description
                   thaliana]
                   136546
Seq. No.
                   143566 1.R1010
Contig ID
5'-most EST
                   q1565829
Method
                   BLASTX
                   q4006886
NCBI GI
BLAST score
                   508
E value
                   2.0e-51
                   152
Match length
                   59
% identity
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                   136547
                   143599 1.R1010
Contig ID
5'-most EST
                   q1053411
Seq. No.
                   136548
                   143646 1.R1010
Contig ID
5'-most EST
                   g2412911
                   136549
Seq. No.
                   143650 1.R1010
Contig ID
5'-most EST
                   g1053472
```

136550

Seq. No.

```
143684 1.R1010
Contig ID
5'-most EST
                  q10537\overline{6}7
                  BLASTN
Method
                   g3702732
NCBI GI
                   325
BLAST score
                   0.0e + 00
E value
Match length
                   365
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGF10, complete sequence [Arabidopsis thaliana]
                   136551
Seq. No.
Contig ID
                   143696_1.R1010
                   g1053523
5'-most EST
                   BLASTX
Method
                   q4455361
NCBI GI
                   504
BLAST score
                   6.0e-51
E value
                   111
Match length
                   87
% identity
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   136552
Seq. No.
                   143707 1.R1010
Contig ID
5'-most EST
                   g1053540
                   BLASTN
Method
                   g4582411
NCBI GI
                   173
BLAST score
                   2.0e-92
E value
Match length
                   326
% identity
                   Arabidopsis thaliana chromosome 1 BAC T23K8 sequence,
NCBI Description
                   complete sequence
                   136553
Seq. No.
                   143708 1.R1010
Contig ID
5'-most EST
                   g1053789
                   BLASTN
Method
                   q2191126
NCBI GI
BLAST score
                   291
                   1.0e-163
E value
                   366
Match length
% identity
NCBI Description Arabidopsis thaliana BAC IG002N01
                   136554
Seq. No.
                   143733 1.R1010
Contig ID
5'-most EST
                   g2047566
Method
                   BLASTX
NCBI GI
                   g3927825
                   120
BLAST score
                   4.0e-50
E value
Match length
                   170
% identity
                   74
                   (AC005727) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                    [Arabidopsis thaliana]
```

Contig ID

5'-most EST



```
136555
Seq. No.
Contig ID
                  143742 1.R1010
                  q1053581
5'-most EST
                  136556
Seq. No.
                  143757 1.R1010
Contig ID
5'-most EST
                  g1053599
Method
                  BLASTX
                  g4558564
NCBI GI
                  462
BLAST score
                  5.0e-46
E value
                  116
Match length
% identity
                  (AC007138) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                  136557
Seq. No.
                  143844 1.R1010
Contig ID
5'-most EST
                  q2412725
                  136558
Seq. No.
                  143849_1.R1010
Contig ID
                  g1053705
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2558938
BLAST score
                  202
E value
                   1.0e-29
                   206
Match length
                   42
% identity
                  (AF024625) arm repeat containing protein [Brassica napus]
NCBI Description
                   136559
Seq. No.
                   143971 1.R1010
Contig ID
5'-most EST
                   g1053856
                   BLASTN
Method
NCBI GI
                   q3522932
BLAST score
                   473
                   0.0e + 00
E value
                   494
Match length
% identity
                   99
                   Arabidopsis thaliana chromosome II BAC F14M4 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   136560
Seq. No.
                   143987 1.R1010
Contig ID
                   q1053879
5'-most EST
                   BLASTN
Method
NCBI GI
                   q1785673
BLAST score
                   378
E value
                   0.0e+00
Match length
                   487
                   95
% identity
NCBI Description A.thaliana mitochondrial genome, part A
Seq. No.
                   136561
```

16295

144001 1.R1010

 $g23936\overline{4}3$



```
136562
Seq. No.
                  144026 1.R1010
Contig ID
                  q25807\overline{5}0
5'-most EST
                  BLASTX
Method
                  g3132477
NCBI GI
BLAST score
                  550
                  2.0e-56
E value
Match length
                  110
                   99
% identity
NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]
                  136563
Seq. No.
                   144165_1.R1010
Contig ID
5'-most EST
                   g2757263
                   BLASTX
Method
                   g2982458
NCBI GI
                   595
BLAST score
                   1.0e-61
E value
                   127
Match length
                   98
% identity
                  (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
                   136564
Seq. No.
                   144238_1.R1010
Contig ID
                   g2047442
5'-most EST
                   BLASTX
Method
                   g3892057
NCBI GI
BLAST score
                   379
                   9.0e-37
E value
Match length
                   99
                   78
% identity
NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana]
                   136565
Seq. No.
                   144532 1.R1010
Contig ID
5!-most EST
                   g1103334
                   136566
Seq. No.
Contig ID
                   144561 1.R1010
                   q1158881
5'-most EST
                   136567
Seq. No.
                   144612 1.R1010
Contig ID
5'-most EST
                   g1103362
                   BLASTX
Method
                   q4468804
NCBI GI
BLAST score
                   417
                   7.0e-41
E value
Match length
                   123
% identity
                   (AL035601) putative protein [Arabidopsis thaliana]
NCBI Description
                   136568
Seq. No.
                   144616 1.R1010
Contig ID
```

q1103366

BLASTN

5'-most EST

Method

Method NCBI GI

BLAST score



```
q2853071
NCBI GI
BLAST score
                   217
                   1.0e-119
E value
                   235
Match length
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7
NCBI Description
                   (ESSA project)
                   136569
Seq. No.
                   144631 1.R1010
Contig ID
                   g11494\overline{4}2
5'-most EST
                   136570
Seq. No.
                   144635 1.R1010
Contig ID
5'-most EST
                   g1109707
Method
                   BLASTX
                   g3287494
NCBI GI
                   333
BLAST score
                   7.0e-31
E value
                   139
Match length
% identity
                   52
                   (D78504) similar to yeast SRP1 [Oryza sativa]
NCBI Description
                   136571
Seq. No.
                   144641_1.R1010
Contig ID
5'-most EST
                   g1109713
                   BLASTX
Method
NCBI GI
                   q3980386
BLAST score
                   735
                   4.0e-78
E value
                   143
Match length
                   99
% identity
                   (AC004561) putative glutathione S-transferase [Arabidopsis
NCBI Description
                   thaliana]
                   136572
Seq. No.
                   144654 1.R1010
Contig ID
                   g1109726
5'-most EST
Method
                   BLASTN
                   g3869067
NCBI GI
BLAST score
                   199
                   1.0e-108
E value
                   245
Match length
                   100
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCK7, complete sequence [Arabidopsis thaliana]
                   136573
Seq. No.
                   144684 1.R1010
Contig ID
5'-most EST
                   g2748813
Seq. No.
                   136574
                   144724 1.R1010
Contig ID
                   q1158274
5'-most EST
```

BLASTX

g3885341 532



```
3.0e-54
E value
                   162
Match length
% identity
                   53
                   (AC005623) unknown protein [Arabidopsis thaliana]
NCBI Description
                   136575
Seq. No.
                   144729 1.R1010
Contig ID
                   q1158279
5'-most EST
                   BLASTN
Method
                   g2564045
NCBI GI
                   312
BLAST score
                   1.0e-175
E value
                   502
Match length
                   92
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K8K14, complete sequence [Arabidopsis thaliana]
                   136576
Seq. No.
                   144747 1.R1010
Contig ID
                   a11582\overline{9}9
5'-most EST
Method
                   BLASTX
                   g4415931
NCBI GI
BLAST score
                   454
                   6.0e-49
E value
Match length
                   115
% identity
                   87
                   (AC006418) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown
                   protein [Arabidopsis thaliana]
                   136577
Seq. No.
                   145411 1.R1010
Contig ID
                   g2580944
5'-most EST
                   BLASTN
Method
                   g4220468
NCBI GI
                   294
BLAST score
                   1.0e-164
E value
                   337
Match length
% identity
                   Arabidopsis thaliana chromosome II BAC T8011 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   136578
Seq. No.
                   145460 1.R1010
Contig ID
                   g2757384
5'-most EST
Method
                   BLASTX
                   q2982452
NCBI GI
                   572
BLAST score
E value
                   5.0e-59
Match length
                   132
 % identity
                   87
                    (AL022223) receptor protein kinase-like protein
NCBI Description
                    [Arabidopsis thaliana]
```

Seq. No. 136579

Contig ID 145670_1.R1010

5'-most EST g1159324



BLASTN Method g4519195 NCBI GI 147 BLAST score 5.0e-77 E value 225 Match length 91 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MQC12, complete sequence 136580 Seq. No. 145923_1.R1010 Contig ID g3450082 5'-most EST BLASTN Method g3641835 NCBI GI BLAST score 350 E value 0.0e+00Match length 519 99 % identity Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 NCBI Description (ESSAII project) 136581 Seq. No. 145938 1.R1010 Contig ID g1159662 5'-most EST Method BLASTN NCBI GI g4557061 225 BLAST score E value 1.0e-123 Match length 449 90 % identity Arabidopsis thaliana chromosome II BAC F23M2 genomic NCBI Description sequence, complete sequence 136582 Seq. No. 146227 1.R1010 Contig ID g1215839 5'-most EST BLASTN Method g2253009 NCBI GI 340 BLAST score 0.0e+00E value 411 Match length 95 % identity Arabidopsis thaliana mRNA for MAP3K delta-1 protein kinase, NCBI Description partial 136583 Seq. No. 146233 1.R1010 Contig ID g1225918 5'-most EST Seq. No. 136584 Contig ID 146245 1.R1010 g2393146 5'-most EST

136585 Seq. No.

146259 1.R1010 Contig ID

5'-most EST q1215872 Method BLASTX

Match length

```
q3319340
NCBI GI
                   480
BLAST score
                   3.0e-48
E value
                   95
Match length
                   100
% identity
                   (AF077407) contains similarity to E. coli cation transport
NCBI Description
                   protein ChaC (GB:D90756) [Arabidopsis thaliana]
                   136586
Seq. No.
                   146331_1.R1010
Contig ID
                   g12159\overline{4}4
5'-most EST
                   BLASTX
Method
                   q4490297
NCBI GI
BLAST score
                   71
                   3.0e+00
E value
                   109
Match length
                   17
% identity
                   (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                   136587
Seq. No.
                   146338 1.R1010
Contig ID
                   q27495\overline{20}
5'-most EST
                   136588
Seq. No.
                   146352 1.R1010
Contig ID
                   g1215969
5'-most EST
Method
                   BLASTX
                   g2462832
NCBI GI
                   484
BLAST score
                   1.0e-48
E value
                   125
Match length
                   65
% identity
                   (AF000657) similar to Bacillus CotA [Arabidopsis thaliana]
NCBI Description
                   136589
Seq. No.
Contig ID
                   146455 1.R1010
5'-most EST
                   g2758462
                   BLASTX
Method
                   q2351097
NCBI GI
BLAST score
                   391
                   2.0e-55
E value
                   206
Match length
                   60
% identity
                   (AB006810) ATMRK1 [Arabidopsis thaliana]
NCBI Description
                   136590
Seq. No.
                   146965 1.R1010
Contig ID
5'-most EST
                   g2048076
                    136591
Seq. No.
                    147359 1.R1010
Contig ID
                    g2047652
 5'-most EST
                   BLASTN
Method
NCBI GI
                    g2827538
BLAST score
                    275
                    1.0e-153
E value
```



Seq. No. 136592

Contig ID 147553 1.R1010

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MFC16, complete sequence [Arabidopsis thaliana]

Seq. No. 136593

Contig ID 147669 1.R1010

5'-most EST g2749065
Method BLASTX
NCBI GI g4559329
BLAST score 279
E value 1.0e-24
Match length 91
% identity 60

NCBI Description (AC007087) putative protein kinase MAP3K [Arabidopsis

thaliana]

Seq. No. 136594

Contig ID 147984_1.R1010

5'-most EST g20481\overline{81}
Method BLASTX
NCBI GI g4753648
BLAST score 692
E value 5.0e-73
Match length 137
% identity 99

NCBI Description (AL049751) putative protein [Arabidopsis thaliana]

Seq. No. 136595

Contig ID 148213 1.R1010

5'-most EST g1327623
Method BLASTX
NCBI GI g2795806
BLAST score 741
E value 1.0e-78
Match length 170
% identity 88

NCBI Description (AC003674) unknown protein [Arabidopsis thaliana]

Seq. No. 136596

Contig ID 148442_1.R1010

 5'-most EST
 g2748790

 Method
 BLASTN

 NCBI GI
 g3510339

 BLAST score
 356

 E value
 0.0e+00



Match length 440 % identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K3K7, complete sequence [Arabidopsis thaliana]

Seq. No. 136597

Contig ID 148493 1.R1010

5'-most EST g1328128

Method BLASTN

NCBI GI g4757678

BLAST score 110

E value 7.0e-55

Match length 325
% identity 97

NCBI Description Arabidopsis thaliana chromosome I BAC F9H16 genomic

sequence, complete sequence

Seq. No. 136598

Contig ID 148539 1.R1010

5'-most EST g2393179
Method BLASTN
NCBI GI g4662647
BLAST score 186
E value 1.0e-100
Match length 450
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC F3K12 genomic

sequence, complete sequence

Seq. No. 136599

Contig ID 148602 1.R1010

5'-most EST g2596170
Method BLASTX
NCBI GI g2494123
BLAST score 397
E value 3.0e-38
Match length 77
% identity 99

NCBI Description (AC002376) Contains similarity to Saccharomyces

hypothetical 52.1 KD protein (gb_Z28075). EST gb_T04617

comes from this gene. [Arabidopsis thaliana]

Seq. No. 136600

Contig ID 148635_1.R1010

5'-most EST g2597530
Method BLASTX
NCBI GI g2621798
BLAST score 303
E value 2.0e-27
Match length 80
% identity 70

NCBI Description (AE000850) transcriptional regulator [Methanobacterium

thermoautotrophicum]

Seq. No. 136601

Contig ID 148719 1.R1010

5'-most EST $q24459\overline{2}3$



```
Method
                   BLASTN
NCBI GI
                   q4417264
BLAST score
                   246
E value
                   1.0e-136
Match length
                   387
% identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F7D8 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136602
Contig ID
                   148840 1.R1010
5'-most EST
                   q1520923
Method
                   BLASTN
NCBI GI
                   q343347
BLAST score
                   261
E value
                   1.0e-145
Match length
                   432
% identity
                   91
NCBI Description
                 Soybean 18S ribosomal RNA gene
Seq. No.
                   136603
Contig ID
                   149018 1.R1010
5'-most EST
                   g1565836
Method
                   BLASTN
NCBI GI
                   g2618603
BLAST score
                   175
E value
                   2.0e-93
Match length
                   212
% identity
                   97
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSL3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136604
Contig ID
                   149158 1.R1010
5'-most EST
                   g1932922
Method
                   BLASTX
NCBI GI
                   g2245053
BLAST score
                   231
E value
                   4.0e-19
Match length
                   81
% identity
                   59
NCBI Description
                  (Z97342) resistance gene homolog [Arabidopsis thaliana]
Seq. No.
                   136605
Contig ID
                   149262 1.R1010
5'-most EST
                  g2759078
Method
                  BLASTN
NCBI GI
                  g2088638
BLAST score
                  361
E value
                  0.0e+00
Match length
                  426
```

% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136606

149299_1.R1010 Contig ID

16303

~ \$e

NCBI GI

E value

BLAST score

Match length

g3193292

7.0e-54

529

125



```
5'-most EST
                   g2047603
Method
                   BLASTN
NCBI GI
                   g4220640
BLAST score
                   160
E value
                   8.0e-85
Match length
                   320
% identity
                   98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MPE11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136607
Contig ID
                   149346 1.R1010
5'-most EST
                   g2047481
Seq. No.
                   136608
Contig ID
                   149348 1.R1010
5'-most EST
                   g2758665
Method
                   BLASTN
NCBI GI
                   g4589428
BLAST score
                   174
E value
                   6.0e-93
Match length
                   408
% identity
                   97
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MFH8, complete sequence
Seq. No.
                   136609
Contig ID
                   149351 1.R1010
5'-most EST
                   g2576672
Method
                   BLASTX
NCBI GI
                   g2213595
BLAST score
                   178
E value
                   6.0e-13
Match length
                   51
% identity
                   63
NCBI Description
                  (AC000348) T7N9.15 [Arabidopsis thaliana]
Seq. No.
                   136610
Contig ID
                   149368 1.R1010
5'-most EST
                   g2047510
Method
                  BLASTX
NCBI GI
                   g2392772
BLAST score
                   163
E value
                  7.0e-21
Match length
                   69
% identity
                  80
NCBI Description
                   (AC002534) putative chloroplast prephenate dehydratase
                   [Arabidopsis thaliana]
Seq. No.
                  136611
Contig ID
                  149383 1.R1010
5'-most EST
                  g2580669
Method
                  BLASTX
```



% identity NCBI Description (AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana] Seq. No. 136612 Contig ID 149678 1.R1010 5'-most EST g2047882 Method BLASTX NCBI GI g4006872 BLAST score 169 E value 5.0e-19 Match length 106 % identity 52

NCBI Description (Z99707) methionyl aminopeptidase-like protein [Arabidopsis thaliana1

Seq. No. 136613 Contig ID 149769 1.R1010 5'-most EST g2047980 Method BLASTN NCBI GI g4757414

BLAST score 205 E value 1.0e-111 Match length 367 % identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No. 136614

Contig ID 149779 1.R1010

5'-most EST g2047991 Method BLASTN NCBI GI g4585952 BLAST score 188 E value 1.0e-101 Match length 362 % identity 91

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F26F24,

complete sequence

Seq. No. 136615

Contig ID 149785 1.R1010 5'-most EST g2580872

Seq. No. 136616

Contig ID 149791 1.R1010

5'-most EST g2580759

Seq. No. 136617

Contig ID 149795 1.R1010

5'-most EST g2393442 Method BLASTN NCBI GI g4757399 BLAST score 196 E value 1.0e-106

Match length 438



% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MEE13, complete sequence

Seq. No. 136618

Contig ID 149823_1.R1010

5'-most EST $g24133\overline{0}8$

Seq. No. 136619

Contig ID 149862_1.R1010

5'-most EST g2048096

Seq. No. 136620

Contig ID 149879 1.R1010

Match length 85 % identity 88

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 136621

Contig ID 149897_1.R1010

5'-most EST g2048133

Seq. No. 136622

Contig ID 150114_1.R1010

5'-most EST g2048366
Method BLASTN
NCBI GI g2191181
BLAST score 176
E value 4.0e-94
Match length 200

% identity 96

NCBI Description Arabidopsis thaliana BAC TM021B04

Seq. No. 136623

Contig ID 150204 1.R1010

5'-most EST g2445909
Method BLASTN
NCBI GI g2182285
BLAST score 318
E value 1.0e-179
Match length 387
% identity 96

NCBI Description Sequence of BAC F5I14 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 136624

Contig ID 150254_1.R1010

5'-most EST $g27588\overline{1}0$

Seq. No. 136625

Contig ID 150422_1.R1010

5'-most EST $g27490\overline{9}0$



```
Method
                   BLASTN
NCBI GI
                   g2335089
BLAST score
                   332
E value
                   0.0e+00
Match length
                   407
% identity
                   96
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T11A7 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136626
Contig ID
                   150464 1.R1010
5'-most EST
                   g2412933
Method
                   BLASTN
NCBI GI
                   q2828183
BLAST score
                   42
E value
                   2.0e-14
Match length
                   99
                   55
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MPL12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  136627
Contig ID
                  150482 1.R1010
5'-most EST
                  g2048777
Method
                  BLASTX
NCBI GI
                  g3702333
BLAST score
                  163
E value
                  1.0e-11
Match length
                  40
% identity
                  65
NCBI Description
                  (AC005397) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  136628
                  150492 1.R1010
Contig ID
5'-most EST
                  g2749179
Method
                  BLASTN
NCBI GI
                  g4220643
BLAST score
                  348
E value
                  0.0e+00
Match length
                  421
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MWD22, complete sequence [Arabidopsis thaliana]
                  136629
Seq. No.
                  150594 1.R1010
5'-most EST
                  g2048900
                  BLASTN
```

Contig ID Method NCBI GI g2645198 BLAST score 231 E value 1.0e-127 Match length 302

% identity 95 NCBI Description Arabidopsis thaliana chromosome I BAC T26J12 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136630

% identity

84



```
Contig ID
                    150643 1.R1010
 5'-most EST
                    g2048950
 Method
                    BLASTX
 NCBI GI
                    g2651307
 BLAST score
                    74
 E value
                    7.0e-25
 Match length
                    91
 % identity
                    55
 NCBI Description
                    (AC002336) putative uroporphyinogen decarboxylase
                    [Arabidopsis thaliana]
 Seq. No.
                    136631
                    150743 1.R1010
 Contig ID
 5'-most EST
                    g2414001
 Method
                    BLASTN
 NCBI GI
                    g3004543
 BLAST score
                    296
 E value
                    1.0e-166
Match length
                    445
 % identity
                    97
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC F19F24 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    136632
 Contig ID
                   150833 1.R1010
 5'-most EST
                   g2446032
 Method
                   BLASTN
 NCBI GI
                   g2894591
 BLAST score
                   59
 E value
                   2.0e-24
Match length
                   324
 % identity
                   95
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21
                    (ESSAII project)
 Seq. No.
                   136633
 Contig ID
                   150889 1.R1010
 5'-most EST
                   g2393163
Method
                   BLASTN
NCBI GI
                   g3894179
BLAST score
                   370
E value
                   0.0e+00
Match length
                   453
                   97
 % identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F13H10 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136634
Contig ID
                   150921 1.R1010
5'-most EST
                   g3450256
Method
                   BLASTN
NCBI GI
                   g3869075
BLAST score
                   78
E value
                   1.0e-35
Match length
                   226
```

16308

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

E value

Match length

1.0e-118

518





MXK3, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                   136635
 Contig ID
                   150953 1.R1010
 5'-most EST
                   g2393227
Method
                   BLASTX
NCBI GI
                   g4510381
BLAST score
                   392
E value
                   6.0e-38
Match length
                   134
% identity
                   67
NCBI Description
                   (AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.
                   136636
                   150985 1.R1010
Contig ID
5'-most EST
                   g2393259
Method
                   BLASTN
NCBI GI
                   g4159706
BLAST score
                   222
E value
                   1.0e-121
Match length
                   284
% identity
                   96
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MGL6, complete sequence
Seq. No.
                   136637
Contig ID
                   151059 1.R1010
5'-most EST
                   g2393333
Method
                   BLASTN
NCBI GI
                   g2924652
BLAST score
                   334
E value
                   0.0e+00
Match length
                   406
% identity
                   96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K9L2, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136638
Contig ID
                   151061 1.R1010
5'-most EST
                   g23933<del>3</del>5
Method
                   BLASTN
NCBI GI
                   g2182289
BLAST score
                   106
E value
                   2.0e-52
Match length
                   281
% identity
                   93
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F11P17 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  136639
Contig ID
                  151062 1.R1010
5'-most EST
                  g2747491
Method
                  BLASTN
NCBI GI
                  g4587986
BLAST score
                  216
```

% identity NCBI Description Arabidopsis thaliana ABA-regulated gene cluster, complete sequence Seq. No. 136640 Contig ID 151069 1.R1010 5'-most EST g2445934 Seq. No. 136641 151076 1.R1010 Contig ID 5'-most EST g2393350 Seq. No. 136642 Contig ID 151099 1.R1010 5'-most EST g2393373 Method BLASTN NCBI GI g4538949 BLAST score 306 E value 1.0e-171 Match length 443 % identity 97 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24 (ESSA project) 136643 Seq. No. 151118 1.R1010 Contig ID 5'-most EST g2393392 Seq. No. 136644 Contig ID 151128 1.R1010

Contig ID 151128_1.R1010
5'-most EST g2393402
Method BLASTX
NCBI GI g3859659
BLAST score 307
E value 6.0e-28
Match length 64
% identity 92

NCBI Description (AL031394) putative potassium transporter AtKT5p (AtKT5)

[Arabidopsis thaliana]

Seq. No. 136645

Contig ID 151136_1.R1010 5'-most EST g2393410

Seq. No. 136646

Contig ID 151322_1.R1010 5'-most EST g3449405

Method BLASTX
NCBI GI g2262113
BLAST score 372
E value 2.0e-35
Match length 76
% identity 96

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 136647

Contig ID 151359 1.R1010



```
5'-most EST
                   q2756851
Method
                   BLASTN
NCBI GI
                   q3492818
BLAST score
                   39
E value
                   2.0e-12
Match length
                   86
% identity
                   86
NCBI Description Quercus suber cDNA for a ribosomal protein RPL41
Seq. No.
                   136648
Contig ID
                   151401 1.R1010
5'-most EST
                   g2393676
Method
                   BLASTN
NCBI GI
                   q4415928
BLAST score
                   281
E value
                   1.0e-157
Match length
                   432
% identity
                   92
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F13A10 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136649
                   151444 1.R1010
Contig ID
5'-most EST
                   g2412726
Method
                   BLASTX
NCBI GI
                   g2443885
BLAST score
                   388
E value
                   1.0e-37
Match length
                   83
% identity
                   90
NCBI Description
                  (AC002294) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   136650
Contig ID
                   151444 2.R1010
5'-most EST
                   g2722213
Method
                   BLASTN
NCBI GI
                  g2182289
BLAST score
                   152
E value
                   3.0e-80
Match length
                  216
% identity
                   94
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F11P17 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  136651
Contig ID
                  151445 1.R1010
5'-most EST
                  g2413317
                  BLASTX
                  g2191131
                  367
                  3.0e-35
Match length
                  68
```

Method NCBI GI BLAST score E value

% identity

NCBI Description (AF007269) A_IG002N01.8 gene product [Arabidopsis thaliana]

Seq. No. 136652

Contig ID 151447_1.R1010

NCBI Description



```
5'-most EST
                    g2412917
Seq. No.
                    136653
                    151495 1.R1010
Contig ID
5'-most EST
                    g2412777
Method
                    BLASTN
NCBI GI
                    g3522932
BLAST score
                    272
E value
                    1.0e-151
Match length
                    287
% identity
                    99
                   Arabidopsis thaliana chromosome II BAC F14M4 genomic
NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    136654
Contig ID
                    151552 1.R1010
5'-most EST
                   g2412834
Seq. No.
                   136655
Contig ID
                   151629 1.R1010
5'-most EST
                   g34501\overline{2}6
Seq. No.
                   136656
Contig ID
                   151649 1.R1010
5'-most EST
                   g27495\overline{7}4
Method
                   BLASTX
NCBI GI
                   g2288999
BLAST score
                   397
E value
                   2.0e-38
Match length
                   112
% identity
                   71
NCBI Description
                   (AC002335) electron transfer flavoprotein ubiquinone
                   oxidoreductase isolog [Arabidopsis thaliana]
Seq. No.
                   136657
Contig ID
                   151680 1.R1010
5'-most EST
                   g2576631
Method
                   BLASTX
NCBI GI
                   g4388834
BLAST score
                   304
E value
                   1.0e-27
Match length
                   114
% identity
                   18
NCBI Description
                   (AC006528) putative disease resistance protein RPP1, 3'
                   partial [Arabidopsis thaliana]
Seq. No.
                   136658
Contig ID
                   151724 1.R1010
5'-most EST
                   g2413011
Method
                   BLASTN
NCBI GI
                   g2160132
BLAST score
                   21
E value
                   5.8e-02
Match length
                   273
% identity
                   62
```

16312

1, complete sequence [Arabidopsis thaliana]

Sequence of BAC F19K23 from Arabidopsis thaliana chromosome



Seq. No. 136659

Contig ID 151734 1.R1010

5'-most EST g2413021

Seq. No. 136660

Contig ID 151822 1.R1010

5'-most EST g2413110 Method BLASTX NCBI GI q548485 BLAST score 175 E value 5.0e-13 Match length 64 % identity 27

NCBI Description POLYGALACTURONASE INHIBITOR PRECURSOR

(POLYGALACTURONASE-INHIBITING PROTEIN)

>gi_478677_pir__S23764 polygalacturanase-inhibiting protein precursor - kidney bean >gi_21029_emb_CAA46016 (X64769) polygalacturanase-inhibiting protein [Phaseolus vulgaris]

Seq. No. 136661

Contig ID 151858 1.R1010

5'-most EST $q27479\overline{15}$ Method BLASTN NCBI GI g2244747 BLAST score 54 E value 2.0e-21 Match length 414

% identity 67

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 136662

Contig ID 151860 1.R1010

5'-most EST g2749543 Method BLASTN NCBI GI q3128166 BLAST score 415 E value 0.0e+00Match length 459 97 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136663

Contig ID 151866 1.R1010

5'-most EST g2413154

Seq. No. 136664

Contig ID 151952 1.R1010

68

5'-most EST g2580778 Method BLASTX NCBI GI g2245014 BLAST score 280 9.0e-25 E value Match length 82 % identity

Contig ID

5'-most EST



```
NCBI Description (Z97341) glucosyltransferase homolog [Arabidopsis thaliana]
  Seq. No.
                    136665
 Contig ID
                    151964 1.R1010
  5'-most EST
                    g3449732
 Method
                    BLASTN
 NCBI GI
                    g2924733
 BLAST score
                    107
 E value
                    4.0e-53
 Match length
                    287
 % identity
                    98
 NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MUF9, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    136666
 Contig ID
                    151980 1.R1010
 5'-most EST
                    g2580711
 Method
                    BLASTN
 NCBI GI
                    g4757403
 BLAST score
                    283
 E value
                    1.0e-158
 Match length
                    291
 % identity
                    99
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
 NCBI Description
                    MJL12, complete sequence
 Seq. No.
                    136667
 Contig ID
                    152004 1.R1010
 5'-most EST
                    g2580734
 Method
                    BLASTX
 NCBI GI
                    g2497753
 BLAST score
                    238
 E value
                    7.0e-20
Match length
                    85
 % identity
                    51
 NCBI Description
                    NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
                    >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein
                    [Prunus dulcis]
 Seq. No.
                    136668
 Contig ID
                    152077 1.R1010
 5'-most EST
                    g2722217
 Seq. No.
                    136669
 Contig ID
                    152119_1.R1010
 5'-most EST
                   g2580655
 Method
                   BLASTN
 NCBI GI
                   g16472
 BLAST score
                   178
 E value
                   2.0e-95
 Match length
                   355
 % identity
                   98
 NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type
 Seq. No.
                   136670
```

152119 2.R1010

g2756756



```
Method
                    BLASTN
 NCBI GI
                    q3402671
 BLAST score
                    269
 E value
                    1.0e-149
 Match length
                    288
                    98
 % identity
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC T16B24 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    136671
 Contig ID
                    152232 1.R1010
 5'-most EST
                    g3450076
 Method
                    BLASTX
 NCBI GI
                    g2129755
 BLAST score
                    184
 E value
                    1.0e-13
Match length
                    103
 % identity
                    39
 NCBI Description
                   tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis
                   thaliana >gi_619753 (U18993) tryptophan synthase alpha
                   chain [Arabidopsis thaliana] >gi_1585768_prf__2201482A Trp
                   synthase: SUBUNIT=alpha [Arabidopsis thaliana]
Seq. No.
                   136672
Contig ID
                   152400 1.R1010
5'-most EST
                   q2413832
Method
                   BLASTX
NCBI GI
                   g4127458
BLAST score
                   492
E value
                   9.0e-52
Match length
                   160
% identity
                   71
NCBI Description
                   (AJ011669) myb cov1 protein [Arabidopsis thaliana]
Seq. No.
                   136673
Contig ID
                   152647 1.R1010
5'-most EST
                   g2748592
Method
                   BLASTN
NCBI GI
                   q3510345
BLAST score
                   108
E value
                   2.0e-53
Match length
                   435
% identity
                   48
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MNJ8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136674
                   152931 1.R1010
                   g27494\overline{2}0
                   BLASTN
                   g2760170
                   174
                   7.0e-93
```

Contig ID 5'-most EST Method NCBI GI BLAST score E value Match length 484 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIO24, complete sequence [Arabidopsis thaliana]

Method

NCBI GI

E value

BLAST score

BLASTX

232

g4007792

4.0e-19



Seq. No. 136675 Contig ID 153137 1.R1010 5'-most EST g2722350 Seq. No. 136676 Contig ID 153146 1.R1010 5'-most EST g2733960 Method BLASTX NCBI GI g2239089 BLAST score 156 E value 3.0e-16 Match length 132 % identity 45 NCBI Description (Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_3288180 emb CAB11466 (Z98758) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] Seq. No. 136677 Contig ID 153248 1.R1010 5'-most EST g2576745 Seq. No. 136678 Contig ID 153317 1.R1010 5'-most EST g2757289Method BLASTX NCBI GI g1809259 BLAST score 229 E value 8.0e-19 Match length 96 % identity 48 NCBI Description (U59318) serine/threonine protein kinase Fen [Lycopersicon esculentum] Seq. No. 136679 Contig ID 153419 1.R1010 5'-most EST g2580751 Method BLASTX NCBI GI g488573 BLAST score 500 E value 1.0e-50 Match length 103 % identity 97 NCBI Description (U09463) histone H3.2 [Medicago sativa] Seq. No. 136680 Contig ID 153480 1.R1010 5'-most EST g2722207 Seq. No. 136681 153613 1.R1010 Contig ID 5'-most EST g2580960



Match length 93 % identity 55

NCBI Description (AL034463) Xenopus 14s cohesin smc1 subunit homolog

[Schizosaccharomyces pombe]

Seq. No. 136682

Contig ID 153842 1.R1010

5'-most EST g2749495
Method BLASTN
NCBI GI g3510340
BLAST score 271

E value 1.0e-151
Match length 332
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDN11, complete sequence [Arabidopsis thaliana]

Seq. No. 136683

Contig ID 153885 1.R1010

5'-most EST g2763414
Method BLASTN
NCBI GI g4079614
BLAST score 337
E value 0.0e+00
Match length 399
% identity 97

NCBI Description Arabidopsis thaliana chromosome I BAC F21M11 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136684

Contig ID 153924_1.R1010

5'-most EST $g34495\overline{3}6$

Seq. No. 136685

Contig ID 154192_1.R1010

5'-most EST $g27572\overline{6}9$

Seq. No. 136686

Contig ID 154410_1.R1010

5'-most EST g2763029
Method BLASTN
NCBI GI g4056429
BLAST score 68
E value 5.0e-30
Match length 240

NCBI Description Arabidopsis thaliana chromosome 1 BAC F508 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 136687

% identity

Contig ID 154481_1.R1010

5'-most EST g2597256
Method BLASTX
NCBI GI g3193287
BLAST score 368
E value 2.0e-44
Match length 136



% identity

NCBI Description (AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No. 136688

Contig ID 154513 1.R1010

5'-most EST q2596786 Method BLASTN NCBI GI q2088638 BLAST score 360 E value 0.0e + 00Match length 461 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC T28M21 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136689

Contig ID 154646 1.R1010

5'-most EST g2757411 Method BLASTX NCBI GI g115783 BLAST score 274 E value 4.0e-26 Match length 65 % identity 97

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543_ (X03909)

chlorophyll a/b bind $\overline{\text{ing}}$ protein (LHCP $\overline{\text{AB}}$ 140) [Arabidopsis

thaliana]

Seq. No. 136690

Contig ID 154648 1.R1010

5'-most EST g2762897 Method BLASTX NCBI GI g2760839 BLAST score 475 9.0e-48 E value Match length 97

% identity 95

NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 136691

Contig ID 154940 1.R1010

5'-most EST $g27642\overline{2}3$ Method BLASTX NCBI GI g4467142 BLAST score 191 E value 8.0e-30 Match length 89 % identity 84

NCBI Description (AL035540) Phospholipase like protein [Arabidopsis

thaliana]

Seq. No. 136692

Contig ID 154959 1.R1010

5'-most EST g2597234



```
Seq. No.
                   136693
Contig ID
                   155142 1.R1010
5'-most EST
                   q2597417
Method
                   BLASTN
NCBI GI
                   g2191126
BLAST score
                   339
E value
                   0.0e + 00
Match length
                   422
% identity
                   96
NCBI Description
                  Arabidopsis thaliana BAC IG002N01
Seq. No.
                   136694
Contig ID
                   155259 1.R1010
5'-most EST
                   g2597534
Seq. No.
                   136695
Contig ID
                   155446 1.R1010
5'-most EST
                   g2733822
Method
                   BLASTX
NCBI GI
                   q2979551
BLAST score
                   298
E value
                   3.0e-27
Match length
                   75
% identity
                   81
                   (AC003680) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   136696
Contig ID
                   155547 1.R1010
5'-most EST
                   g2619116
Method
                  BLASTN
NCBI GI
                   g3650026
BLAST score
                   182
E value
                   5.0e-98
Match length
                   281
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T26I20 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  136697
Contig ID
                  155756 1.R1010
5'-most EST
                  g2763201
Method
                  BLASTX
NCBI GI
                  g3548801
BLAST score
                  316
E value
                  5.0e-29
Match length
                  79
% identity
                  76
                  (AC005313) putative transmembrane protein [Arabidopsis
```

NCBI Description

thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative

integral membrane protein [Arabidopsis thaliana]

Seq. No. Contig ID 136698

155836 1.R1010

5'-most EST g2763181 Method BLASTX NCBI GI g4206122



BLAST score 453 E value 4.0e-45 Match length 106 % identity 79

NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum

crystallinum]

Seq. No. 136699

Contig ID 155927 1.R1010

5'-most EST g2722281

Method BLASTX

NCBI GI g3021266

BLAST score 556

E value 4.0e-57

Match length 105

% identity 100

NCBI Description (AL022347) serine/threonine kinase - like protein

[Arabidopsis thaliana] >gi_3292840_emb_CAA19830_ (AL031018)

serine/threonine kinase - like protein [Arabidopsis

thaliana]

Seq. No. 136700

Contig ID 156076 1.R1010

5'-most EST g2722689
Method BLASTX
NCBI GI g4490336
BLAST score 445
E value 4.0e-44
Match length 99
% identity 88

NCBI Description (AL035656) auxin-induced protein-like [Arabidopsis

thaliana]

Seq. No. 136701

Contig ID 156128 1.R1010

5'-most EST g2722938
Method BLASTN
NCBI GI g2645198
BLAST score 271
E value 1.0e-151
Match length 319
% identity 98

NCBI Description Arabidopsis thaliana chromosome I BAC T26J12 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136702

Contig ID 156576 1.R1010

5'-most EST g2722992
Method BLASTN
NCBI GI g3242700
BLAST score 249
E value 1.0e-138
Match length 303
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]



Seq. No. 136703 Contig ID 156646 1.R1010 5'-most EST $q27230\overline{1}4$ Method BLASTN NCBI GI g3449314 BLAST score 243 E value 1.0e-134 Match length 321 % identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K22F20, complete sequence [Arabidopsis thaliana]

Seq. No. 136704

Contig ID 156705_1.R1010

5'-most EST g2723073
Method BLASTN
NCBI GI g3241917
BLAST score 232
E value 1.0e-127
Match length 443
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19B1, complete sequence [Arabidopsis thaliana]

Seq. No. 136705

Contig ID . 156930_1.R1010

5'-most EST g2757807
Method BLASTN
NCBI GI g4490324
BLAST score 323
E value 0.0e+00
Match length 394
% identity 61

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14

(ESSA project)

Seq. No. 136706

Contig ID 156959_1.R1010

5'-most EST g3719094
Method BLASTN
NCBI GI g2351064
BLAST score 384
E value 0.0e+00
Match length 442
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No. 136707

Contig ID 157055_1.R1010

5'-most EST $g27332\overline{3}7$

Seq. No. 136708

Contig ID 157153 1.R1010

 5'-most EST
 g2733336

 Method
 BLASTX

 NCBI GI
 g2827549



```
BLAST score
E value
                   4.0e-62
Match length
                   139
% identity
                   87
NCBI Description
                   (AL021635) glycoprotein endopeptidase - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   136709
Contia ID
                   157252 1.R1010
5'-most EST
                   g27494\overline{2}3
Seq. No.
                   136710
Contig ID
                   157333 1.R1010
5'-most EST
                   g2733518
Method
                   BLASTX
NCBI GI
                   g4263795
BLAST score
                   313
E value
                   4.0e-48
Match length
                   100
% identity
                   95
NCBI Description
                   (AC006068) putative glucosyltransferase [Arabidopsis
                   thaliana]
Seq. No.
                   136711
Contig ID
                   157478 1.R1010
5'-most EST
                   g2733662
Method
                   BLASTN
NCBI GI
                   g4432829
BLAST score
                   252
E value
                   1.0e-139
Match length
                   256
% identity
                   100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T1B3 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136712
Contig ID
                   157665 1.R1010
5'-most EST
                   g2747888
Method
                   BLASTN
NCBI GI
                   g2564050
BLAST score
                   207
E value
                   1.0e-113
Match length
                   321
% identity
                   95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUA22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  136713
Contig ID
                  157724 1.R1010
```

5'-most EST g2733913 Method BLASTX NCBI GI g2924785 BLAST score 231 E value 4.0e-19 Match length 118 % identity 47

NCBI Description (AC002334) similar to disease resistance protein

Contig ID 5'-most EST



[Arabidopsis thaliana]

```
Seq. No.
                   136714
Contig ID
                   157758 1.R1010
5'-most EST
                   g2747822
Method
                   BLASTN
NCBI GI
                   g3449327
BLAST score
                   303
E value
                   1.0e-170
Match length
                   402
% identity
                   96
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCA23, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136715
Contig ID
                   157847 1.R1010
5'-most EST
                   g2739561
Method
                   BLASTX
NCBI GI
                   g3184292
BLAST score
                   292
E value
                   3.0e-26
Match length
                   52
% identity
                   90
                   (AC004136) putative nucleic acid binding protein, 5'
NCBI Description
                   partial [Arabidopsis thaliana]
Seq. No.
                   136716
Contig ID
                   157935 1.R1010
5'-most EST
                   g2748061
Method
                   BLASTN
NCBI GI
                   g3128166
BLAST score
                   277
E value
                   1.0e-154
Match length
                   339
% identity
                   98
                  Arabidopsis thaliana chromosome II BAC F4I1 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136717
Contig ID
                   158087 1.R1010
5'-most EST
                   g3450414
Method
                   BLASTX
NCBI GI
                   g3043426
BLAST score
                   83
E value
                   1.6e-01
Match length
                   83
% identity
                   62
NCBI Description
                  (AJ005345) hypothetical protein [Cicer arietinum]
Seq. No.
                   136718
Contig ID
                   158102 1.R1010
5'-most EST
                  g27475\overline{1}6
Seq. No.
                  136719
```

158219 1.R1010

g2747633

5'-most EST

BLAST score

Method

NCBI GI

g2749505

g3406034

BLASTN

78



```
Seq. No.
                   136720
Contig ID
                   158286 1.R1010
5'-most EST
                   g27590\overline{1}8
Method
                   BLASTN
NCBI GI
                   g2351068
BLAST score
                   273
E value
                   1.0e-152
Match length
                   319
% identity
                   97
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MRH10, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136721
Contig ID
                   158439 1.R1010
5'-most EST
                   g2747855
Method
                   BLASTN
NCBI GI
                   g2656026
BLAST score
                   74
                   2.0e-33
E value
Match length
                   195
% identity
                   99
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MDF20
Seq. No.
                   136722
Contig ID
                   158493 1.R1010
5'-most EST
                   g2749539
Method
                   BLASTX
NCBI GI
                   g3395440
BLAST score
                   233
E value
                   3.0e-19
Match length
                   78
% identity
                   56
NCBI Description
                  (AC004683) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   136723
Contig ID
                   159057 1.R1010
5'-most EST
                   g3228580
Method
                   BLASTX
NCBI GI
                   q3033400
BLAST score
                   195
E value
                   2.0e-14
Match length
                   141
% identity
                   68
NCBI Description
                   (AC004238) putative Ser/Thr protein kinase [Arabidopsis
                   thalianal
Seq. No.
                   136724
Contig ID
                   159570 1.R1010
5'-most EST
                   g2748992
Seq. No.
                   136725
Contig ID
                   159862 1.R1010
```



E value 1.0e-35 Match length 125 % identity 92

NCBI Description BAC F18A17 from chromosome V containing TINY at 60.5 cM,

complete sequence [Arabidopsis thaliana]

Seq. No. 136726

Contig ID 159870_1.R1010

5'-most EST $g27492\overline{9}3$

Seq. No. 136727

Contig ID 160574_1.R1010

5'-most EST g2756835

Method BLASTX

NCBI GI g2335099

BLAST score 355

E value 3.0e-35

Match length 75% identity 91

NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

Seq. No. 136728

Contig ID 160711_1.R1010

5'-most EST g2756973
Method BLASTX
NCBI GI g3860250
BLAST score 301
E value 3.0e-27
Match length 104
% identity 58

NCBI Description (AC005824) putative chloroplast prephenate dehydratase

[Arabidopsis thaliana]

Seq. No. 136729

Contig ID 160869 1.R1010

5'-most EST g2757133
Method BLASTN
NCBI GI g2815519
BLAST score 153
E value 2.0e-80
Match length 328
% identity 98

NCBI Description Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm,

complete sequence [Arabidopsis thaliana]

Seq. No. 136730

Contig ID 161344 1.R1010

5'-most EST g2759232
Method BLASTX
NCBI GI g2342686
BLAST score 397
E value 6.0e-43
Match length 96
% identity 96

NCBI Description (AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb_Z49209). ESTs gb_T44436,gb_42252 come from this

gene. [Arabidopsis thaliana]



```
Seq. No.
                    136731
Contig ID
                    161391 1.R1010
5'-most EST
                   g27643\overline{4}7
Method
                   BLASTX
NCBI GI
                   g3850585
BLAST score
                    445
E value
                   3.0e-44
Match length
                   109
% identity
                   81
NCBI Description
                   (AC005278) ESTs gb H36966, gb R65511, gb T42324 and
                   gb_T20569 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   136732
Contig ID
                   161493 1.R1010
5'-most EST
                   g27590\overline{9}3
Method
                   BLASTX
NCBI GI
                   g4220452
BLAST score
                   524
E value
                   2.0e-53
Match length
                   117
% identity
                   44
                   (AC006216) Similar to gi 3413714 T19L18.21 putative
NCBI Description
                   myrosinase-binding protein from Arabidopsis thaliana BAC
                   gb_AC004747. ESTs gb_T44298, gb_T42447, gb_R64761 and
                   gb_I100206 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   136733
Contig ID
                   161946 1.R1010
5'-most EST
                   g27634<del>7</del>7
Method
                   BLASTX
NCBI GI
                   g2062159
BLAST score
                   512
E value
                   4.0e-52
Match length
                   126
% identity
                   47
NCBI Description
                   (AC001645) jasmonate inducible protein isolog [Arabidopsis
                   thaliana]
Seq. No.
                   136734
Contig ID
                   163021 1.R1010
5'-most EST
                   g34495<del>6</del>1
Method
                   BLASTX
NCBI GI
                   g3928543
BLAST score
                   48
E value
                   3.0e-09
Match length
                   52
% identity
                   67
NCBI Description
                   (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
                   thaliana]
```

Seq. No. 136735

Contig ID 163311_1.R1010 5'-most EST g2759588

7 MOSC EST 92739366

Seq. No. 136736

Contig ID 163603_1.R1010

Match length

NCBI Description

% identity

66

55



```
5'-most EST
                   g2762416
Method
                   BLASTN
NCBI GI
                   q4335744
BLAST score
                   263
E value
                   1.0e-146
Match length
                   354
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T4M8 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136737
Contig ID
                   164898 1.R1010
5'-most EST
                   g2763371
Method
                   BLASTN
NCBI GI
                   q3449329
BLAST score
                   352
E value
                   0.0e + 00
Match length
                   452
% identity
                   96
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDH9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136738
Contig ID
                   164933 1.R1010
5'-most EST
                   g2763405
Method
                   BLASTX
NCBI GI
                  g3445210
BLAST score
                   549
E value
                   3.0e-56
Match length
                   119
% identity
                   87
NCBI Description
                  (AC004786) putative flavonol 3-o-glucosyltransferase
                   [Arabidopsis thaliana]
Seq. No.
                  136739
Contig ID
                  165000 1.R1010
5'-most EST
                   q2763473
Method
                  BLASTN
NCBI GI
                  q4263774
BLAST score
                  362
E value
                  0.0e + 00
Match length
                  438
% identity
                  59
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20F21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  136740
Contig ID
                  165223 1.R1010
5'-most EST
                  g2763770
Method
                  BLASTX
NCBI GI
                  q3297820
BLAST score
                  149
E value
                  2.0e-09
```

16327

(AL031032) putative protein [Arabidopsis thaliana]

```
Seq. No.
                   136741
Contig ID
                  167194 1.R1010
5'-most EST
                  g3719179
Method
                  BLASTN
NCBI GI
                  g2351064
BLAST score
                  393
E value
                  0.0e + 00
Match length
                  440
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDJ22, complete sequence [Arabidopsis thaliana]
                  136742
Seq. No.
                  167214 1.R1010
Contig ID
5'-most EST
                  g3719121
Method
                  BLASTN
NCBI GI
                  g2351064
BLAST score
                  260
                 ~1.0e-144
E value
Match length
                  310
% identity
                  96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDJ22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  136743
Contig ID
```

167372 1.R1010 5'-most EST q3868952 Method BLASTX NCBI GI g4262237 BLAST score 351 E value 3.0e-33 Match length 109 % identity 67 NCBI Description (AC006200) hypothetical protein [Arabidopsis thaliana]

 Seq. No.
 136744

 Seq. ID
 ARABL1-01-Q1-B1-F4

 Method
 BLASTX

 NCBI GI
 g549063

 BLAST score
 225

NCBI GI g549063
BLAST score 225
E value 4.0e-19
Match length 53
% identity 81

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 136745

Seq. ID ARABL1-01-Q1-B2-B2

Method BLASTX
NCBI GI g1172872
BLAST score 290
E value 2.0e-26
Match length 89
% identity 69

NCBI Description CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718



drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible

cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No. 136746

Seq. ID ARABL1-01-Q1-B2-D2

Method BLASTX NCBI GI q3688799 BLAST score 670 E value 1.0e-70 Match length 134 % identity 99

NCBI Description (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis

thalianal

Seq. No. 136747

Seq. ID ARABL1-01-Q1-B2-E6

Method BLASTX NCBI GI q4056456 BLAST score 276 E value 2.0e-24 Match length 57 % identity 98

NCBI Description (AC005990) Strong similarity to gb U20808 auxin-induced

> protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb AA395179 come from this gene. [Arabidopsis thaliana]

Seq. No. 136748

Seq. ID ARABL1-01-Q1-B2-E8

Method BLASTN NCBI GI g4512656 BLAST score 353 E value 0.0e+00Match length 407 100 % identity

Arabidopsis thaliana chromosome II BAC F7D19 genomic NCBI Description

sequence, complete sequence

Seq. No. 136749

Seq. ID ARABL1-01-Q1-B2-F5

Method BLASTN NCBI GI g2351065 BLAST score 78 E value 1.0e-36 Match length 78 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MHF15, complete sequence [Arabidopsis thaliana]

Seq. No. 136750

Seq. ID ARABL1-01-Q1-B2-F6

Method BLASTX NCBI GI g131398 BLAST score 533



E value Match length 123 % identity

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714 pir F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 136751

Seq. ID ARABL1-01-Q1-B2-G2

Method BLASTN NCBI GI g3868723 BLAST score 208 E value 1.0e-113 Match length 394 % identity 98

NCBI Description Arabidopsis thaliana chromosome V map 60.5 cM, complete

sequence [Arabidopsis thaliana]

Seq. No. 136752

Seq. ID ARABL1-01-Q1-E1-B6

Method BLASTN NCBI GI g3449331 BLAST score 133 E value 5.0e-69 Match length 173 % identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNC17, complete sequence [Arabidopsis thaliana]

Seq. No. 136753

Seq. ID ARABL1-01-Q1-E1-B9

Method BLASTX NCBI GI g3123296 BLAST score 244 E value 9.0e-21 Match length 59 % identity 85

NCBI Description CALMODULIN-RELATED PROTEIN 3, TOUCH-INDUCED >qi 598067

(L34546) calmodulin-related protein [Arabidopsis thaliana]

Seq. No. 136754

ARABL1-01-Q1-E1-E12 Seq. ID

Method BLASTN NCBI GI g2564045 BLAST score 364 E value 0.0e+00Match length 393 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K8K14, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                   136755
Seq. ID
                   ARABL1-01-Q1-E1-E8
Method
                   BLASTN
NCBI GI
                   g4512656
BLAST score
                   163
E value
                   7.0e-87
Match length
                   179
% identity
                   98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
                   sequence, complete sequence
Seq. No.
                   136756
Seq. ID
                   ARABL1-01-Q1-E1-F1
Method
                  BLASTN
NCBI GI
                   g2564051
BLAST score
                   187
E value
                   1.0e-101
Match length
                   203
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MWD9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  136757
Seq. ID
                  ARABL1-01-Q1-E1-F5
Method
                  BLASTN
NCBI GI
                  g2351065
BLAST score
                  62
E value
                  5.0e-27
Match length
                  78
% identity
                  95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MHF15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  136758
                  ARABL1-019-Q1-B1-B10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2262097
BLAST score
                  339
E value
                  0.0e+00
Match length
                  339
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome IV BAC T19F6 genomic
                  sequence, complete sequence
Seq. No.
                  136759
Seq. ID
                  ARABL1-019-Q1-B1-C3
Method
                  BLASTN
                  g4325340
                  299
                  1.0e-167
                  299
```

NCBI GI BLAST score E value Match length % identity 100

NCBI Description Arabidopsis thaliana BAC T1J1

Seq. No. 136760

Seq. ID ARABL1-019-Q1-B1-C5

Method BLASTX

NCBI GI g2388577 BLAST score 609 E value 1.0e-63 Match length 120 % identity 98 NCBI Description (AC000098) Similar to Arabidopsis putative ion-channel PID:g2262157 (gb_AC002329). [Arabidopsis thaliana] Seq. No. 136761 Seq. ID ARABL1-019-Q1-B1-E12 Method BLASTN NCBI GI q3492855 BLAST score 320 E value 1.0e-180 Match length 320 % identity 100 Genomic sequence for Arabidopsis thaliana BAC F20N2, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 136762 Seq. ID ARABL1-019-Q1-B1-E7 Method BLASTN NCBI GI q3869070 BLAST score 216 E value 1.0e-118 Match length 251 % identity 96 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGO3, complete sequence [Arabidopsis thaliana] Seq. No. 136763

Seq. ID ARABL1-019-Q1-B1-F3

Method BLASTX NCBI GI g2832717 BLAST score 445 E value 3.0e-44Match length 104 % identity 77

NCBI Description (AJ003114) alkaline/neutral invertase [Lolium temulentum]

Seq. No. 136764

Seq. ID ARABL1-019-Q1-B1-F6

Method BLASTX NCBI GI g2924509 BLAST score 251 E value 2.0e-21 Match length 105 % identity 48

NCBI Description (AL022023) subtilisin proteinase-like [Arabidopsis

thaliana]

Seq. No. 136765

Seq. ID ARABL1-019-Q1-B1-F8

Method BLASTX NCBI GI g2119846 BLAST score 723 E value 7.0e-77



Match length 139 % identity 100

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 136766

Seq. ID ARABL1-019-Q1-B1-F9

Method BLASTX
NCBI GI g3236237
BLAST score 335
E value 1.0e-31
Match length 61
% identity 100

NCBI Description (AC004684) putative ribotol dehydrogenase [Arabidopsis

thaliana]

Seq. No. 136767

Seq. ID ARABL1-019-Q1-B1-H8

Method BLASTN
NCBI GI g4193383
BLAST score 81
E value 4.0e-38
Match length 140
% identity 93

NCBI Description Arabidopsis thaliana ribosomal protein S27 (ARS27A) gene,

complete cds

Seq. No. 136768

Seq. ID ARABL1-02-Q1-B1-E7

Method BLASTN
NCBI GI 94757392
BLAST score 136
E value 6.0e-71
Match length 136
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K14A17, complete sequence

Seq. No. 136769

Seq. ID ARABL1-02-Q1-B1-E9

Method BLASTN
NCBI GI 94263753
BLAST score 237
E value 1.0e-131
Match length 237
% identity 100

NCBI Description Arabidopsis thaliana chromosome V map near 60.5 cM,

complete sequence [Arabidopsis thaliana]

Seq. No. 136770

Seq. ID ARABL1-02-Q1-B1-G5

Method BLASTN



```
NCBI GI
                   q3869066
BLAST score
                   127
E value
                   2.0e-65
Match length
                   148
% identity
                   95
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MBM17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136771
Seq. ID
                   ARABL1-02-Q1-B1-H5
Method
                   BLASTN
NCBI GI
                   q887938
BLAST score
                   30
E value
                   2.0e-07
Match length
                   169
% identity
                   95
NCBI Description
                  Arabidopsis thaliana clone YAP317 GAST1 protein homolog
                   mRNA, complete cds
Seq. No.
                   136772
Seq. ID
                   ARABL1-02-Q1-E1-B10
Method
                   BLASTN
NCBI GI
                   q4314374
BLAST score
                   235
E value
                   1.0e-129
Match length
                   247
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F10A12 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136773
Seq. ID
                  ARABL1-02-Q1-E1-B3
                  BLASTX
                   g2507587
                  235
                  1.0e-19
                   41
% identity
                  100
NCBI Description
```

Method NCBI GI BLAST score E value Match length

METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G) >gi_1361998_pir S57861 metallothionein 2a - Arabidopsis thaliana >gi_555976 (U15108) metallothionein-like protein

[Arabidopsis thaliana] >gi_1580892_prf__2116236A

metallothionein 1 [Arabidopsis thaliana]

Seq. No. 136774

Seq. ID ARABL1-02-Q1-E1-D11

Method BLASTN NCBI GI g2262155 BLAST score 212 E value 1.0e-116 Match length 256 % identity 95

NCBI Description DNA sequence of Arabidopsis thaliana BAC F5J6 from

chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No. 136775

Seq. ID ARABL1-02-Q1-E1-D5



```
Method
                   BLASTN
NCBI GI
                   g3402745
BLAST score
                   160
E value
                   4.0e-85
Match length
                   180
% identity
                   67
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5
                   (ESSAII project)
Seq. No.
                   136776
Seq. ID
                  ARABL1-02-Q1-E1-D8
Method
                  BLASTN
NCBI GI
                  q4757392
BLAST score
                  124
E value
                  9.0e-64
Match length
                  136
% identity
                   98
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                  K14A17, complete sequence
Seq. No.
                  136777
Seq. ID
                  ARABL1-02-Q1-E1-F5
Method
                  BLASTX
NCBI GI
                  g1174850
BLAST score
                  203
E value
                  5.0e-16
Match length
                  69
% identity
                  64
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN
                  LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)
Seq. No.
                  136778
Seq. ID
                  ARABL1-02-Q1-E1-G11
Method
                  BLASTN
NCBI GI
                  g4512690
BLAST score
                  102
E value
                  1.0e-50
Match length
                  126
```

% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No. 136779

Seq. ID ARABL1-02-Q1-E1-G5

Method BLASTN NCBI GI q3869066 BLAST score 119 E value 1.0e-60 Match length 148 % identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBM17, complete sequence [Arabidopsis thaliana]

Seq. No. 136780

ARABL1-020-Q1-B1-A4 Seq. ID

Method BLASTX NCBI GI g4490330



```
BLAST score
E value
                   4.0e-47
Match length
                   90
                   93
% identity
NCBI Description
                   (AL035656) splicing factor-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   136781
Seq. ID
                   ARABL1-020-Q1-B1-B5
Method
                   BLASTN
NCBI GI
                   q4539448
BLAST score
                   110
E value
                   3.0e-55
Match length
                   175
% identity
                   90
                  Arabidopsis thaliana DNA chromosome 4, BAC clone
NCBI Description
                   (ESSA project)
Seq. No.
                   136782
Seq. ID
                   ARABL1-020-Q1-B1-E12
Method
                  BLASTX
NCBI GI
                   q2914700
BLAST score
                   500
E value
                   8.0e-51
Match length
                   117
% identity
                   85
NCBI Description
                   (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
                   thaliana]
Seq. No.
                  136783
Seq. ID
                  ARABL1-020-Q1-B1-G8
Method
                  BLASTX
NCBI GI
                  g2911060
BLAST score
                  312
E value
                  7.0e-29
Match length
                  75
                  57
% identity
NCBI Description
                   (AL021961) putative protein [Arabidopsis thaliana]
                  >gi_3297826_emb_CAA19884.1_ (AL031032) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                  136784
Seq. ID
                  ARABL1-020-Q1-B1-H4
Method
                  BLASTN
NCBI GI
                  g4589427
```

BLAST score 129 E value 3.0e-66 Match length 337 % identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MFG13, complete sequence

Seq. No. 136785

Seq. ID ARABL1-020-Q1-B1-H8

Method BLASTX NCBI GI g2879811 BLAST score 204



```
E value
                   2.0e-16
Match length
                   39
% identity
                   95
NCBI Description
                  (AJ223316) ribosomal protein L30 [Lupinus luteus]
Seq. No.
                   136786
Seq. ID
                  ARABL1-021-Q1-B1-B4
Method
                  BLASTX
NCBI GI
                  g2829910
BLAST score
                  242
E value
                  1.0e-20
Match length
                  115
% identity
                  14
NCBI Description
                  (AC002291) Unknown protein, contains regulator of
                  chromosome condensation motifs [Arabidopsis thaliana]
Seq. No.
                  136787
Seq. ID
                  ARABL1-021-Q1-B1-D10
Method
                  BLASTX
NCBI GI
                  g445612
BLAST score
                  199
E value
                  1.0e-15
Match length
                  86
% identity
                  74
NCBI Description ribosomal protein S19 [Solanum tuberosum]
Seq. No.
                  136788
Seq. ID
                  ARABL1-021-Q1-B1-D8
Method
                  BLASTN
NCBI GI
                  g4544405
BLAST score
                  155
E value
                  8.0e-82
Match length
                  327
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F28I8 genomic
                  sequence, complete sequence
Seq. No.
                  136789
Seq. ID
                  ARABL1-021-Q1-B1-D9
Method
                  BLASTN
NCBI GI
                  g3738313
BLAST score
                  308
E value
                  1.0e-173
Match length
                  312
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T29E15 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```

Seq. No. 136790

Seq. ID ARABL1-021-Q1-B1-E1 Method

BLASTX NCBI GI g1773014 BLAST score 233 E value 8.0e-20 Match length 82 % identity 59

NCBI Description (Y10338) chloride channel Stclc1 [Solanum tuberosum]



Seq. No. 136791

Seq. ID ARABL1-021-Q1-B1-E2

Method BLASTX NCBI GI g131398 BLAST score 288 E value 7.0e-26 Match length 85 % identity 69

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 136792

Seq. ID ARABL1-021-Q1-B1-E7

Method BLASTX NCBI GI q464987 BLAST score 199 E value 2.0e-15 Match length 125 % identity 100

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN

LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)

>gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana

>gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin

conjugating enzyme [Arabidopsis thaliana]

Seq. No. 136793

Seq. ID ARABL1-021-Q1-B1-F2

Method BLASTX NCBI GI g3080389 BLAST score 542 E value 1.0e-55 Match length 107 % identity 100

NCBI Description (AL022603) putative membrane associated protein

[Arabidopsis thaliana]

Seq. No. 136794

Seq. ID ARABL1-021-Q1-B1-F4

Method BLASTN NCBI GI g3327922 BLAST score 49 E value 7.0e-19 Match length 137 % identity

Arabidopsis thaliana chromosome II BAC T31E10 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                   136795
Seq. ID
                   ARABL1-021-Q1-B1-G2
Method
                   BLASTX
NCBI GI
                   g3142294
BLAST score
                   281
E value
                   5.0e-25
Match length
                   68
                   97
% identity
NCBI Description
                   (AC002411) Strong similarity to initiation factor eIF-2,
                   gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and
                   gb_N37529 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   136796
Seq. ID
                  ARABL1-021-Q1-B1-G5
Method
                   BLASTX
NCBI GI
                   g2392895
BLAST score
                   703
E value
                   2.0e-74
Match length
                   134
                   100
% identity
NCBI Description
                   (AF017056) brassinosteroid insensitive 1 [Arabidopsis
                   thaliana]
Seq. No.
                  136797
Seq. ID
                  ARABL1-021-Q1-B1-H12
Method
                  BLASTX
NCBI GI
                  q733554
BLAST score
                  114
E value
                  8.0e-22
Match length
                  87
% identity
                  55
NCBI Description
                  (U23450) similar to RNA-binding protein [Caenorhabditis
                  elegans]
Seq. No.
                  136798
Seq. ID
                  ARABL1-021-Q1-B1-H4
Method
                  BLASTX
NCBI GI
                  g166410
BLAST score
                  334
E value
                  3.0e-31
Match length
                  101
% identity
                  64
NCBI Description
                  (L07291) Alfin-1 [Medicago sativa]
Seq. No.
                  136799
Seq. ID
                  ARABL1-021-Q1-B1-H8
Method
                  BLASTX
                  g115767
                  261
```

NCBI GI BLAST score E value 5.0e-23 Match length 49 % identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir_ A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368 emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]





>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 136800

Seq. ID ARABL1-022-Q1-B1-A10

Method BLASTN
NCBI GI g4734011
BLAST score 195

E value 1.0e-105 Match length 403 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F24C20 genomic

sequence, complete sequence

Seq. No. 136801

Seq. ID ARABL1-022-Q1-B1-A7

Method BLASTX
NCBI GI g3212859
BLAST score 394
E value 1.0e-38
Match length 81
% identity 96

NCBI Description (AC004005) hypothetical protein [Arabidopsis thaliana]

Seq. No. 136802

Seq. ID ARABL1-022-Q1-B1-B7

Method BLASTN
NCBI GI g4079614
BLAST score 20
E value 1.4e-01
Match length 168
% identity 99

NCBI Description Arabidopsis thaliana chromosome I BAC F21M11 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136803

Seq. ID ARABL1-022-Q1-B1-C7

Method BLASTN
NCBI GI g2656028
BLAST score 169
E value 3.0e-90
Match length 247
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNF13

Seq. No. 136804

Seq. ID ARABL1-022-Q1-B1-G3

Method BLASTN
NCBI GI g3367500
BLAST score 100
E value 5.0e-49
Match length 289
% identity 100

NCBI Description REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1

TO: 93489, complete sequence [Arabidopsis thaliana]



Seq. No. 136805

Seq. ID ARABL1-022-Q1-B1-H1

Method BLASTX
NCBI GI g2119846
BLAST score 584
E value 9.0e-61
Match length 108
% identity 100

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
photosystem II type I chlorophyll a /b binding protein
[Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
II type I chlorophyll a/b binding protein [Arabidopsis
thaliana] >gi_3327371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis

thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 136806

Seq. ID ARABL1-023-Q1-B1-A11

Method BLASTX
NCBI GI g3924594
BLAST score 535
E value 7.0e-55
Match length 123
% identity 60

NCBI Description (AF069442) putative ribonucleoprotein [Arabidopsis

thaliana] >gi_4262139_gb_AAD14439 (AC005275) putative

ribonucleoprotein [Arabidopsis thaliana]

Seq. No. 136807

Seq. ID ARABL1-023-Q1-B1-A12

Method BLASTX
NCBI GI g1168201
BLAST score 598
E value 3.0e-62
Match length 122
% identity 100

NCBI Description 14-3-3-LIKE PROTEIN RCI2 >gi_1076394_pir__S47970 RCI1B

protein - Arabidopsis thaliana >gi 531379 emb CAA52238

(X74141) RCI1B [Arabidopsis thaliana]

Seq. No. 136808

Seq. ID ARABL1-023-Q1-B1-A4

Method BLASTX
NCBI GI g3046696
BLAST score 400
E value 2.0e-39
Match length 78
% identity 100

NCBI Description (AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No. 136809

Seq. ID ARABL1-023-Q1-B1-A5

Method BLASTX
NCBI GI g2493129
BLAST score 398
E value 3.0e-39
Match length 79



% identity 97

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B SUBUNIT) >gi_459198 (U07052) vacuolar H+-ATPase subunit B

[Gossypium hirsutum]

Seq. No. 136810

Seq. ID ARABL1-023-Q1-B1-C3

Method BLASTX
NCBI GI g3738340
BLAST score 221
E value 2.0e-18
Match length 60
% identity 72

NCBI Description (AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No. 136811

Seq. ID ARABL1-023-Q1-B1-D8

Method BLASTX
NCBI GI g115783
BLAST score 276
E value 7.0e-25
Match length 56
% identity 96

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 136812

Seq. ID ARABL1-023-Q1-B1-H3

Method BLASTN
NCBI GI g2138315
BLAST score 137
E value 3.0e-71
Match length 242
% identity 98

NCBI Description Arabidopsis thaliana root hair defective 3 (RHD3) gene,

complete cds

Seq. No. 136813

Seq. ID ARABL1-023-Q1-B1-H5

Method BLASTX
NCBI GI g131143
BLAST score 454
E value 1.0e-45
Match length 86
% identity 94

NCBI Description PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A1

>gi_72670_pir__AlNTP7 photosystem I P700 apoprotein A1 common tobacco chloroplast >gi_11830_emb_CAA77352_ (Z00044)

PSI P700 apoprotein Al [Nicotiana tabacum]

>gi_225198_prf 1211235AC photosystem I P700 apoprotein A1

[Nicotiana tabacum]

Seq. No. 136814

Seq. ID ARABL1-024-Q1-B1-B5

Method BLASTX

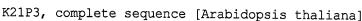


```
NCBI GI
                  q544424
BLAST score
                  215
E value
                  2.0e-17
Match length
                  42
% identity
                  100
                  GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__$30147
NCBI Description
                  glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                  >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
                  [Arabidopsis thaliana] >gi 166837 (L00648) RNA-binding
                  protein [Arabidopsis thaliana]
                  >gi 4567224 gb AAD23639.1 AC007119 5 (AC007119)
                  glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
Seq. No.
                  136815
Seq. ID
                  ARABL1-024-Q1-B1-E3
Method
                  BLASTN
NCBI GI
                  g1532162
BLAST score
                  138
E value
                  1.0e-71
Match length
                  348
% identity
                  97
NCBI Description Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3,
                  AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14
                  genes, partial cds, AT.I.24-7, ascorbate peroxidase
                  (ATHAPX1), EF-lalpha-A1, -A2 and -A3 (EF-lalpha) and AT.I
Seq. No.
                  136816
Seq. ID
                  ARABL1-024-Q1-B1-E7
Method
                  BLASTN
NCBI GI
                  g4589439
BLAST score
                  41
E value
                  3.0e-14
Match length
                  105
                  85
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQM1, complete sequence
Seq. No.
                  136817
Seq. ID
                  ARABL1-024-Q1-B1-E9
Method
                  BLASTN
NCBI GI
                  q3702731
BLAST score
                  103
E value
                  3.0e-51
Match length
                  126
                  95
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFC19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  136818
Seq. ID
                  ARABL1-024-Q1-B1-F8
Method
                  BLASTN
NCBI GI
                  q3449313
BLAST score
                  229
```

E value 1.0e-126 Match length 333 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:





 Seq. No.
 136819

 Seq. ID
 ARABL1-024-Q1-B1-F9

 Method
 BLASTN

 NCBI GI
 g3869068

 BLAST score
 148

E value 1.0e-77 Match length 344 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC16, complete sequence [Arabidopsis thaliana]

Seq. No. 136820

Seq. ID ARABL1-024-Q1-B1-G6

Method BLASTN
NCBI GI g298035
BLAST score 67
E value 7.0e-30
Match length 67
% identity 100

NCBI Description A.thaliana Lhcb4 gene

Seq. No. 136821

Seq. ID ARABL1-024-Q1-B1-H6

Method BLASTX
NCBI GI g2119846
BLAST score 546
E value 2.0e-56
Match length 101
% identity 100

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 136822

Seq. ID ARABL1-025-Q1-B1-A8

Method BLASTX
NCBI GI g115783
BLAST score 557
E value 2.0e-57
Match length 105
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 136823

Seq. ID ARABL1-025-Q1-B1-C12

Method BLASTX NCBI GI g4741954 BLAST score 153



E value 1.0e-10 Match length 28 % identity 100

NCBI Description (AF134127) Lhcb4.2 protein [Arabidopsis thaliana]

Seq. No. 136824

Seq. ID ARABL1-025-Q1-B1-C4

Method BLASTN
NCBI GI 94539331
BLAST score 155
E value 8.0e-82
Match length 331
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13

(ESSA project)

Seq. No. 136825

Seq. ID ARABL1-025-Q1-B1-D1

Method BLASTX
NCBI GI g4415912
BLAST score 369
E value 2.0e-35
Match length 109
% identity 63

NCBI Description (AC006282) putative protease [Arabidopsis thaliana]

Seq. No. 136826

Seq. ID ARABL1-025-Q1-B1-D3

Method BLASTN
NCBI GI 94388816
BLAST score 163
E value 1.0e-86
Match length 288
% identity 99

MCBI Description Arabidopsis thaliana chromosome II BAC F9B22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136827

Seq. ID ARABL1-025-Q1-B1-F9

Method BLASTX
NCBI GI g2118220
BLAST score 388
E value 1.0e-37
Match length 113
% identity 50

NCBI Description H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain

(clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16

kDa proteolipid [Arabidopsis thaliana]

>gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar

H+-transporting ATPase 16K chain [Arabidopsis thaliana]
>gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting
ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]
>gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar
H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. ID Method



```
136828
Seq. No.
Seq. ID
                  ARABL1-025-Q1-B1-G9
Method
                  BLASTN
NCBI GI
                  g790686
                  92
BLAST score
                  1.0e-44
E value
                  100
Match length
% identity
                   98
                  Arabidopsis thaliana zinc finger protein (ZFP8) mRNA,
NCBI Description
                  complete cds
                  136829
Seq. No.
                  ARABL1-026-Q1-B1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3309259
BLAST score
                  162
E value
                   4.0e-86
                   272
Match length
% identity
                   99
                  Arabidopsis thaliana BAC F4H6, chromosome IV, complete
NCBI Description
                   sequence
                   136830
Seq. No.
Seq. ID
                  ARABL1-026-Q1-B1-A12
Method
                  BLASTX
NCBI GI
                   q1651828
                   294
BLAST score
                   1.0e-26
E value
Match length
                   99
% identity
                   60
                  (D90900) dihydrolipoamide dehydrogenase [Synechocystis sp.]
NCBI Description
Seq. No.
                   136831
Seq. ID
                   ARABL1-026-Q1-B1-C6
Method
                   BLASTN
NCBI GI
                   q4220468
BLAST score
                   260
E value
                   1.0e-144
Match length
                   260
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC T8011 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136832
                   ARABL1-026-Q1-B1-D5
Seq. ID
                   BLASTN
Method
                   q16375
NCBI GI
BLAST score
                   99
                   9.0e-49
E value
                   103
Match length
                   99
% identity
                  A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding
NCBI Description
                   protein
Seq. No.
                   136833
```

ARABL1-026-Q1-B1-F4

BLASTN



q4589421 NCBI GI BLAST score 183 E value 2.0e-98 Match length 319 % identity 99 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K5K13, complete sequence Seq. No. 136834 Seq. ID ARABL1-026-Q1-B1-F5 Method BLASTX NCBI GI g3738316 BLAST score 209 E value 9.0e-17 Match length 50 % identity 80 NCBI Description (AC005170) unknown protein [Arabidopsis thaliana] Seq. No. 136835 Seq. ID ARABL1-026-Q1-B1-H9 Method BLASTN NCBI GI g2335089 BLAST score 235 E value 1.0e-129 Match length 357 % identity 97 NCBI Description Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 136836 Seq. ID ARABL1-027-Q1-B1-A1 Method BLASTN NCBI GI q2924734 BLAST score 21 E value 8.2e-02 Match length 377 % identity 89 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana] Seq. No. 136837 Seq. ID ARABL1-027-Q1-B1-B7 Method BLASTN g3402671 209 1.0e-114

NCBI GI BLAST score E value Match length 209 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T16B24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136838

Seq. ID ARABL1-027-Q1-B1-C3

Method BLASTN NCBI GI g4586349 BLAST score 55 E value 4.0e-22



Match length 97
% identity 90
NCBI Description Arabidopsis thaliana DNA for glucose-1-phosphate adenylyltransferase, complete cds

 Seq. No.
 136839

 Seq. ID
 ARABL1-027-Q1-B1-C6

 Method
 BLASTN

 NCBI GI
 g3702737

 BLAST score
 126

 E value
 1.0e-64

E value 1.0e
Match length 210
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSN2, complete sequence [Arabidopsis thaliana]

Seq. No. 136840

Seq. ID ARABL1-027-Q1-B1-E11

Method BLASTX
NCBI GI g4567268
BLAST score 359
E value 2.0e-34
Match length 78
% identity 100

NCBI Description (AC006841) putative fructose biphosphate aldolase

[Arabidopsis thaliana]

Seq. No. 136841

Seq. ID ARABL1-027-Q1-B1-E2

Method BLASTX
NCBI GI g4581201
BLAST score 192
E value 7.0e-15
Match length 55
% identity 71

NCBI Description (Y17911) cyclic nucleotide and calmodulin-regulated ion

channel [Arabidopsis thaliana]

Seq. No. 136842

Seq. ID ARABL1-027-Q1-B1-E5

Method BLASTX
NCBI GI g2618725
BLAST score 244
E value 7.0e-21
Match length 45
% identity 100

NCBI Description (U49074) IAA18 [Arabidopsis thaliana]

Seq. No. 136843

Seq. ID ARABL1-027-Q1-B1-E6

Method BLASTN
NCBI GI g2351069
BLAST score 152
E value 4.0e-80
Match length 285
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

% identity





Seq. No. 136844 Seq. ID ARABL1-027-Q1-B1-E9 Method BLASTN NCBI GI g4220637 BLAST score 283 E value 1.0e-158 Match length 304 % identity 98 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1, complete sequence [Arabidopsis thaliana] Seq. No. 136845 Seq. ID ARABL1-027-Q1-B1-G12 Method BLASTX NCBI GI g3451075 BLAST score 351 E value 2.0e-33 Match length 102 % identity 62 NCBI Description (AL031326) putative protein [Arabidopsis thaliana] Seq. No. 136846 Seq. ID ARABL1-027-Q1-B1-G6 Method BLASTX NCBI GI g4510348 BLAST score 511 E value 2.0e-52 Match length 89 % identity 100 NCBI Description (AC006921) unknown protein [Arabidopsis thaliana] 136847 Seq. No. Seq. ID ARABL1-027-Q1-B1-G7 Method BLASTN NCBI GI g4159706 BLAST score 54 7.0e-22 E value Match length 155 96 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence Seq. No. 136848 Seq. ID ARABL1-027-Q1-B1-G8 Method BLASTX NCBI GI g1086252 BLAST score 337 E value 7.0e-32 Match length 91

NCBI Description sucrose cleavage protein - Potato >gi_707001_bbs_157931 (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]

[Solanum tuberosum]



```
Seq. No.
                   136849
Seq. ID
                   ARABL1-028-Q1-B1-A2
Method
                   BLASTN
NCBI GI
                   g1490552
BLAST score
                   294
E value
                   1.0e-165
                   297
Match length
% identity
                   100
NCBI Description
                  Arabidopsis thaliana S-adenosylmethionine decarboxylase
                   (SAMdc) mRNA, complete cds
Seq. No.
                   136850
Seq. ID
                  ARABL1-028-Q1-B1-B11
Method
                   BLASTX
NCBI GI
                   g4646206
BLAST score
                   411
E value
                   2.0e-40
Match length
                   107
% identity
                   71
NCBI Description
                   (AC007230) Contains similarity to gb_D13630 KIAA0005 gene
                   from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360,
                   gb_T20468, gb_T45191 and gb_AI100459 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  136851
Seq. ID
                  ARABL1-028-Q1-B1-B3
Method
                  BLASTX
NCBI GI
                  g421929
BLAST score
                  365
E value
                  4.0e-35
Match length
                  98
% identity
                  11
NCBI Description
                  ubiquitin - tomato >gi_312160 emb_CAA51679_ (X73156)
                  ubiquitin [Lycopersicon esculentum]
Seq. No.
                  136852
Seq. ID
                  ARABL1-028-Q1-B1-B6
Method
                  BLASTX
NCBI GI
                  g2494041
BLAST score
                  182
E value
                  2.0e-16
Match length
                  77
% identity
                  57
NCBI Description
                  DIAMINOPIMELATE EPIMERASE >gi 1653875 dbj BAA18785
                  (D90917) diaminopimelate epimerase [Synechocystis sp.]
Seq. No.
                  136853
Seq. ID
                  ARABL1-028-Q1-B1-B7
Method
                  BLASTX
                  g2119848
                  450
                  4.0e-45
```

NCBI GI BLAST score E value Match length 91 % identity 92

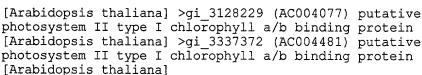
NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 -Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein

Match length

% identity

183





```
Seq. No.
                   136854
Seq. ID
                   ARABL1-028-Q1-B1-C5
Method
                   BLASTX
NCBI GI
                   g166410
BLAST score
                   226
E value
                   9.0e-19
Match length
                   59
% identity
                   71
NCBI Description (L07291) Alfin-1 [Medicago sativa]
Seq. No.
                   136855
Seq. ID
                   ARABL1-028-Q1-B1-D5
Method
                  BLASTX
NCBI GI
                   g4469020
BLAST score
                   322
E value
                   7.0e-30
Match length
                   76
% identity
                   79
                  (AL035602) putative protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   136856
Seq. ID
                  ARABL1-028-Q1-B1-F1
Method
                  BLASTN
NCBI GI
                  g2894591
BLAST score
                  133
E value
                  8.0e-69
Match length
                  247
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21
NCBI Description
                   (ESSAII project)
Seq. No.
                  136857
Seq. ID
                  ARABL1-028-Q1-B1-F7
Method
                  BLASTX
NCBI GI
                  g2160175
BLAST score
                  458
E value
                  4.0e-46
Match length
                  91
                  100
% identity
NCBI Description
                  (AC000132) Strong similarity to Dianthus cysteine
                  proteinase (gb U17135). [Arabidopsis thaliana]
Seq. No.
                  136858
Seq. ID
                  ARABL1-028-Q1-B1-G8
Method
                  BLASTN
NCBI GI
                  g4235150
BLAST score
                  183
E value
                  9.0e-99
```



Arabidopsis thaliana chromosome I BAC T25B24 genomic NCBI Description sequence, complete sequence

136859 Seq. No.

Seq. ID ARABL1-028-Q1-B1-H4

Method BLASTN NCBI GI g3212846 BLAST score 347 E value 0.0e+00Match length 350 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136860

Seq. ID ARABL1-029-Q1-B1-B1

Method BLASTN NCBI GI g2924652 BLAST score 29 E value 7.0e-07 Match length 211 % identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9L2, complete sequence [Arabidopsis thaliana]

Seq. No. 136861

Seq. ID ARABL1-029-Q1-B1-C1

Method BLASTX NCBI GI g4490736 BLAST score 365 E value 2.0e-35 Match length 69

% identity 57

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 136862

Seq. ID ARABL1-029-Q1-B1-C5

Method BLASTN NCBI GI q3859658 BLAST score 166 E value 2.0e-88 Match length 327 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1

(ESSAII project)

Seq. No. 136863

Seq. ID ARABL1-029-Q1-B1-D3

Method BLASTX NCBI GI g2507281 BLAST score 408 E value 3.0e-40 Match length 74 % identity 100

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi 1668706 emb CAA66048

(X97380) atran2 [Arabidopsis thaliana]



Seq. No. 136864

Seq. ID ARABL1-029-Q1-B1-F5

Method BLASTN
NCBI GI g4220645
BLAST score 150
E value 4.0e-79
Match length 206

% identity 97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYA6, complete sequence [Arabidopsis thaliana]

Seq. No. 136865

Seq. ID ARABL1-029-Q1-B1-F6

Method BLASTN
NCBI GI 94235150
BLAST score 72
E value 1.0e-32
Match length 177
% identity 94

NCBI Description Arabidopsis thaliana chromosome I BAC T25B24 genomic

sequence, complete sequence

Seq. No. 136866

Seq. ID ARABL1-029-Q1-B1-G7

Method BLASTN
NCBI GI g2358139
BLAST score 75
E value 1.0e-34
Match length 100
% identity 81

NCBI Description Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete

sequence [Arabidopsis thaliana]

Seq. No. 136867

Seq. ID ARABL1-03-Q1-B1-D11

Method BLASTX
NCBI GI g2244999
BLAST score 626
E value 1.0e-65
Match length 121
% identity 100

NCBI Description (Z97341) similarity to phaseolin G-box binding protein PG2

[Arabidopsis thaliana]

Seq. No. 136868

Seq. ID ARABL1-03-Q1-B1-D12

Method BLASTN
NCBI GI g3169169
BLAST score 90
E value 1.0e-43
Match length 90
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F21P24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136869

Seq. ID ARABL1-03-Q1-B1-D9



Method BLASTX
NCBI GI g1181533
BLAST score 348
E value 5.0e-33
Match length 106
% identity 62

NCBI Description (L41245) thionin [Arabidopsis thaliana]

>gi_1586834_prf__2204399B thionin [Arabidopsis thaliana]

Seq. No. 136870

Seq. ID ARABL1-03-Q1-B1-E7

Method BLASTN
NCBI GI g4220635
BLAST score 137
E value 4.0e-71
Match length 291
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDB19, complete sequence [Arabidopsis thaliana]

Seq. No. 136871

Seq. ID ARABL1-03-Q1-B1-F3

Method BLASTX
NCBI GI g1363492
BLAST score 279
E value 4.0e-25
Match length 78
% identity 63

NCBI Description outer envelope membrane protein OEP75 precursor - garden

pea >gi_576507 (L36858) outer membrane protein [Pisum sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

Seq. No. 136872

Seq. ID ARABL1-03-Q1-B1-F9

Method BLASTN
NCBI GI 94589439
BLAST score 279
E value 1.0e-156
Match length 279
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQM1, complete sequence

Seq. No. 136873

Seq. ID ARABL1-03-Q1-B1-H1

Method BLASTX
NCBI GI g3901294
BLAST score 248
E value 3.0e-21
Match length 95
% identity 56

NCBI Description (AF089711) rpp8 [Arabidopsis thaliana]

Seq. No. 136874

Seq. ID ARABL1-030-Q1-B1-B3

Method BLASTN



```
NCBI GI
                   q3985958
BLAST score
                   129
                   2.0e-66
E value
Match length
                   257
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MZN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   136875
Seq. ID
                   ARABL1-030-Q1-B1-B6
Method
                   BLASTN
NCBI GI
                   q4115930
BLAST score
                   123
E value
                   4.0e-63
Match length
                   127
% identity
                   99
NCBI Description Arabidopsis thaliana BAC T4B21
Seq. No.
                   136876
Seq. ID
                   ARABL1-030-Q1-B1-C6
Method
                   BLASTN
NCBI GI
                   q4519197
BLAST score
                   66
                   3.0e-29
E value
Match length
                   106
% identity
                   64
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MTC11, complete sequence
Seq. No.
                   136877
Seq. ID
                   ARABL1-030-Q1-B1-D4
Method
                   BLASTX
NCBI GI
                   g2252840
BLAST score
                   254
E value
                   3.0e-22
Match length
                   68
% identity
                   69
NCBI Description
                   (AF013293) contains regions of similarity to Haemophilus
                   influenzae permease (SP:P38767) [Arabidopsis thaliana]
                   136878
Seq. No.
Seq. ID
                  ARABL1-030-Q1-B1-H8
Method
                  BLASTN
NCBI GI
                   g4581103
BLAST score
                   75
E value
                   3.0e-34
Match length
                   135
                   89
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T24I21 genomic
                  sequence, complete sequence
Seq. No.
                  136879
```

Seq. ID ARABL1-031-Q1-B1-A11

Method BLASTX
NCBI GI g3935145
BLAST score 181
E value 9.0e-14



Match length 66 % identity 55

NCBI Description (AC005106) T25N20.9 [Arabidopsis thaliana]

Seq. No. 136880

Seq. ID ARABL1-031-Q1-B1-C1

Method BLASTN NCBI GI g3869063

BLAST score 55

E value 2.0e-22 Match length 190 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K17022, complete sequence [Arabidopsis thaliana]

Seq. No. 136881

Seq. ID ARABL1-031-Q1-B1-E8

Method BLASTX
NCBI GI g2398531
BLAST score 450
E value 7.0e-45
Match length 99
% identity 87

NCBI Description (Y13726) Transcription factor [Arabidopsis thaliana]

Seq. No. 136882

Seq. ID ARABL1-031-Q1-B1-F6

Method BLASTX
NCBI GI g2342690
BLAST score 413
E value 1.0e-40
Match length 102
% identity 73

NCBI Description (AC000106) Similar to Homo copine I (gb_U83246).

[Arabidopsis thaliana]

Seq. No. 136883

Seq. ID ARABL1-031-Q1-B1-G5

Method BLASTX
NCBI GI g2500430
BLAST score 675
E value 3.0e-71
Match length 130
% identity 100

NCBI Description 40S RIBOSOMAL PROTEIN S16

Seq. No. 136884

Seq. ID ARABL1-031-Q1-E1-A7

Method BLASTX
NCBI GI g1408471
BLAST score 351
E value 2.0e-33
Match length 71
% identity 97

NCBI Description (U48938) actin depolymerizing factor 1 [Arabidopsis

thaliana] >gi 3851707 (AF102173) actin depolymerizing

factor 1 [Arabidopsis thaliana]



Seq. No. 136885

Seq. ID ARABL1-031-Q1-E1-A8

Method BLASTN
NCBI GI g1061039
BLAST score 193
E value 1.0e-104
Match length 213

Match length 213 % identity 98

NCBI Description A.thaliana mRNA for sterol-C-methyltransferase

Seq. No. 136886

Seq. ID ARABL1-031-Q1-E1-B12

Method BLASTX
NCBI GI g548484
BLAST score 355
E value 4.0e-34
Match length 80
% identity 82

NCBI Description PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (CYCLOOXYGENASE -2)

(COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2)

(PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) >gi_543442_pir__JC2030 prostaglandin-endoperoxide

synthase (EC 1.14.99.1)-2 - rat >gi_414813 (L25925) cyclooxygenase-2 [Rattus norvegicus] >gi_516872 (U04300) mitogen inducible cyclooxygenase [Rattus norvegicus] >gi_743591_prf__2013181A growth factor-inducible

cyclooxygenase [Rattus norvegicus]

Seq. No. 136887

Seq. ID ARABL1-031-Q1-E1-D4

Method BLASTN
NCBI GI g1469227
BLAST score 45
E value 4.0e-16
Match length 64

% identity 94

NCBI Description B.oleracea mRNA for hypothetical protein

Seq. No. 136888

Seq. ID ARABL1-031-Q1-E1-F2

Method BLASTN
NCBI GI g3445196
BLAST score 332
E value 0.0e+00
Match length 332
% identity 84

NCBI Description Arabidopsis thaliana chromosome II BAC T20K9 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136889

Seq. ID ARABL1-031-Q1-E1-G9

Method BLASTX
NCBI GI g2143942
BLAST score 186
E value 2.0e-14
Match length 33



```
% identity
NCBI Description prostaglandin G/H synthase 1 - rat (fragment)
Seq. No.
                  136890
Seq. ID
                  ARABL1-032-Q1-B1-B12
Method
                  BLASTX
NCBI GI
                  g2129773
BLAST score
                  378
E value
                  2.0e-36
Match length
                  70
% identity
NCBI Description
                  xyloglucan endotransglycosylase-related protein XTR3 -
                  Arabidopsis thaliana (fragment) >gi_1244752 (U43485)
                  xyloglucan endotransglycosylase-related protein
                  [Arabidopsis thaliana]
Seq. No.
                  136891
Seq. ID
                  ARABL1-032-Q1-B1-C8
Method
                  BLASTN
NCBI GI
                  g2351065
BLAST score
                  87
E value
                  2.0e-41
Match length
                  203
% identity
                  86
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHF15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  136892
Seq. ID
                  ARABL1-032-Q1-B1-C9
Method
                  BLASTX
NCBI GI
                  g1495259
BLAST score
                  171
E value
                  2.0e-12
Match length
                  55
% identity
                  56
NCBI Description
                  (X97826) orf04 [Arabidopsis thaliana]
Seq. No.
                  136893
Seq. ID
                  ARABL1-032-Q1-B1-D4
Method
                  BLASTN
NCBI GI
                  g4467131
BLAST score
                  180
E value
                  5.0e-97
Match length
                  180
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13
                  (ESSA project)
Seq. No.
                  136894
Seq. ID
                  ARABL1-032-Q1-B1-D6
```

Method BLASTN NCBI GI g2828180 BLAST score 81 E value 4.0e-38 Match length 121 % identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

% identity

91





MDK4, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                   136895
Seq. ID
                   ARABL1-032-Q1-B1-E3
Method
                   BLASTN
NCBI GI
                   g2244788
BLAST score
                   176
E value
                   1.0e-94
Match length
                   176
% identity
                   100
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
Seq. No.
                   136896
Seq. ID
                  ARABL1-032-Q1-B1-F1
Method
                  BLASTN
NCBI GI
                  g3063690
BLAST score
                   172
E value
                   5.0e-92
Match length
                   294
% identity
                   100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11
                   (ESSAII project)
Seq. No.
                  136897
Seq. ID
                  ARABL1-032-Q1-B1-G5
Method
                  BLASTX
NCBI GI
                  q134976
BLAST score
                  97
E value
                  8.0e-04
Match length
                  88
% identity
                  83
NCBI Description
                  GLUCOSE TRANSPORTER (SUGAR CARRIER) >gi_81619_pir__$12042
                   glucose transport protein STP1 - Arabidopsis thaliana
                  >gi_16520_emb_CAA39037_ (X55350) glucose transporter
                   [Arabidopsis thaliana]
Seq. No.
                  136898
Seq. ID
                  ARABL1-032-Q1-B1-H10
Method
                  BLASTN
NCBI GI
                  g2618601
BLAST score
                  273
E value
                  1.0e-152
Match length
                  273
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MHJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  136899
                  ARABL1-032-Q1-B1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2995989
BLAST score
                  59
E value
                  6.0e-25
Match length
                  95
```

NCBI Description Arabidopsis thaliana dormancy-associated protein (DRM1)

% identity

NCBI Description

97



mRNA, complete cds

```
136900
Seq. No.
Seq. ID
                   ARABL1-032-Q1-E1-A6
Method
                   BLASTN
NCBI GI
                   g12139
BLAST score
                   39
E value
                   7.0e-13
Match length
                   76
% identity
                   87
                  Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and
NCBI Description
                   trnG coding for ribosomal protein S2, one CF(1) and three
                  CF(O) subunits of ATP synthase and tRNA-Arg and tRNA-Gly
Seq. No.
                  136901
Seq. ID
                  ARABL1-032-Q1-E1-B3
Method
                  BLASTN
NCBI GI
                  g2323343
BLAST score
                  227
E value
                   1.0e-125
Match length
                   300
% identity
                   92
NCBI Description
                  Arabidopsis thaliana alpha-glucosidase 1 (Aglu1) gene,
                  complete cds
Seq. No.
                  136902
Seq. ID
                  ARABL1-032-Q1-E1-B9
Method
                  BLASTX
NCBI GI
                  g3355465
BLAST score
                  230
E value
                  1.0e-19
Match length
                  66
% identity
                   68
NCBI Description
                   (AC004218) putative Ser/Thr protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  136903
Seq. ID
                  ARABL1-032-Q1-E1-E3
Method
                  BLASTN
NCBI GI
                  g2244788
BLAST score
                  174
E value
                  2.0e-93
Match length
                  186
% identity
                  98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  136904
Seq. ID
                  ARABL1-032-Q1-E1-G3
Method
                  BLASTN
NCBI GI
                  g4567300
BLAST score
                  230
E value
                  1.0e-126
Match length
                  255
```

sequence, complete sequence

Arabidopsis thaliana chromosome II P1 MHK10 genomic

Seq. No.

Seq. ID

Method

136910

BLASTX

ARABL1-033-Q1-B1-B3



```
136905
Seq. No.
Seq. ID
                  ARABL1-033-Q1-B1-A10
Method
                  BLASTX
NCBI GI
                  g3478637
                  196
BLAST score
                  2.0e-15
E value
Match length
                  81
% identity
                  44
NCBI Description
                 (AC005546) R29425 1 [Homo sapiens]
Seq. No.
                  136906
                  ARABL1-033-Q1-B1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g16375
BLAST score
                  54
                  4.0e-22
E value
                  54
Match length
                  100
% identity
NCBI Description A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding
                  protein
Seq. No.
                  136907
                  ARABL1-033-Q1-B1-A9
Seq. ID
Method
                  BLASTN
                  g2264317
NCBI GI
BLAST score
                  138
                  8.0e-72
E value
                  239
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUG13, complete sequence [Arabidopsis thaliana]
Seq. No.
                  136908
Seq. ID
                  ARABL1-033-Q1-B1-B10
                  BLASTX
Method
NCBI GI
                  g4510345
BLAST score
                  339
E value
                  3.0e-32
                  76
Match length
                  79
% identity
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.
                  136909
Seq. ID
                  ARABL1-033-Q1-B1-B2
Method
                  BLASTN
NCBI GI
                  g4733953
BLAST score
                  96
                  3.0e-47
E value
                  96
Match length
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F13011 genomic
                  sequence, complete sequence
```



```
NCBI GI
                  q4102703
BLAST score
                  504
                  3.0e-51
E value
Match length
                  99
% identity
                  100
NCBI Description
                  (AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis
                  thaliana]
Seq. No.
                  136911
Seq. ID
                  ARABL1-033-Q1-B1-B7
Method
                  BLASTN
NCBI GI
                  q4249393
BLAST score
                  306
E value
                  1.0e-172
Match length
                  306
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC T9J23 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  136912
Seq. No.
                  ARABL1-033-Q1-B1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4263697
BLAST score
                  502
E value
                  4.0e-51
Match length
                  99
                  99
% identity
NCBI Description
                  (AC006223) putative ribosomal protein L27 [Arabidopsis
                  thaliana]
                  136913
Seq. No.
Seq. ID
                  ARABL1-033-Q1-B1-D9
Method
                  BLASTN
NCBI GI
                  q4757405
BLAST score
                  128
E value
                  7.0e-66
Match length
                  248
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MOJ10, complete sequence
Seq. No.
                  136914
Seq. ID
                  ARABL1-033-Q1-B1-E10
Method
                  BLASTX
NCBI GI
                  q131398
BLAST score
                  348
E value
                  3.0e-33
Match length
                  71
                  100
% identity
NCBI Description
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                  >gi 72714 pir F2MU10 photosystem II 10K protein precursor
```

- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

Match length

% identity

65

74



come from this gene. [Arabidopsis

```
Seq. No.
                   136915
Seq. ID
                   ARABL1-033-Q1-B1-E7
Method
                   BLASTN
NCBI GI
                   q1354271
BLAST score
                   20
E value
                   1.8e-01
Match length
                  220
                   98
% identity
NCBI Description Arabidopsis thaliana aspartic proteinase mRNA, partial cds
Seq. No.
                  136916
Seq. ID
                  ARABL1-033-Q1-B1-F10
Method
                  BLASTX
NCBI GI
                  q4240120
BLAST score
                  395
E value
                  8.0e-39
Match length
                  74
                  100
% identity
NCBI Description
                  (AB007801) cytochrome b5 [Arabidopsis thaliana]
Seq. No.
                  136917
                  ARABL1-033-Q1-B1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  a2119846
BLAST score
                  681
E value
                  6.0e-72
Match length
                  129
% identity
                  99
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi_16364_emb_CAA45790 (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  136918
Seq. ID
                  ARABL1-033-Q1-B1-F9
Method
                  BLASTN
NCBI GI
                  g2244788
BLAST score
                  104
E value
                  2.0e-51
Match length
                  250
% identity
                  97
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  136919
Seq. ID
                  ARABL1-033-Q1-B1-G10
Method
                  BLASTX
NCBI GI
                  g3885511
BLAST score
                  233
E value
                  8.0e-20
```



NCBI Description (AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No. 136920

Seq. ID ARABL1-033-Q1-B1-G2

Method BLASTX
NCBI GI g2264373
BLAST score 617
E value 2.0e-64
Match length 114
% identity 100

NCBI Description (AC002354) putative NAM/no apical meristem protein

[Arabidopsis thaliana]

Seq. No. 136921

Seq. ID ARABL1-033-Q1-B1-G5

Method BLASTX
NCBI GI g3123188
BLAST score 583
E value 2.0e-60
Match length 111
% identity 96

NCBI Description CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis

thaliana] >gi_\(\overline{2}\)511726 (AF021937) catalase 3 [Arabidopsis

thaliana]

Seq. No. 136922

Seq. ID ARABL1-033-Q1-B1-G7

Method BLASTN
NCBI GI g4662609
BLAST score 81
E value 6.0e-38
Match length 133
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5,

complete sequence

Seq. No. 136923

Seq. ID ARABL1-033-Q1-B1-H9

Method BLASTX
NCBI GI g3152581
BLAST score 365
E value 3.0e-35
Match length 82
% identity 83

NCBI Description (AC002986) Similar to E. coli sulfurtransferase (rhodanese)

gb_AE00338. ESTs gb_T03984, gb_T03983 and gb_W43228 come

from this gene. [Arabidopsis thaliana]

Seq. No. 136924

Seq. ID ARABL1-033-Q1-E1-A9

Method BLASTN
NCBI GI g2264317
BLAST score 99
E value 7.0e-49
Match length 119
% identity 96



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No. 136925

Seq. ID ARABL1-033-Q1-E1-B3

Method BLASTN
NCBI GI g4102702
BLAST score 331
E value 0.0e+00
Match length 331
% identity 100

NCBI Description Arabidopsis thaliana ribulose-5-phosphate-3-epimerase mRNA,

complete cds

Seq. No. 136926

Seq. ID ARABL1-033-Q1-E1-C9

Method BLASTN
NCBI GI g555975
BLAST score 99
E value 8.0e-49
Match length 135
% identity 93

NCBI Description Arabidopsis thaliana metallothionein-like protein (AtMT-K)

mRNA, complete cds

Seq. No. 136927

Seq. ID ARABL1-033-Q1-E1-D4

Method BLASTN
NCBI GI g2828182
BLAST score 241
E value 1.0e-133
Match length 241
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No. 136928

Seq. ID ARABL1-033-Q1-E1-E1

Method BLASTN
NCBI GI g4584339
BLAST score 181
E value 1.0e-97
Match length 206
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC T23A1 genomic

sequence, complete sequence

Seq. No. 136929

Seq. ID ARABL1-033-Q1-E1-E8

Method BLASTX
NCBI GI g132102
BLAST score 506
E value 2.0e-51
Match length 89
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR

(RUBISCO SMALL SUBUNIT 2B) >gi_68061 pir RKMUB2



ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_(X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No. 136930

Seq. ID ARABL1-033-Q1-E1-G2

Method BLASTN
NCBI GI g2264367
BLAST score 346
E value 0.0e+00
Match length 346
% identity 100

NCBI Description Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm,

complete sequence [Arabidopsis thaliana]

Seq. No. 136931

Seq. ID ARABL1-033-Q1-E1-G7

Method BLASTN
NCBI GI 94662609
BLAST score 72
E value 1.0e-32
Match length 125
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5,

complete sequence

Seq. No. 136932

Seq. ID ARABL1-033-Q1-E1-H9

Method BLASTX
NCBI GI g3152581
BLAST score 174
E value 1.0e-12
Match length 42
% identity 83

NCBI Description (AC002986) Similar to E. coli sulfurtransferase (rhodanese)

gb AE00338. ESTs gb T03984, gb T03983 and gb W43228 come

from this gene. [Arabidopsis thaliana]

Seq. No. 136933

Seq. ID ARABL1-034-Q1-B1-A10

Method BLASTN
NCBI GI g4753195
BLAST score 78
E value 4.0e-36
Match length 198
% identity 96

NCBI Description Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5

cM, complete sequence

Seq. No. 136934

Seq. ID ARABL1-034-Q1-B1-A2

Method BLASTX
NCBI GI g861155
BLAST score 274
E value 2.0e-24
Match length 77



% identity 61

NCBI Description (Z35162) beta-fructofuranosidase; cell wall invertase I;

fructosidase [Vicia faba]

Seq. No. 136935

Seq. ID ARABL1-034-Q1-B1-A3

Method BLASTX
NCBI GI g2493144
BLAST score 404
E value 1.0e-39
Match length 95
% identity 57

NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE

16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132

H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis

thaliana]

Seq. No. 136936

Seq. ID ARABL1-034-Q1-B1-B11

Method BLASTN
NCBI GI g166810
BLAST score 190
E value 1.0e-103
Match length 194
% identity 99

NCBI Description Arabidopsis thaliana Columbia protein kinase mRNA, complete

cds

Seq. No. 136937

Seq. ID ARABL1-034-Q1-B1-C10

Method BLASTN
NCBI GI g3805839
BLAST score 104
E value 2.0e-51
Match length 224
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14

(ESSAII project)

Seq. No. 136938

Seq. ID ARABL1-034-Q1-B1-C5

Method BLASTX
NCBI GI g2129773
BLAST score 518
E value 6.0e-53
Match length 113
% identity 87

NCBI Description xyloglucan endotransglycosylase-related protein XTR3 -

Arabidopsis thaliana (fragment) >gi_1244752 (U43485) xyloglucan endotransglycosylase-related protein

[Arabidopsis thaliana]

Seq. No. 136939

Seq. ID ARABL1-034-Q1-B1-C7

Method BLASTX



NCBI GI g4755189 BLAST score 300 E value 2.0e-27 Match length 119 % identity 66

NCBI Description (AC007018) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 136940

Seq. ID ARABL1-034-Q1-B1-D10

Method BLASTX
NCBI GI g3298536
BLAST score 415
E value 4.0e-41
Match length 82
% identity 100

NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]

Seq. No. 136941

Seq. ID ARABL1-034-Q1-B1-D11

Method BLASTX
NCBI GI g1076678
BLAST score 388
E value 5.0e-38
Match length 78
% identity 100

NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No. 136942

Seq. ID ARABL1-034-Q1-B1-D8

Method BLASTX
NCBI GI g3766248
BLAST score 203
E value 6.0e-16
Match length 57
% identity 67

NCBI Description (Y18227) blue copper binding-like protein [Arabidopsis

thaliana]

Seq. No. 136943

Seq. ID ARABL1-034-Q1-B1-E11

Method BLASTX
NCBI GI g2827546
BLAST score 287
E value 4.0e-26
Match length 77
% identity 65

NCBI Description (AL021635) cytochrome P450 like protein [Arabidopsis

thaliana]

Seq. No. 136944

Seq. ID ARABL1-034-Q1-B1-E8

Method BLASTX
NCBI GI g2129550
BLAST score 618
E value 1.0e-64
Match length 121
% identity 69



NCBI Description calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi 836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi 836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1 (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana] Seq. No. 136945 Seq. ID ARABL1-034-Q1-B1-E9 Method BLASTN NCBI GI q4741959 BLAST score 213 E value 1.0e-116

% identity 97 NCBI Description Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete cds

Seq. No. 136946

Match length

Seq. ID ARABL1-034-Q1-B1-F1

243

Method BLASTN NCBI GI g2618599 BLAST score 347 0.0e+00E value Match length 347 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBD2, complete sequence [Arabidopsis thaliana]

Seq. No. 136947

Seq. ID ARABL1-034-Q1-B1-F2

Method BLASTX NCBI GI g4559384 BLAST score 436 E value 2.0e-43 Match length 115 % identity 83

NCBI Description (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No. 136948

Seq. ID ARABL1-034-Q1-B1-G10

Method BLASTN NCBI GI q4309719 BLAST score 244 E value 1.0e-135 Match length 248 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T30D6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136949

Seq. ID ARABL1-034-Q1-B1-G11

Method BLASTX NCBI GI g124372 BLAST score 360



E value 1.0e-34
Match length 68
% identity 100

NCBI Description ACETOLACTATE SYNTHASE PRECURSOR (ACETOHYDROXY-ACID

SYNTHASE) (ALS) >gi 68240 pir YCMU acetolactate synthase

(EC 4.1.3.18) precursor - Arabidopsis thaliana

>gi_226221_prf__1501386B acetolactate synthase [Arabidopsis

thaliana]

Seq. No.

136950

Seq. ID Method ARABL1-034-Q1-B1-G6

Method BLASTN
NCBI GI g4006885
BLAST score 100
E value 6.0e-49
Match length 336

Match length 336 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No.

136951

Seq. ID

ARABL1-034-Q1-B1-H10

Method BLASTX
NCBI GI g2497886
BLAST score 197
E value 1.0e-15
Match length 39
% identity 100

NCBI Description METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B)

>gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis
thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis

thaliana]

Seq. No.

136952

Seq. ID

ARABL1-034-Q1-B1-H11

Method BLASTX
NCBI GI g464986
BLAST score 258
E value 9.0e-23
Match length 48
% identity 100

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC

6.3.2.19) UBC9 - Arabidopsis thaliana

>gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)

ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis thaliana]

>gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

Seq. No. 136953

Seq. ID ARABL1-034-Q1-B1-H9

Method BLASTX NCBI GI g4185505

```
BLAST score
E value
                  1.0e-21
Match length
                  61
                  80
% identity
                  (AF101038) nonspecific lipid-transfer protein precursor
NCBI Description
                  [Brassica napus]
                  136954
Seq. No.
Seq. ID
                  ARABL1-034-Q1-E1-F6
Method
                  BLASTX
NCBI GI
                  g4755190
BLAST score
                  242
E value
                  1.0e-20
Match length
                  60
% identity
                  73
                  (AC007018) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  136955
Seq. ID
                  ARABL1-035-Q1-B1-A2
Method
                  BLASTN
NCBI GI
                  g3128142
BLAST score
                  252
E value
                  1.0e-140
Match length
                  272
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQN23, complete sequence [Arabidopsis thaliana]
Seq. No.
                  136956
Seq. ID
                  ARABL1-035-Q1-B1-B1
Method
                  BLASTN
NCBI GI
                  g4159706
BLAST score
                  82
E value
                  6.0e-39
Match length
                  82
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGL6, complete sequence
                  136957
Seq. No.
Seq. ID
                  ARABL1-035-Q1-B1-B2
Method
                  BLASTX
```

Method BLASTX
NCBI GI 94455214
BLAST score 92
E value 5.0e-42
Match length 109
% identity 98

NCBI Description (AL035440) putative dihydrolipoamide succinyltransferase

[Arabidopsis thaliana]

Seq. No. 136958

Seq. ID ARABL1-035-Q1-B1-B3

Method BLASTX
NCBI GI g131398
BLAST score 440
E value 8.0e-44
Match length 105



% identity 86

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 136959

Seq. ID ARABL1-035-Q1-B1-B5

Method BLASTX
NCBI GI g4584548
BLAST score 648
E value 4.0e-68
Match length 120
% identity 100

NCBI Description (AL049608) putative protein [Arabidopsis thaliana]

Seq. No. 136960

Seq. ID ARABL1-035-Q1-B1-B6

Method BLASTX
NCBI GI g4335734
BLAST score 96
E value 2.0e-03
Match length 53
% identity 25

NCBI Description (AC006248) putative calmodulin [Arabidopsis thaliana]

Seq. No. 136961

Seq. ID ARABL1-035-Q1-B1-C10

Method BLASTX
NCBI GI g1710530
BLAST score 592
E value 1.0e-61
Match length 110
% identity 96

NCBI Description 60S RIBOSOMAL PROTEIN L27A >qi 2129719 pir S71256

ribosomal protein L27a - Arabidopsis thaliana

>gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein

L27a [Arabidopsis thaliana]

Seq. No. 136962

Seq. ID ARABL1-035-Q1-B1-E1

Method BLASTN
NCBI GI g1688071
BLAST score 66
E value 3.0e-29
Match length 106
% identity 91

NCBI Description Arabidopsis thaliana biotin holocarboxylase synthetase

mRNA, complete cds

Seq. No. 136963

Seq. ID ARABL1-035-Q1-B1-E12



```
Method BLASTX
NCBI GI g2894596
BLAST score 311
E value 4.0e-29
Match length 62
% identity 100
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
```

Seq. No. 136964

Seq. ID ARABL1-035-Q1-B1-E6

Method BLASTN
NCBI GI g3449327
BLAST score 190
E value 1.0e-103
Match length 217
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCA23, complete sequence [Arabidopsis thaliana]

Seq. No. 136965

Seq. ID ARABL1-035-Q1-B1-F1

Method BLASTX
NCBI GI g4580460
BLAST score 372
E value 7.0e-36
Match length 89
% identity 83

NCBI Description (AC006081) putative 26S Protease Subunit 4 [Arabidopsis

thaliana]

Seq. No. 136966

Seq. ID ARABL1-035-Q1-B1-F2

Method BLASTX
NCBI GI g4678259
BLAST score 391
E value 4.0e-38
Match length 101
% identity 74

NCBI Description (AL049657) putative protein [Arabidopsis thaliana]

Seq. No. 136967

Seq. ID ARABL1-035-Q1-B1-G8

Method BLASTX
NCBI GI g1071912
BLAST score 227
E value 7.0e-19
Match length 45
% identity 100

NCBI Description cysteine synthase (EC 4.2.99.8) cpACS1 - Arabidopsis

thaliana >gi_572517_emb_CAA57344_ (X81698) cysteine

synthase [Arabidopsis thaliana]

Seq. No. 136968

Seq. ID ARABL1-035-Q1-E1-A11

Method BLASTN
NCBI GI g4193383
BLAST score 111

E value Match length 115 % identity 99

Arabidopsis thaliana ribosomal protein S27 (ARS27A) gene, NCBI Description

complete cds

Seq. No. 136969

Seq. ID ARABL1-035-Q1-E1-B1

Method BLASTN NCBI GI q4159706 BLAST score 82 E value 6.0e-39 Match length 82

100 % identity

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MGL6, complete sequence

Seq. No. 136970

ARABL1-035-Q1-E1-D4 Seq. ID

Method BLASTN NCBI GI g4757392 BLAST score 251 E value 1.0e-139 Match length 251 % identity 100

Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: NCBI Description

K14A17, complete sequence

Seq. No. 136971

Seq. ID ARABL1-035-Q1-E1-E12

Method BLASTX NCBI GI g2894596 BLAST score 311 E value 4.0e-29 Match length 62

% identity 100

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 136972

Seq. ID ARABL1-035-Q1-E1-E6

Method BLASTN NCBI GI g3449327 BLAST score 190 E value 1.0e-103 Match length 217 96 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MCA23, complete sequence [Arabidopsis thaliana]

136973 Seq. No.

Seq. ID ARABL1-035-Q1-E1-G3

Method BLASTN NCBI GI g2815404 BLAST score 134 2.0e-69 E value Match length 238 % identity 90



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No. 136974

Seq. ID ARABL1-036-Q1-B1-A3

Method BLASTN NCBI GI g3128135 BLAST score 80 E value 5.0e-37 Match length 348

% identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19E1, complete sequence [Arabidopsis thaliana]

Seq. No. 136975

Seq. ID ARABL1-036-Q1-B1-A5

95

Method BLASTX NCBI GI g16374 BLAST score 161 2.0e-11 E value Match length 29 % identity 100

NCBI Description (X03908) chlorophyll a/b binding protein (LHCP AB 180)

[Arabidopsis thaliana]

136976 Seq. No.

Seq. ID ARABL1-036-Q1-B1-B1

Method BLASTX NCBI GI q3688175 BLAST score 451 E value 5.0e-45 Match length 107 % identity 81

NCBI Description (AL031804) gamma-VPE (vacuolar processing enzyme)

[Arabidopsis thaliana]

136977 Seq. No.

Seq. ID ARABL1-036-Q1-B1-B11

Method BLASTN NCBI GI g4335744 BLAST score 73 E value 8.0e-33 Match length 197 84 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC T4M8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136978

Seq. ID ARABL1-036-Q1-B1-B3

Method BLASTN NCBI GI g4691223 BLAST score 102 E value 2.0e-50 Match length 203 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15

(ESSA project)

% identity

NCBI Description

89

(ESSAII project)



```
Seq. No.
                  136979
Seq. ID
                  ARABL1-036-Q1-B1-B7
Method
                  BLASTX
NCBI GI
                  g2160142
BLAST score
                  405
E value
                  1.0e-39
Match length
                  104
% identity
                  80
NCBI Description
                  (AC000375) Strong similarity to Arabidopsis APR2
                   (gb_U56921). [Arabidopsis thaliana] >gi_2738758 (AF016283)
                  5'-adenylylsulfate reductase [Arabidopsis thaliana]
Seq. No.
                  136980
Seq. ID
                  ARABL1-036-Q1-B1-B8
Method
                  BLASTN
NCBI GI
                  g3250673
BLAST score
                  187
E value
                  1.0e-101
Match length
                  378
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5
                  (ESSAII project)
Seq. No.
                  136981
Seq. ID
                  ARABL1-036-Q1-B1-C7
Method
                  BLASTX
NCBI GI
                  q1929056
BLAST score
                  293
                  2.0e-26
E value
                  99
Match length
% identity
                  54
NCBI Description
                  (Y12090) putative 3,4-dihydroxy-2-butanone kinase
                   [Lycopersicon esculentum]
Seq. No.
                  136982
Seq. ID
                  ARABL1-036-Q1-B1-E5
Method
                  BLASTN
NCBI GI
                  g3763944
BLAST score
                  170
E value
                  5.0e-91
Match length
                  170
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23
                  (ESSAII project)
                  136983
Seq. No.
Seq. ID
                  ARABL1-036-Q1-B1-F11
Method
                  BLASTN
NCBI GI
                  g2864607
BLAST score
                  23
E value
                  2.0e-03
Match length
                  67
```

Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6



```
Seq. No.
                  ARABL1-036-Q1-B1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2398679
BLAST score
                  313
E value
                  5.0e-29
Match length
                  66
% identity
                  89
                  (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
NCBI Description
                  synthase [Morinda citrifolia]
Seq. No.
                  136985
Seq. ID
                  ARABL1-036-Q1-B1-G12
Method
                  BLASTX
NCBI GI
                  q3885892
BLAST score
                  532
E value
                  1.0e-54
Match length
                  112
% identity
NCBI Description
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.
                  136986
Seq. ID
                  ARABL1-036-Q1-B1-H6
Method
                  BLASTN
NCBI GI
                  q2358139
BLAST score
                  144
E value
                  3.0e-75
Match length
                  401
% identity
                  100
                  Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete
NCBI Description
                  sequence [Arabidopsis thaliana]
Seq. No.
                  136987
Seq. ID
                  ARABL1-036-Q1-B1-H8
Method
                  BLASTX
NCBI GI
                  g2338712
BLAST score
                  262
E value
                  8.0e-23
                  69
Match length
                  74
% identity
                  (AF013959) metallothionein-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  136988
Seq. ID
                  ARABL1-036-Q1-E1-A5
                  BLASTX
Method
NCBI GI
                  g16374
BLAST score
                  161
                  2.0e-11
E value
Match length
                  29
% identity
                  100
```

(X03908) chlorophyll a/b binding protein (LHCP AB 180) NCBI Description

[Arabidopsis thaliana]

Seq. No. 136989

Seq. ID ARABL1-036-Q1-E1-B3

Method BLASTN



```
NCBI GI
                  q4691223
BLAST score
                  207
                  1.0e-113
E value
Match length
                  391
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
                  (ESSA project)
                  136990
Seq. No.
Seq. ID
                  ARABL1-036-Q1-E1-B8
Method
                  BLASTN
NCBI GI
                  q3250673
BLAST score
                  303
E value
                  1.0e-170
Match length
                  350
% identity
                  56
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5
NCBI Description
                  (ESSAII project)
```

 Seq. No.
 136991

 Seq. ID
 ARABL1-036-Q1-E1-C6

 Method
 BLASTN

 NCBI GI
 g4204948

 BLAST score
 182

BLAST score 182 E value 7.0e-98 Match length 189 % identity 99

NCBI Description Arabidopsis thaliana serine/threonine protein phosphatase

2A-4 catalytic subunit gene, complete cds

Seq. No. 136992

Seq. ID ARABL1-036-Q1-E1-E5

Method BLASTN
NCBI GI g3763944
BLAST score 170
E value 5.0e-91
Match length 170
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23

(ESSAII project)

Seq. No. 136993

Seq. ID ARABL1-036-Q1-E1-F6

Method BLASTN
NCBI GI g3702735
BLAST score 322
E value 0.0e+00
Match length 343
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQL5, complete sequence [Arabidopsis thaliana]

Seq. No. 136994

Seq. ID ARABL1-036-Q1-E1-H3

Method BLASTN NCBI GI g4538949 BLAST score 99



E value 2.0e-48 Match length 270 % identity 85

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24

(ESSA project)

Seq. No. 136995

Seq. ID ARABL1-037-Q1-B1-A12

Method BLASTN
NCBI GI g2564050
BLAST score 120
E value 2.0e-61
Match length 132
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUA22, complete sequence [Arabidopsis thaliana]

Seq. No. 136996

Seq. ID ARABL1-037-Q1-B1-A7

Method BLASTN
NCBI GI g4662609
BLAST score 190
E value 1.0e-103
Match length 211
% identity 97

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5,

complete sequence

Seq. No. 136997

Seq. ID ARABL1-037-Q1-B1-A8

Method BLASTX
NCBI GI g2809232
BLAST score 476
E value 5.0e-48
Match length 110
% identity 81

NCBI Description (AC002560) F21B7.1 [Arabidopsis thaliana]

Seq. No. 136998

Seq. ID ARABL1-037-Q1-B1-B7

Method BLASTN
NCBI GI 94567300
BLAST score 68
E value 1.0e-30
Match length 68
% identity 100

NCBI Description Arabidopsis thaliana chromosome II P1 MHK10 genomic

sequence, complete sequence

Seq. No. 136999

Seq. ID ARABL1-037-Q1-B1-C5

Method BLASTN
NCBI GI g16375
BLAST score 65
E value 1.0e-28
Match length 65
% identity 100



NCBI Description A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding protein

Seq. No. 137000

Seq. ID ARABL1-037-Q1-B1-D10

Method BLASTN
NCBI GI g4159706
BLAST score 149
E value 1.0e-78
Match length 149
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGL6, complete sequence

Seq. No. 137001

Seq. ID ARABL1-037-Q1-B1-E1

Method BLASTX
NCBI GI g115785
BLAST score 272
E value 3.0e-24
Match length 51
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-2) (LHCP) >gi_82380_pir_S04028 chlorophyll

a/b-binding protein 2 precursor - barley

>gi_18943_emb_CAA31232_ (X12735) LHC precursor protein (AA

-34 to 230) [Hordeum vulgare]

Seq. No. 137002

Seq. ID ARABL1-037-Q1-B1-F9

Method BLASTN
NCBI GI g4538949
BLAST score 156
E value 9.0e-83
Match length 156
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24

(ESSA project)

Seq. No. 137003

Seq. ID ARABL1-037-Q1-B1-G12

Method BLASTN
NCBI GI g2623294
BLAST score 91
E value 3.0e-44
Match length 99
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T20B5 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137004

Seq. ID ARABL1-037-Q1-B1-G6

Method BLASTN
NCBI GI g3241924
BLAST score 79
E value 2.0e-36
Match length 205



% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNC6, complete sequence [Arabidopsis thaliana]

Seq. No. 137005

Seq. ID ARABL1-037-Q1-B1-H10

Method BLASTX
NCBI GI g2829920
BLAST score 170
E value 1.0e-12
Match length 35

NCBI Description (AC002291) Similar to 'MADS box' transcription factors

[Arabidopsis thaliana]

Seq. No. 137006

% identity

Seq. ID ARABL1-037-Q1-E1-B12

100

Method BLASTX
NCBI GI g1769849
BLAST score 290
E value 2.0e-26
Match length 55
% identity 100

NCBI Description (275663) chlorophyll a/b binding protein [Apium graveolens]

Seq. No. 137007

Seq. ID ARABL1-037-Q1-E1-B7

Method BLASTN
NCBI GI g4567300
BLAST score 68
E value 1.0e-30
Match length 68
% identity 100

NCBI Description Arabidopsis thaliana chromosome II P1 MHK10 genomic

sequence, complete sequence

Seq. No. 137008

Seq. ID ARABL1-037-Q1-E1-C11

Method BLASTN
NCBI GI g886427
BLAST score 86
E value 7.0e-41
Match length 178
% identity 87

NCBI Description A.thaliana mRNA for zeta-crystallin homologue

Seq. No. 137009

Seq. ID ARABL1-037-Q1-E1-C5

Method BLASTN
NCBI GI g16375
BLAST score 53
E value 2.0e-21
Match length 65
% identity 95

NCBI Description A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding

protein



Seq. No. 137010

Seq. ID ARABL1-037-Q1-E1-D10

Method BLASTN
NCBI GI g4159706
BLAST score 144
E value 1.0e-75
Match length 152
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGL6, complete sequence

Seq. No. 137011

Seq. ID ARABL1-037-Q1-E1-E6

Method BLASTN
NCBI GI g4063730
BLAST score 358
E value 0.0e+00
Match length 358
% identity 100

NCBI Description Arabidopsis thaliana BAC F21J6 from chromosome V,

containing KNAT3 and mapping near 60.5 cM, complete

sequence [Arabidopsis thaliana]

Seq. No. 137012

Seq. ID ARABL1-038-Q1-B1-A11

Method BLASTX
NCBI GI g3738261
BLAST score 211
E value 4.0e-17
Match length 100
% identity 56

NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus

nigra]

Seq. No. 137013

Seq. ID ARABL1-038-Q1-B1-A12

Method BLASTX
NCBI GI g3286693
BLAST score 547
E value 2.0e-56
Match length 104
% identity 100

NCBI Description (Y15433) 33 kDa polypeptide of oxygen-evolving complex

(OEC) in photosystem II [Arabidopsis thaliana]

Seq. No. 137014

Seq. ID ARABL1-038-Q1-B1-B7

Method BLASTX
NCBI GI g2493144
BLAST score 404
E value 1.0e-39
Match length 95
% identity 57

NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE

16 KD PROTEOLIPID SUBUNIT) >gi 2118221 pir__S60132

H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585)



vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
thaliana]

Seq. No. 137015

Seq. ID ARABL1-038-Q1-B1-B9

Method BLASTX
NCBI GI g3287862
BLAST score 465
E value 8.0e-47
Match length 85
% identity 100

NCBI Description PUTATIVE TRYPSIN INHIBITOR T01024.27 PRECURSOR >gi 2289007

(AC002335) trypsin inhibitor 2 precursor isolog

[Arabidopsis thaliana]

Seq. No. 137016

Seq. ID ARABL1-038-Q1-B1-D10

Method BLASTN
NCBI GI g4757403
BLAST score 40
E value 3.0e-13
Match length 114
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MJL12, complete sequence

Seq. No. 137017

Seq. ID ARABL1-038-Q1-B1-D3

Method BLASTX
NCBI GI g2315463
BLAST score 235
E value 8.0e-20
Match length 98
% identity 50

NCBI Description (AF016449) similar to enzymes that act through an ATP

dependent binding of AMP; most similar to CoA ligases

[Caenorhabditis elegans]

Seq. No. 137018

Seq. ID ARABL1-038-Q1-B1-E11

Method BLASTN
NCBI GI g4335744
BLAST score 71
E value 1.0e-31
Match length 167
% identity 86

NCBI Description Arabidopsis thaliana chromosome II BAC T4M8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137019

Seq. ID ARABL1-038-Q1-B1-F11

Method BLASTX
NCBI GI g2146733
BLAST score 364
E value 6.0e-35
Match length 82
% identity 79





```
NCBI Description GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana
```

137020 Seq. No. Seq. ID ARABL1-038-Q1-B1-F12 Method BLASTN NCBI GI g3522932 BLAST score 272 1.0e-151 E value 304 Match length 97 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137021

Seq. ID ARABL1-038-Q1-B1-F7

Method BLASTX
NCBI GI g3033397
BLAST score 261
E value 7.0e-23
Match length 51
% identity 100

NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]

Seq. No. 137022

Seq. ID ARABL1-038-Q1-B1-G10

Method BLASTN
NCBI GI g2924651
BLAST score 159
E value 3.0e-84
Match length 313
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K2A18, complete sequence [Arabidopsis thaliana]

Seq. No. 137023

Seq. ID ARABL1-038-Q1-B1-G11

Method BLASTX
NCBI GI g464987
BLAST score 456
E value 9.0e-46
Match length 84
% identity 100

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN

LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)

>gi_421858_pir__S32672 ubiquitin--protein ligase (EC

6.3.2.19) UBC10 - Arabidopsis thaliana

>gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating
enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin

conjugating enzyme [Arabidopsis thaliana]

Seq. No. 137024

Seq. ID ARABL1-038-Q1-B1-G2

Method BLASTX
NCBI GI g3402685
BLAST score 625
E value 2.0e-65
Match length 123



% identity 99

NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 137025

Seq. ID ARABL1-038-Q1-B1-G4

Method BLASTX
NCBI GI g2119848
BLAST score 336
E value 6.0e-32
Match length 70
% identity 93

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 -

Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]

Seq. No. 137026

Seq. ID ARABL1-038-Q1-B1-G6

Method BLASTN
NCBI GI g3869075
BLAST score 370

E value 0.0e+00 Match length 382

% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXK3, complete sequence [Arabidopsis thaliana]

Seq. No. 137027

Seq. ID ARABL1-038-Q1-B1-H11

Method BLASTX
NCBI GI g2507587
BLAST score 284
E value 1.0e-25
Match length 57
% identity 88

NCBI Description METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G)

>gi_1361998_pir__S57861 metallothionein 2a - Arabidopsis
thaliana >gi 555976 (U15108) metallothionein-like protein

[Arabidopsis thaliana] >gi 1580892 prf 2116236A

metallothionein 1 [Arabidopsis thaliana]

Seq. No. 137028

Seq. ID ARABL1-038-Q1-E1-A9

Method BLASTX
NCBI GI g131398
BLAST score 258
E value 2.0e-22
Match length 81
% identity 69

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]



>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
come from this gene. [Arabidopsis

Seq. No. 137029

Seq. ID ARABL1-038-Q1-E1-B10

Method BLASTX
NCBI GI g2119846
BLAST score 323
E value 3.0e-30
Match length 62
% identity 100

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 137030

Seq. ID ARABL1-038-Q1-E1-B7

Method BLASTX
NCBI GI g1200116
BLAST score 168
E value 7.0e-12
Match length 50
% identity 76

NCBI Description (X95752) c subunit of V-type ATPase [Nicotiana tabacum]

Seq. No. 137031

Seq. ID ARABL1-038-Q1-E1-D11

Method BLASTN
NCBI GI g2618603
BLAST score 114
E value 2.0e-57
Match length 242
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSL3, complete sequence [Arabidopsis thaliana]

Seq. No. 137032

Seq. ID ARABL1-038-Q1-E1-D3

Method BLASTN
NCBI GI g3046855
BLAST score 170
E value 1.0e-90
Match length 385
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MSL1, complete sequence [Arabidopsis thaliana]

Seq. No. 137033

Seq. ID ARABL1-038-Q1-E1-D9

Method BLASTX



NCBI GI g2213597 BLAST score 191 E value 1.0e-14 Match length 48 % identity 79

NCBI Description (AC000348) T7N9.17 [Arabidopsis thaliana]

Seq. No. 137034

Seq. ID ARABL1-038-Q1-E1-F8

Method BLASTN
NCBI GI g16375
BLAST score 146
E value 1.0e-76
Match length 146
% identity 100

NCBI Description A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding

protein

Seq. No. 137035

Seq. ID ARABL1-038-Q1-E1-G10

Method BLASTX
NCBI GI g2435518
BLAST score 223
E value 2.0e-18
Match length 42
% identity 86

NCBI Description (AF024504) contains similarity to C3HC4-type zinc fingers

[Arabidopsis thaliana]

Seq. No. 137036

Seq. ID ARABL1-038-Q1-E1-G11

Method BLASTX
NCBI GI g464987
BLAST score 198
E value 2.0e-15
Match length 36
% identity 97

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN

LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)

>gi_421858_pir__S32672 ubiquitin--protein ligase (EC

6.3.2.19) UBC10 - Arabidopsis thaliana

>gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating
enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin

conjugating enzyme [Arabidopsis thaliana]

Seq. No. 137037

Seq. ID ARABL1-038-Q1-E1-G2

Method BLASTN
NCBI GI g3402671
BLAST score 325
E value 0.0e+00
Match length 325
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T16B24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137038

```
Seq. ID

ARABL1-038-Q1-E1-G6

Method

BLASTN

NCBI GI

BLAST score

116

E value

1.0e-58

Match length

36

identity

96

NCBI Description

Arabidopsis thaliana ge
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

```
      Seq. No.
      137039

      Seq. ID
      ARABL1-038-Q1-E1-G8

      Method
      BLASTN

      NCBI GI
      q3337347
```

NCBI GI g3337347
BLAST score 139
E value 1.0e-72
Match length 143
% identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

 Seq. No.
 137040

 Seq. ID
 ARABL1-038-Q1-E1-H10

 Method
 BLASTX

 NCBI GI
 a643469

NCBI GI g643469
BLAST score 238
E value 4.0e-20
Match length 59
% identity 73

NCBI Description (U19886) unknown [Lycopersicon esculentum]

Seq. No. 137041

Seq. ID ARABL1-038-Q1-E1-H7

Method BLASTX
NCBI GI g99696
BLAST score 299
E value 3.0e-27
Match length 60
% identity 98

NCBI Description glutamate--ammonia ligase (EC 6.3.1.2) precursor,

chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln

synthetase [Arabidopsis thaliana]

Seq. No. 137042

Seq. ID ARABL1-039-Q1-B1-A7

Method BLASTX
NCBI GI g2651297
BLAST score 329
E value 1.0e-30
Match length 84
% identity 75

NCBI Description (AC002336) putative expansin [Arabidopsis thaliana]

Seq. No. 137043



```
Seq. ID
                  ARABL1-039-Q1-B1-B1
Method
                  BLASTX
NCBI GI
                  q4678226
BLAST score
                  511
                  5.0e-52
E value
Match length
                  119
% identity
                  88
NCBI Description
                  (AC007135) putative 40S ribosomal protein S14 [Arabidopsis
                  thaliana]
Seq. No.
                  137044
Seq. ID
                  ARABL1-039-Q1-B1-B3
Method
                  BLASTX
NCBI GI
                  q4741952
BLAST score
                  265
E value
                  9.0e-24
Match length
                  50
% identity
                  100
NCBI Description
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
                  137045
Seq. No.
Seq. ID
                  ARABL1-039-Q1-B1-B7
Method
                  BLASTX
NCBI GI
                  q4584110
BLAST score
                  320
E value
                  1.0e-29
Match length
                  121
% identity
                  51
NCBI Description
                  (AJ133639) SAH7 protein [Arabidopsis thaliana]
Seq. No.
                  137046
Seq. ID
                  ARABL1-039-Q1-B1-C8
Method
                  BLASTX
NCBI GI
                  q399298
BLAST score
                  217
E value
                  1.0e-17
Match length
                  66
% identity
                  70
NCBI Description
                  STRESS-INDUCED KIN2 PROTEIN (COLD-INDUCED COR6.6 PROTEIN)
                  >gi_1084343_pir__S22529 cold-regulated protein kin2 -
                  Arabidopsis thaliana >gi_16230 emb CAA38894 (X55053) cold
                  regulated [Arabidopsis thaliana]
Seq. No.
                  137047
Seq. ID
                  ARABL1-039-Q1-B1-D2
Method
                  BLASTN
NCBI GI
                  q4803835
BLAST score
                  322
E value
                  0.0e+00
                  322
Match length
% identity
                  Arabidopsis thaliana mRNA for a dynamin-like protein ADL3,
NCBI Description
                  complete cds
```

Seq. No. 137048

Seq. ID ARABL1-039-Q1-B1-E1

Method BLASTN



NCBI GI g4586241 BLAST score 110 E value 2.0e-55 Match length 110 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18

(ESSA project)

Seq. No. 137049

Seq. ID ARABL1-039-Q1-B1-E10

Method BLASTX
NCBI GI g1076302
BLAST score 529
E value 4.0e-54
Match length 108
% identity 100

NCBI Description cold-regulated protein cor15a precursor - Arabidopsis

thaliana >gi_413922_emb_CAA45499_ (X64138) cor15 [Arabidopsis thaliana] >gi 507149 (U01377) cor15a

[Arabidopsis thaliana]

>gi_4559337_gb_AAD22999.1_AC007087_18 (AC007087) cold-regulated protein cor15a precursor [Arabidopsis

thaliana] >gi_444330_prf__1906379A cor15 gene [Arabidopsis

thaliana]

Seq. No. 137050

Seq. ID ARABL1-039-Q1-B1-E9

Method BLASTN
NCBI GI g3063438
BLAST score 60
E value 5.0e-26
Match length 60
% identity 100

NCBI Description Complete sequence of Arabidopsis F22013, complete sequence

[Arabidopsis thaliana]

Seq. No. 137051

Seq. ID ARABL1-039-Q1-B1-F2

Method BLASTX
NCBI GI g2497886
BLAST score 300
E value 3.0e-27
Match length 54
% identity 100

NCBI Description METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B)

>gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis
thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis

thaliana]

Seq. No. 137052

Seq. ID ARABL1-039-Q1-B1-F4

Method BLASTN
NCBI GI g4218109
BLAST score 211
E value 1.0e-115
Match length 275
% identity 94



NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 (ESSAII project)

Seq. No. 137053

Seq. ID ARABL1-039-Q1-B1-F7

Method BLASTN
NCBI GI g2351069
BLAST score 275
E value 1.0e-153
Match length 393
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSH12, complete sequence [Arabidopsis thaliana]

Seq. No. 137054

Seq. ID ARABL1-039-Q1-B1-G10

Method BLASTN
NCBI GI g4115352
BLAST score 317
E value 1.0e-178
Match length 317
% identity 79

NCBI Description Arabidopsis thaliana chromosome II BAC T15J14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137055

Seq. ID ARABL1-039-Q1-B1-H1

Method BLASTN
NCBI GI g4584841
BLAST score 64
E value 1.0e-27
Match length 289
% identity 66

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T23E23,

complete sequence

Seq. No. 137056

Seq. ID ARABL1-039-Q1-B1-H2

Method BLASTN
NCBI GI g3860243
BLAST score 69
E value 9.0e-31
Match length 194
% identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC F15K20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137057

Seq. ID ARABL1-039-Q1-E1-A9

Method BLASTX
NCBI GI g541858
BLAST score 361
E value 2.0e-34
Match length 62
% identity 100

NCBI Description endoxyloglucan transferase - Arabidopsis thaliana

>gi 469484 dbj BAA03921 (D16454) endo-xyloglucan

Seq. No.

Seq. ID

137063

ARABL1-039-Q1-E1-D6

```
transferase [Arabidopsis thaliana] >gi_4063757 (AC005561)
```

```
endo-xyloglucan transferase [Arabidopsis thaliana]
                  137058
Seq. No.
Seq. ID
                  ARABL1-039-Q1-E1-B12
Method
                  BLASTX
                  g3176874
NCBI GI
                  170
BLAST score
                  4.0e-12
E value
Match length
                  45
% identity
                  76
NCBI Description
                  (AF065639) cucumisin-like serine protease [Arabidopsis
                  thaliana]
Seq. No.
                  137059
Seq. ID
                  ARABL1-039-Q1-E1-B3
Method
                  BLASTX
NCBI GI
                  g4741952
BLAST score
                  255
                  1.0e-22
E value
Match length
                  50
% identity
                  96
NCBI Description
                 (AF134126) Lhcb3 protein [Arabidopsis thaliana]
                  137060
Seq. No.
                  ARABL1-039-Q1-E1-C11
Seq. ID
Method
                  BLASTX
                  g3540181
NCBI GI
BLAST score
                  204
                  4.0e-16
E value
                  70
Match length
                  56
% identity
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
                  137061
Seq. No.
Seq. ID
                  ARABL1-039-Q1-E1-C4
                  BLASTN
Method
NCBI GI
                  q4589421
BLAST score
                  72
                  8.0e-33
E value
Match length
                  112
% identity
                  97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                  K5K13, complete sequence
                  137062
Seq. No.
Seq. ID
                  ARABL1-039-Q1-E1-D4
Method
                  BLASTX
NCBI GI
                  q1370186
BLAST score
                  190
                  2.0e-14
E value
Match length
                  40
% identity
NCBI Description
                 (Z73942) RAB7C [Lotus japonicus]
```



```
BLASTN
Method
                  g2462930
NCBI GI
                  79
BLAST score
                  2.0e-36
E value
Match length
                  100
% identity
                  100
                  dArabidopsis thaliana mRNA for UDP-glucose:sterol
NCBI Description
                  glucosyltransferase
Seq. No.
                  137064
                  ARABL1-039-Q1-E1-E1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4586241
BLAST score
                  110
E value
                  2.0e-55
Match length
                  110
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18
NCBI Description
                  (ESSA project)
                  137065
Seq. No.
Seq. ID
                  ARABL1-039-Q1-E1-E9
Method
                  BLASTN
NCBI GI
                  g3063438
BLAST score
                  60
                5.0e-26
E value
Match length
                  60
% identity
                  100
                  Complete sequence of Arabidopsis F22013, complete sequence
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  137066
Seq. ID
                  ARABL1-039-Q1-E1-F7
Method
                  BLASTN
                  g2351069
NCBI GI
BLAST score
                  152
E value
                  2.0e-80
                  164
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSH12, complete sequence [Arabidopsis thaliana]
                  137067
Seq. No.
                  ARABL1-04-Q1-B1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4741952
BLAST score
                  646
                  8.0e-68
E value
                  122
Match length
                  75
% identity
```

NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No. 137068

Seq. ID ARABL1-04-Q1-B1-B6

Method BLASTX NCBI GI q4662642 BLAST score 668



```
2.0e-70
E value
Match length
                   128
% identity
                   100
                  (AC006429) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   137069
Seq. No.
Seq. ID
                   ARABL1-04-Q1-B1-B8
Method
                   BLASTX
NCBI GI
                   g464986
BLAST score
                   558
E value
                   2.0e-57
Match length
                   104
% identity
                   99
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                   >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana
                   >gi 297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639)
                   ubiquitin conjugating enzyme [Arabidopsis thaliana]
                   >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
enzyme E2 [Arabidopsis thaliana]
                   >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
                   ligase UBC9 [Arabidopsis thaliana]
Seq. No.
                   137070
Seq. ID
                   ARABL1-04-Q1-B1-C3
Method
                   BLASTX
NCBI GI
                   g3170230
BLAST score
                   462
                   3.0e-46
E value
                   134
Match length
% identity
                   66
                   (AF041848) fructose-6-phosphate 2-kinase
NCBI Description
                   /fructose-2,6-bisphosphatase [Spinacia oleracea]
                   137071
Seq. No.
Seq. ID
                   ARABL1-04-Q1-B1-C8
Method
                   BLASTX
NCBI GI
                   g1709534
                   590
BLAST score
                   3.0e-61
E value
Match length
                   133
                   89
% identity
                  DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE A (P5CS A)
NCBI Description
                   [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK);
                   GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR)
                   (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE)
                   (GLUTAMYL-GAMMA-SEMIALDE... >gi_2129572_pir__S66637
                   delta-1-pyrroline-5-carboxylate synthetase - Arabidopsis
                   thaliana >gi 829100 emb CAA60740 (X87330)
                   pyrroline-5-carboxylate synthetase [Arabidopsis thaliana]
                   >gi 870866 emb CAA60446 (X86777) pyrroline-5-carboxylate
                   synthetase A [Arabidopsis thaliana]
```

delta-1-pyrroline 5-carboxylase synthetase, P5C1

>gi_1041248_emb_CAA61593_ (X89414) pyrroline-5-carboxylate synthase [Arabidopsis thaliana] >gi 2642162 (AC003000)



[Arabidopsis thaliana]

```
137072
Seq. No.
Seq. ID
                  ARABL1-04-Q1-B1-D1
Method
                  BLASTN
NCBI GI
                  g3335331
                  327
BLAST score
E value
                  0.0e + 00
Match length
                  327
                  100
% identity
                  Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  137073
Seq. ID
                  ARABL1-04-Q1-B1-D5
Method
                  BLASTX
NCBI GI
                  g4469022
BLAST score
                  427
E value
                  2.0e-42
Match length
                  86
                  98
% identity
NCBI Description
                   (AL035602) cytochrome P450-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  137074
Seq. ID
                  ARABL1-04-Q1-B1-D6
Method
                  BLASTX
NCBI GI
                  q430947
BLAST score
                  541
E value
                  2.0e-55
Match length
                  133
% identity
                  80
NCBI Description
                   (U01103) PSI type III chlorophyll a/b-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                  137075
Seq. ID
                  ARABL1-04-Q1-B1-E8
Method
                  BLASTX
NCBI GI
                  g2127972
BLAST score
                  159
                   9.0e-11
E value
                  54
Match length
                   50
% identity
                  HIT protein homolog - Methanococcus jannaschii
NCBI Description
Seq. No.
                  137076
Seq. ID
                  ARABL1-04-Q1-B1-F1
Method
                  BLASTX
NCBI GI
                  g3068713
BLAST score
                   505
                   3.0e-51
E value
                  131
Match length
% identity
                  81
NCBI Description
                  (AF049236) unknown [Arabidopsis thaliana]
```

16395

137077

ARABL1-04-Q1-B1-G1

Seq. No. Seq. ID

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The second secon
```

```
Method BLASTN
NCBI GI g4572664
BLAST score 128
E value 9.0e-66
Match length 249
% identity 86
```

NCBI Description Arabidopsis thaliana chromosome II BAC F25P17 genomic

sequence, complete sequence

Seq. No. 137078

Seq. ID ARABL1-04-Q1-B1-G3

Method BLASTN
NCBI GI g3152602
BLAST score 135
E value 5.0e-70
Match length 135
% identity 50

NCBI Description Arabidopsis thaliana chromosome II BAC F27L4 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137079

Seq. ID ARABL1-04-Q1-B1-G5

Method BLASTX
NCBI GI g4678261
BLAST score 463
E value 2.0e-46
Match length 94
% identity 100

NCBI Description (AL049657) putative proteasome regulatory subunit

[Arabidopsis thaliana]

Seq. No. 137080

Seq. ID ARABL1-04-Q1-B1-H6

Method BLASTN
NCBI GI g2656028
BLAST score 219
E value 1.0e-120
Match length 324
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNF13

Seq. No. 137081

Seq. ID ARABL1-040-Q1-B1-A11

Method BLASTX
NCBI GI 94185599
BLAST score 153
E value 5.0e-10
Match length 107
% identity 37

NCBI Description (AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana

triflora]

Seq. No. 137082

Seq. ID ARABL1-040-Q1-B1-A2

Method BLASTX NCBI GI g543751



BLAST score 164 E value 7.0e-12 Match length 31 % identity 100

NCBI Description 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE) (ETHYLENE-FORMING ENZYME) (EFE) >gi 541861 pir JT0755

ethylene-forming enzyme - Arabidopsis thaliana

>gi_16254_emb_CAA47251_ (X66719) ethylene-forming enzyme

[Arabidopsis thaliana]

Seq. No. 137083

Seq. ID ARABL1-040-Q1-B1-D7

Method BLASTN
NCBI GI g4662628
BLAST score 106
E value 2.0e-52
Match length 210
% identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC F27010 genomic

sequence, complete sequence

Seq. No. 137084

Seq. ID ARABL1-040-Q1-B1-D9

Method BLASTX
NCBI GI 94585882
BLAST score 482
E value 1.0e-48
Match length 92
% identity 100

NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 137085

Seq. ID ARABL1-040-Q1-B1-E11

Method BLASTX
NCBI GI g115783
BLAST score 479
E value 2.0e-48
Match length 90
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 137086

Seq. ID ARABL1-040-Q1-B1-E8

Method BLASTX
NCBI GI g3335372
BLAST score 256
E value 4.0e-22
Match length 112
% identity 45

NCBI Description (AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No. 137087

Seq. ID ARABL1-040-Q1-B1-G9



```
Method
NCBI GI
                  a3241923
BLAST score
                  158
                  6.0e-84
E value
                  158
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MMN10, complete sequence [Arabidopsis thaliana]
                  137088
Seq. No.
                  ARABL1-040-Q1-B1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2760606
BLAST score
                  432
                  9.0e-43
E value
Match length
                  109
                  72
% identity
                  (AB001568) phospholipid hydroperoxide glutathione
NCBI Description
                  peroxidase-like protein [Arabidopsis thaliana] >gi_3004869
                   (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis
                  thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500)
                  phospholipid hydroperoxide glutathione peroxidase
                   [Arabidopsis thaliana]
Seq. No.
                  137089
                  ARABL1-040-Q1-E1-C12
Seq. ID
                  BLASTN
Method
                  q2088638
NCBI GI
BLAST score
                  389
E value
                  0.0e + 00
Match length
                  389
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T28M21 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   137090
Seq. ID
                  ARABL1-040-Q1-E1-D5
Method
                  BLASTN
NCBI GI
                   q2584827
BLAST score
                   92
E value
                   3.0e-44
Match length
                   293
                   97
% identity
                  Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   137091
Seq. ID
                   ARABL1-040-Q1-E1-E10
Method
                   BLASTN
NCBI GI
                   g3063690
BLAST score
                   164
```

3.0e-87 E value 196 Match length 96 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11

(ESSAII project)



```
Seq. No.
Seq. ID
                  ARABL1-040-Q1-E1-F12
Method
                  BLASTN
NCBI GI
                  g1707006
BLAST score
                  113
                  4.0e-57
E value
Match length
                  157
                  93
% identity
                  Arabidopsis thaliana chromosome II BAC T1B8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  137093
Seq. ID
                  ARABL1-040-Q1-E1-F4
Method
                  BLASTX
NCBI GI
                  q131398
BLAST score
                  283
                  2.0e-25
E value
Match length
                  65
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                  >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                   - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >gi_3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide gb X55970. ESTs gb_Z17693, gb_N37616,
                  gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                  gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
                  come from this gene. [Arabidopsis
Seq. No.
                  137094
                  ARABL1-040-Q1-E1-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3241927
                  200
BLAST score
E value
                  1.0e-108
                  309
Match length
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTE17, complete sequence [Arabidopsis thaliana]
                  137095
Seq. No.
Seq. ID
                  ARABL1-040-Q1-E1-G9
                  BLASTN
Method
                  g3241923
NCBI GI
BLAST score
                  158
E value
                   6.0e-84
                  158
Match length
```

100 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MMN10, complete sequence [Arabidopsis thaliana]

137096 Seq. No.

Seq. ID ARABL1-040-Q1-E1-H1

Method BLASTN NCBI GI g2618599 BLAST score 310 E value 1.0e-174



Match length 100 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone: NCBI Description

MBD2, complete sequence [Arabidopsis thaliana]

137097 Seq. No.

ARABL1-041-Q1-B1-A10 Seq. ID

Method BLASTX g2244904 NCBI GI 476 BLAST score 6.0e-48 E value 117 Match length 90 % identity

(Z97339) similar to hypothetical protein C02F5.7 - Caenorha NCBI Description

[Arabidopsis thaliana]

137098 Seq. No.

ARABL1-041-Q1-B1-B9 Seq. ID

BLASTN Method g4191760 NCBI GI 86 BLAST score 4.0e-41 E value 130 Match length 92 % identity

Genomic sequence for Arabidopsis thaliana BAC F17F8, NCBI Description

complete sequence [Arabidopsis thaliana]

137099 Seq. No.

ARABL1-041-Q1-B1-C7 Seq. ID

BLASTN Method q4220640 NCBI GI 344 BLAST score 0.0e + 00E value 344 Match length 100 % identity

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MPE11, complete sequence [Arabidopsis thaliana]

137100 Seq. No.

ARABL1-041-Q1-B1-C8 Seq. ID

BLASTN Method g3522932 NCBI GI BLAST score 44 2.0e-15 E value Match length 99 93 % identity

Arabidopsis thaliana chromosome II BAC F14M4 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

137101 Seq. No.

ARABL1-041-Q1-B1-E9 Seq. ID

BLASTN Method g4262221 NCBI GI 226 BLAST score 1.0e-124 E value 229 Match length 100 % identity



NCBI Description Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137102

Seq. ID ARABL1-041-Q1-B1-F4

Method BLASTX
NCBI GI g2338712
BLAST score 243
E value 1.0e-20
Match length 46
% identity 98

NCBI Description (AF013959) metallothionein-like protein [Arabidopsis

thaliana]

Seq. No. 137103

Seq. ID ARABL1-041-Q1-B1-G4

Method BLASTX
NCBI GI g1922242
BLAST score 199
E value 2.0e-15
Match length 36
% identity 100

NCBI Description (Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No. 137104

Seq. ID ARABL1-041-Q1-B1-G5

Method BLASTN
NCBI GI g2749918
BLAST score 100
E value 2.0e-49
Match length 121
% identity 94

NCBI Description Arabidopsis thaliana chromosome I BAC F3I6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137105

Seq. ID ARABL1-041-Q1-B1-G7

Method BLASTX
NCBI GI 94584540
BLAST score 427
E value 3.0e-42
Match length 106
% identity 84

NCBI Description (AL049608) putative protein [Arabidopsis thaliana]

Seq. No. 137106

Seq. ID ARABL1-041-Q1-B1-H5

Method BLASTX
NCBI GI g3169287
BLAST score 640
E value 3.0e-67
Match length 128
% identity 99

NCBI Description (AF050673) vacuolar H+-ATPase catalytic subunit [Gossypium

hirsutum]

Seq. No. 137107



Seq. ID ARABL1-041-Q1-B1-H7

Method BLASTN
NCBI GI g2281648
BLAST score 165
E value 1.0e-87
Match length 165
% identity 100

NCBI Description Arabidopsis thaliana AP2 domain containing protein RAP2.12

mRNA, partial cds

Seq. No. 137108

Seq. ID ARABL1-041-Q1-B1-H9

Method BLASTX
NCBI GI g586145
BLAST score 149
E value 1.0e-09
Match length 99
% identity 40

NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT

PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP)

>gi_488848_emb_CAA55894_ (X79332) Rieske iron sulphur

protein [Solanum tuberosum]

Seq. No. 137109

Seq. ID ARABL1-041-Q1-E1-A12

Method BLASTN
NCBI GI g2264304
BLAST score 325
E value 0.0e+00
Match length 333
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBG8, complete sequence [Arabidopsis thaliana]

Seq. No. 137110

Seq. ID ARABL1-041-Q1-E1-B7

Method BLASTX
NCBI GI g3123296
BLAST score 219
E value 6.0e-18
Match length 43
% identity 100

NCBI Description CALMODULIN-RELATED PROTEIN 3, TOUCH-INDUCED >gi 598067

(L34546) calmodulin-related protein [Arabidopsis thaliana]

Seq. No. 137111

Seq. ID ARABL1-041-Q1-E1-C10

Method BLASTN
NCBI GI g2098816
BLAST score 176
E value 2.0e-94
Match length 350
% identity 100

NCBI Description Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No. 137112

Seq. ID ARABL1-041-Q1-E1-C9

Method NCBI GI



```
Method
                   BLASTN
NCBI GI
                   q2347177
BLAST score
                   45
E value
                   3.0e-16
Match length
                   153
                   82
% identity
                  Arabidopsis thaliana catalase 3 (CAT3) gene, complete cds
NCBI Description
                  137113
Seq. No.
Seq. ID
                  ARABL1-041-Q1-E1-D11
Method
                  BLASTN
NCBI GI
                   q2264305
BLAST score
                   266
E value
                   1.0e-148
                   373
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBK23, complete sequence [Arabidopsis thaliana]
                   137114
Seq. No.
                  ARABL1-041-Q1-E1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2398679
BLAST score
                   411
                   2.0e-40
E value
                   84
Match length
                   92
% identity
                   (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
NCBI Description
                   synthase [Morinda citrifolia]
Seq. No.
                   137115
Seq. ID
                   ARABL1-041-Q1-E1-E3
Method
                   BLASTX
NCBI GI
                   q3123188
BLAST score
                   252
                   1.0e-21
E value
Match length
                   51
% identity
                   94
                   CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis
NCBI Description
                   thaliana] >gi 2511726 (AF021937) catalase 3 [Arabidopsis
                   thaliana]
                   137116
Seq. No.
Seq. ID
                   ARABL1-041-Q1-E1-E9
Method
                   BLASTN
NCBI GI
                   g4262221
BLAST score
                   217
                   1.0e-119
E value
Match length
                   229
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC F10A8 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   137117
Seq. ID
                   ARABL1-041-Q1-E1-G5
```

16403

BLASTN

g2749918



BLAST score E value 2.0e-49 Match length 121 94 % identity

Arabidopsis thaliana chromosome I BAC F3I6 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137118

Seq. ID ARABL1-041-Q1-E1-H7

Method BLASTN NCBI GI g2281648 BLAST score 351 E value 0.0e + 00Match length 351 % identity 100

Arabidopsis thaliana AP2 domain containing protein RAP2.12 NCBI Description

mRNA, partial cds

Seq. No. 137119

Seq. ID ARABL1-042-Q1-B1-A10

Method BLASTX g1170089 NCBI GI BLAST score 224 E value 6.0e-19 Match length 46 % identity 100

NCBI Description GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)

>gi 481822 pir S39542 probable glutathione transferase (EC

2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione

S-transferase [Arabidopsis thaliana]

Seq. No. 137120

Seq. ID ARABL1-042-Q1-B1-A9

Method BLASTX NCBI GI q3121825 BLAST score 245 E value 7.0e-21 Match length 93 % identity 56

2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC NCBI Description

ANTIOXIDANT PROTEIN) >gi 1498247 emb CAA63910 (X94219)

bas1 protein [Spinacia oleracea]

Seq. No. 137121

Seq. ID ARABL1-042-Q1-B1-B10

Method BLASTX NCBI GI q3367576 BLAST score 523 2.0e-53 E value Match length 126 % identity

NCBI Description (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

137122 Seq. No.

Seq. ID ARABL1-042-Q1-B1-B11



Method BLASTN a4220638 NCBI GI BLAST score 384 0.0e + 00E value 387 Match length 100 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MIF21, complete sequence [Arabidopsis thaliana]

Seq. No. 137123

Seq. ID ARABL1-042-Q1-B1-C9

Method BLASTX NCBI GI q2119848 BLAST score 273 2.0e-24 E value 66 Match length % identity

chlorophyll a/b-binding protein type I precursor Lhb1B1 -NCBI Description

Arabidopsis thaliana >gi 16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]

137124 Seq. No.

Seq. ID ARABL1-042-Q1-B1-E12

Method BLASTX NCBI GI g4583542 BLAST score 477 4.0e-48 E value Match length 126 % identity 83

(Y16847) 16 kDa polypeptide of oxygen-evolving complex NCBI Description

[Arabidopsis thaliana]

137125 Seq. No.

ARABL1-042-Q1-B1-E3 Seq. ID

Method BLASTN g2673901 NCBI GI 142 BLAST score 2.0e-74 E value 142 Match length 100 % identity

Arabidopsis thaliana chromosome II BAC T24P15 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.

137126

Seq. ID ARABL1-042-Q1-B1-G4

BLASTX Method NCBI GI g3242075 BLAST score 144 3.0e-09 E value Match length 31 % identity

NCBI Description (Z97059) S-adenosyl-L-homocysteine hydrolase [Arabidopsis

NCBI GI

E value Match length

BLAST score

g297877

200 1.0e-109

221



```
thaliana]
                  137127
Seq. No.
                  ARABL1-042-Q1-E1-C11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2959729
BLAST score
                  62
                  2.0e-26
E value
Match length
                  160
% identity
                  100
NCBI Description Arabidopsis thaliana mRNA for GATA transcription factor
Seq. No.
                  137128
Seq. ID
                  ARABL1-042-Q1-E1-D6
Method
                  BLASTN
NCBI GI
                  q4220640
BLAST score
                  158
E value
                  8.0e-84
Match length
                  210
                  94
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MPE11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  137129
Seq. ID
                  ARABL1-042-Q1-E1-E2
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                  330
E value
                  6.0e-31
Match length
                  63
% identity
                  100
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
                  137130
Seq. No.
Seq. ID
                  ARABL1-042-Q1-E1-E3
                  BLASTN
Method
                  g2673901
NCBI GI
                  142
BLAST score
                  2.0e-74
E value
                  142
Match length
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC T24P15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  137131
Seq. No.
Seq. ID
                  ARABL1-042-Q1-E1-F6
Method
                  BLASTN
```



% identity 97
NCBI Description A.thaliana UBC10 mRNA for ubiquitin conjugating enzyme
homolog >gi_349212_gb_L00640_ATHUBCC Arabidopsis thaliana
ubiquitin conjugating enzyme mRNA, complete cds

Seq. No. 137132

Seq. ID ARABL1-042-Q1-E1-G2

Method BLASTN
NCBI GI g499161
BLAST score 58
E value 2.0e-24
Match length 141
% identity 84

NCBI Description A.thaliana mRNA Athb-6

Seq. No. 137133

Seq. ID ARABL1-042-Q1-E1-H12

Method BLASTN
NCBI GI g3449327
BLAST score 296
E value 1.0e-166
Match length 296
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCA23, complete sequence [Arabidopsis thaliana]

Seq. No. 137134

Seq. ID ARABL1-043-Q1-B1-A6

Method BLASTX
NCBI GI g2828293
BLAST score 226
E value 2.0e-48
Match length 95
% identity 94

NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No. 137135

Seq. ID ARABL1-043-Q1-B1-A8

Method BLASTN
NCBI GI g16300
BLAST score 34
E value 7.0e-10
Match length 169
% identity 95

NCBI Description A.thaliana mRNA for glycine rich protein

>gi_166836_gb L00648_ATHRBPA Arabidopsis thaliana

RNA-binding protein mRNA, complete cds

Seq. No. 137136

Seq. ID ARABL1-043-Q1-B1-B10

Method BLASTX
NCBI GI g2894601
BLAST score 336
E value 8.0e-32
Match length 79
% identity 76

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Method

NCBI GI

BLASTX

g4038352



```
Seq. No.
                  137137
Seq. ID
                  ARABL1-043-Q1-B1-B8
Method
                  BLASTX
NCBI GI
                  g3128177
BLAST score
                  632
E value
                  3.0e-66
                  126
Match length
% identity
                  100
                  (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  137138
Seq. ID
                  ARABL1-043-Q1-B1-C2
Method
                  BLASTX
NCBI GI
                  q4522006
BLAST score
                  375
                  2.0e-36
E value
Match length
                  77
                  99
% identity
                  (AC007069) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  137139
Seq. No.
Seq. ID
                  ARABL1-043-Q1-B1-C3
Method
                  BLASTN
NCBI GI
                  q3169169
BLAST score
                  355
                  0.0e + 00
E value
Match length
                  359
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F21P24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  137140
Seq. ID
                  ARABL1-043-Q1-B1-C4
Method
                  BLASTN
NCBI GI
                  q4589439
BLAST score
                  96
E value
                  9.0e-47
Match length
                  169
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQM1, complete sequence
Seq. No.
                  137141
Seq. ID
                  ARABL1-043-Q1-B1-C5
Method
                  BLASTX
                  g2795809
NCBI GI
BLAST score
                  542
E value
                  1.0e-55
                  123
Match length
                  79
% identity
                  (AC003674) putative expansin [Arabidopsis thaliana]
NCBI Description
                  137142
Seq. No.
Seq. ID
                  ARABL1-043-Q1-B1-E10
```



BLAST score 346 E value 1.0e-32 Match length 124 % identity 54

NCBI Description (AF098951) breast cancer resistance protein [Homo sapiens]

Seq. No. 137143

Seq. ID ARABL1-043-Q1-B1-E9

Method BLASTX
NCBI GI g3287693
BLAST score 670
E value 1.0e-70
Match length 125
% identity 100

NCBI Description (AC003979) Similar to LIM17 gene product gb_1653769 from

the genome of Synechocystis sp. gb D90916. [Arabidopsis

thaliana]

Seq. No. 137144

Seq. ID ARABL1-043-Q1-B1-G12

Method BLASTN
NCBI GI g4325340
BLAST score 223
E value 1.0e-122
Match length 338
% identity 99

NCBI Description Arabidopsis thaliana BAC T1J1

Seq. No. 137145

Seq. ID ARABL1-043-Q1-B1-G4

Method BLASTN
NCBI GI g3985952
BLAST score 249
E value 1.0e-138
Match length 286
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MRC8, complete sequence [Arabidopsis thaliana]

Seq. No. 137146

Seq. ID ARABL1-043-Q1-E1-A6

Method BLASTN
NCBI GI g2828278
BLAST score 138
E value 9.0e-72
Match length 254
% identity 89

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16

(ESSAII project)

Seq. No. 137147

Seq. ID ARABL1-043-Q1-E1-A8

Method BLASTN
NCBI GI g166656
BLAST score 129
E value 1.0e-66
Match length 184



% identity

NCBI Description Arabidopsis thaliana Ccr2 mRNA, partial ORF

Seq. No.

137148

Seq. ID

ARABL1-043-Q1-E1-B2

Method

BLASTN

NCBI GI BLAST score g3702728

E value

166 2.0e-88

Match length

299

% identity

95

NCBI Description

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19M13, complete sequence [Arabidopsis thaliana]

Seq. No.

137149

Seq. ID

ARABL1-043-Q1-E1-B7

Method NCBI GI BLASTX g2507587

BLAST score

235

E value

1.0e-19

Match length % identity

41 100

NCBI Description

METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G)

>gi 1361998 pir S57861 metallothionein 2a - Arabidopsis thaliana >gi_555976 (U15108) metallothionein-like protein

[Arabidopsis thaliana] >gi_1580892_prf__2116236A

metallothionein 1 [Arabidopsis thaliana]

Seq. No.

137150 BLASTN

g2642427

Seq. ID

ARABL1-043-Q1-E1-C3

Method NCBI GI BLAST score E value

2.0e-54 216

109

% identity NCBI Description

Match length

99 Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.

137151

Seq. ID

ARABL1-043-Q1-E1-C6

Method NCBI GI BLASTN g3169169

BLAST score E value

96

Match length

6.0e-47 152

% identity

NCBI Description

Arabidopsis thaliana chromosome II BAC F21P24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.

137152

Seq. ID Method

ARABL1-043-Q1-E1-D3

NCBI GI

BLASTN q2832358

BLAST score

52

E value Match length

9.0e-21 108



% identity 87
NCBI Description Arabidopsis thaliana mRNA for HMG betal protein

MODI Description intertacepose charter

Seq. No. 137153

Seq. ID ARABL1-044-Q1-B1-A6

Method BLASTN
NCBI GI g3445196
BLAST score 44
E value 2.0e-15

Match length 191 % identity 82

NCBI Description Arabidopsis thaliana chromosome II BAC T20K9 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137154

Seq. ID ARABL1-044-Q1-B1-B1

Method BLASTX
NCBI GI g115783
BLAST score 512
E value 3.0e-52
Match length 96
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 137155

Seq. ID ARABL1-044-Q1-B1-B4

Method BLASTN
NCBI GI g4589415
BLAST score 119
E value 2.0e-60
Match length 179
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K14A3, complete sequence

Seq. No. 137156

Seq. ID ARABL1-044-Q1-B1-C11

Method BLASTX
NCBI GI g2598589
BLAST score 219
E value 8.0e-18
Match length 73
% identity 56

NCBI Description (Y15367) MtN19 [Medicago truncatula]

Seq. No. 137157

Seq. ID ARABL1-044-Q1-B1-C2

Method BLASTN
NCBI GI g3005688
BLAST score 215
E value 1.0e-117
Match length 362
% identity 100

NCBI Description Arabidopsis thaliana AT4 mRNA sequence



```
137158
Seq. No.
Seq. ID
                  ARABL1-044-Q1-B1-C8
                  BLASTN
Method
NCBI GI
                  g2760164
                  398
BLAST score
                  0.0e+00
E value
                  398
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K18P6, complete sequence [Arabidopsis thaliana]
                  137159
Seq. No.
                  ARABL1-044-Q1-B1-D8
Seq. ID
Method
                  BLASTN
                  g4455229
NCBI GI
BLAST score
                  252
                  1.0e-139
E value
                  380
Match length
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23
NCBI Description
                   (ESSAII project)
                  137160
Seq. No.
Seq. ID
                  ARABL1-044-Q1-B1-D9
Method
                  BLASTX
                  g4468999
NCBI GI
                  108
BLAST score
                  8.0e-05
E value
                  97
Match length
% identity
                  20
                  (Z97342) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                  137161
Seq. No.
Seq. ID
                  ARABL1-044-Q1-B1-G2
                  BLASTX
Method
NCBI GI
                  g2828292
BLAST score
                  492
                  8.0e-50
E value
                  92
Match length
                  100
% identity
                   (AL021687) neoxanthin cleavage enzyme-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  137162
Seq. No.
Seq. ID
                  ARABL1-044-Q1-B1-G8
                  BLASTX
Method
NCBI GI
                  g4544374
BLAST score
                  201
                   6.0e-16
E value
Match length
                  54
                  74
% identity
                  (AC006920) unknown protein [Arabidopsis thaliana]
NCBI Description
```

16412

137163

BLASTX

ARABL1-044-Q1-B1-H5

Seq. No. Seq. ID

Method

Seq. No.

Seq. ID

Method

NCBI GI

E value

BLAST score

137168

BLASTN

85

g2760316

3.0e-40

ARABL1-044-Q1-E1-E10



```
NCBI GI
                   a4583542
BLAST score
                   495
E value
                   4.0e-50
Match length
                   130
                   83
% identity
NCBI Description
                   (Y16847) 16 kDa polypeptide of oxygen-evolving complex
                   [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  137164
                  ARABL1-044-Q1-B1-H7
Method
                  BLASTX
NCBI GI
                  q2281631
BLAST score
                   591
E value
                  2.0e-61
Match length
                  110
                   100
% identity
                   (AF003096) AP2 domain containing protein RAP2.3
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  137165
Seq. ID
                  ARABL1-044-Q1-E1-A12
Method
                  BLASTX
NCBI GI
                  g3582341
BLAST score
                  220
                   5.0e-18
E value
Match length
                  85
% identity
                   60
NCBI Description
                   (AC005496) putative flavonol 3-o-glucosyltransferase
                   [Arabidopsis thaliana]
Seq. No.
                   137166
Seq. ID
                  ARABL1-044-Q1-E1-D5
Method
                  BLASTX
NCBI GI
                   g3763923
BLAST score
                   233
                   1.0e-19
E value
Match length
                   50
% identity
                   90
NCBI Description
                  (AC004450) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   137167
Seq. ID
                  ARABL1-044-Q1-E1-D8
Method
                  BLASTN
NCBI GI
                   g4678258
BLAST score
                   245
E value
                  1.0e-135
Match length
                   339
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F617
                   (ESSA project)
```



```
Match length 117 % identity 93
```

NCBI Description The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 137169

Seq. ID ARABL1-044-Q1-E1-E11

Method BLASTN
NCBI GI g1708776
BLAST score 335
E value 0.0e+00
Match length 355
% identity 99

NCBI Description A.thaliana mRNA for potassium channel

Seq. No. 137170

Seq. ID ARABL1-044-Q1-E1-E2

Method BLASTN
NCBI GI g2760167
BLAST score 193
E value 1.0e-105
Match length 193
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCO15, complete sequence [Arabidopsis thaliana]

Seq. No. 137171

Seq. ID ARABL1-044-Q1-E1-E6

Method BLASTN
NCBI GI g2780191
BLAST score 167
E value 3.0e-89
Match length 207
% identity 95

NCBI Description Arabidopsis thaliana nap gene

Seq. No. 137172

Seq. ID ARABL1-044-Q1-E1-F2

Method BLASTN
NCBI GI 94559344
BLAST score 178
E value 8.0e-96
Match length 182
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F27C12 genomic

sequence, complete sequence

Seq. No. 137173

Seq. ID ARABL1-044-Q1-E1-G8

Method BLASTX
NCBI GI 94544374
BLAST score 247
E value 1.0e-21
Match length 49
% identity 92

NCBI Description (AC006920) unknown protein [Arabidopsis thaliana]



Seq. No. 137174

Seq. ID ARABL1-045-Q1-B1-A8

Method BLASTX NCBI GI q4586256 BLAST score 552 E value 8.0e-57 Match length 127 % identity 86

NCBI Description (AL049640) probable photosystem I chain XI precursor

[Arabidopsis thaliana]

Seq. No. 137175

Seq. ID ARABL1-045-Q1-B1-B1

Method BLASTX NCBI GI q1769905 BLAST score 437 E value 2.0e-43 Match length 123 % identity 69

NCBI Description (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)

[Arabidopsis thaliana]

Seq. No. 137176

Seq. ID ARABL1-045-Q1-B1-B10

Method BLASTN g2760316 NCBI GI BLAST score 380 E value 0.0e + 00Match length 384 % identity 100

NCBI Description The sequence of BAC F1N21 from Arabidopsis thaliana

chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 137177

Seq. ID ARABL1-045-Q1-B1-B6

Method BLASTX NCBI GI g2119846 BLAST score 637 E value 8.0e-67 Match length 122 % identity

NCBI Description

chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 137178

Seq. ID ARABL1-045-Q1-B1-C5

Method BLASTN NCBI GI g3098611 BLAST score 306 E value 1.0e-172 Match length 360 97 % identity



NCBI Description Arabidopsis thaliana senescence associated gene (SAG20) mRNA, partial cds

Seq. No. 137179

Seq. ID ARABL1-045-Q1-B1-C6

Method BLASTN
NCBI GI g3098611
BLAST score 113
E value 7.0e-57
Match length 197
% identity 91

NCBI Description Arabidopsis thaliana senescence associated gene (SAG20)

mRNA, partial cds

Seq. No. 137180

Seq. ID ARABL1-045-Q1-B1-D1

Method BLASTX
NCBI GI g3766248
BLAST score 440
E value 1.0e-43
Match length 102
% identity 81

NCBI Description (Y18227) blue copper binding-like protein [Arabidopsis

thaliana]

Seq. No. 137181

Seq. ID ARABL1-045-Q1-B1-D3

Method BLASTN
NCBI GI g3766106
BLAST score 25
E value 2.0e-04
Match length 181
% identity 69

NCBI Description Arabidopsis thaliana chromosome 1 BAC F9K20 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 137182

Seq. ID ARABL1-045-Q1-B1-D9

Method BLASTN
NCBI GI g397481
BLAST score 26
E value 6.0e-05
Match length 275
% identity 95

NCBI Description A.thaliana hsc70 mRNA for heat shock cognate protein

Seq. No. 137183

Seq. ID ARABL1-045-Q1-B1-E11

Method BLASTX
NCBI GI g1890352
BLAST score 678
E value 1.0e-71
Match length 126
% identity 60

NCBI Description (X91398) transcription factor L2 [Arabidopsis thaliana]

Seq. No. 137184



```
ARABL1-045-Q1-B1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4490323
                  536
BLAST score
                  6.0e-55
E value
                  132
Match length
% identity
                  (AJ131464) nitrate transporter [Arabidopsis thaliana]
NCBI Description
                  137185
Seq. No.
Seq. ID
                  ARABL1-045-Q1-B1-E8
Method
                  BLASTX
NCBI GI
                  q4585977
                  379
BLAST score
                  1.0e-36
E value
Match length
                  82
                  78
% identity
                  (AC005287) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  137186
Seq. No.
                  ARABL1-045-Q1-B1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4455318
BLAST score
                  290
                  3.0e-26
E value
Match length
                  117
                   50
% identity
                  (AL035528) glycine hydroxymethyltransferase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   137187
Seq. No.
                   ARABL1-045-Q1-B1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4688596
BLAST score
                   463
E value
                   2.0e-46
Match length
                   104
                   86
% identity
                   (AJ005682) inositol 1,4,5-trisphosphate 5-phosphatase
NCBI Description
                   [Arabidopsis thaliana]
                   137188
Seq. No.
                   ARABL1-045-Q1-E1-A5
Seq. ID
Method
                   BLASTN
                   g4220510
NCBI GI
BLAST score
                   216
E value
                   1.0e-118
Match length
                   240
                   97
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
                   (ESSAII project)
```

137189 Seq. No.

Seq. ID ARABL1-045-Q1-E1-B9

BLASTN Method NCBI GI g4519183

BLAST score 117



1.0e-59 E value Match length 121 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K15C23, complete sequence

137190 Seq. No.

Seq. ID ARABL1-046-Q1-B1-A10

Method BLASTX g2464914 NCBI GI BLAST score 272 E value 5.0e-24 Match length 106 % identity 55

NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]

137191 Seq. No.

Seq. ID ARABL1-046-Q1-B1-B12

Method BLASTN NCBI GI g3641835 BLAST score 173 7.0e-93 E value 173 Match length % identity 81

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20

(ESSAII project)

Seq. No. 137192

Seq. ID ARABL1-046-Q1-B1-C12

Method BLASTX g125576 NCBI GI 394 BLAST score 2.0e-38 E value Match length 100 % identity 81

NCBI Description PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)

(PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana

>gi 16441 emb CAA41155 (X58149) Ribulose-5-phosphate

kinase [Arabidopsis thaliana]

Seq. No. 137193

Seq. ID ARABL1-046-Q1-B1-C8

Method BLASTX NCBI GI g4091810 BLAST score 647 E value 5.0e-68 Match length 127 % identity 98

NCBI Description (AF053345) fatty acid elongase 3-ketoacyl-CoA synthase 1

[Arabidopsis thaliana]

137194 Seq. No.

Seq. ID ARABL1-046-Q1-B1-G8

Method BLASTX NCBI GI g1769905 BLAST score 437



E value 2.0e-43
Match length 123
% identity 69

NCBI Description (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)

[Arabidopsis thaliana]

Seq. No. 137195

Seq. ID ARABL1-046-Q1-B1-H1

Method BLASTX
NCBI GI g4512684
BLAST score 453
E value 3.0e-45
Match length 99
% identity 92

NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]

>gi_4559324_gb_AAD22986.1_AC007087_5 (AC007087) unknown

protein [Arabidopsis thaliana]

Seq. No. 137196

Seq. ID ARABL1-046-Q1-B1-H5

Method BLASTN
NCBI GI g4056476
BLAST score 68
E value 2.0e-30
Match length 108
% identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC F3G5 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137197

Seq. ID ARABL1-046-Q1-E1-D11

Method BLASTN
NCBI GI g2924733
BLAST score 272
E value 1.0e-151
Match length 308
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUF9, complete sequence [Arabidopsis thaliana]

Seq. No. 137198

Seq. ID ARABL1-046-Q1-E1-H9

Method BLASTX
NCBI GI g115385
BLAST score 233
E value 1.0e-19
Match length 44
% identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 137199

Seq. ID ARABL1-047-Q1-B1-A1

Method BLASTX
NCBI GI g2738248
BLAST score 297



E value 2.0e-27 Match length 78 % identity 79

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No. 137200

Seq. ID ARABL1-047-Q1-B1-A12

Method BLASTN
NCBI GI g4263753
BLAST score 257
E value 1.0e-143
Match length 261
% identity 100

NCBI Description Arabidopsis thaliana chromosome V map near 60.5 cM,

complete sequence [Arabidopsis thaliana]

Seq. No. 137201

Seq. ID ARABL1-047-Q1-B1-A5

Method BLASTN
NCBI GI g4757414
BLAST score 40
E value 2.0e-13
Match length 44
% identity 62

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYF24, complete sequence

Seq. No. 137202

Seq. ID ARABL1-047-Q1-B1-A6

Method BLASTX
NCBI GI g2119848
BLAST score 249
E value 9.0e-22
Match length 47
% identity 100

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 -

Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]

Seq. No. 137203

Seq. ID ARABL1-047-Q1-B1-A8

Method BLASTX
NCBI GI g2119848
BLAST score 259
E value 6.0e-23
Match length 49
% identity 100

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 -

Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative



photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

137204 Seq. No. Seq. ID ARABL1-047-Q1-B1-B1 Method BLASTX NCBI GI g132090 322 BLAST score E value 3.0e-30

Match length 62 % identity 100

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

137205 Seq. No.

Seq. ID ARABL1-047-Q1-B1-B11

Method BLASTN NCBI GI q4689466 BLAST score 55 7.0e-23 E value Match length 80 100 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC T23015 genomic

sequence, complete sequence

Seq. No. 137206

Seq. ID ARABL1-047-Q1-B1-B12

Method BLASTN NCBI GI q3075383 BLAST score 137 E value 3.0e-71 Match length 246 100 % identity

Arabidopsis thaliana chromosome II BAC T1D16 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

137207

Seq. No. Seq. ID ARABL1-047-Q1-B1-B4

Method BLASTX NCBI GI g3914917 BLAST score 204 E value 2.0e-16 39 Match length % identity 100

NCBI Description 40S RIBOSOMAL PROTEIN S3A

137208 Seq. No.

Seq. ID ARABL1-047-Q1-B1-B7

Method BLASTX NCBI GI g4586256 BLAST score 268



E value 6.0e - 24Match length 73 % identity 75 (AL049640) probable photosystem I chain XI precursor NCBI Description [Arabidopsis thaliana] 137209 Seq. No. Seq. ID ARABL1-047-Q1-B1-B9 Method BLASTX NCBI GI g1086263 BLAST score 234 E value 7.0e-20 Match length 84 58 % identity TMV resistance protein N - tobacco (Nicotiana glutinosa) NCBI Description >gi 558887 (U15605) N [Nicotiana glutinosa]

Seq. No. 137210

Seq. ID ARABL1-047-Q1-B1-C11 Method BLASTN NCBI GI q4589427 BLAST score 261 E value 1.0e-145 Match length 261 100 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MFG13, complete sequence

Seq. No. 137211 Seq. ID ARABL1-047-Q1-B1-C12

Method BLASTN NCBI GI g2924655 BLAST score 214 1.0e-117 E value Match length 263 100 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MKD10, complete sequence [Arabidopsis thaliana]

137212 Seq. No.

Seq. ID ARABL1-047-Q1-B1-C2

BLASTX Method NCBI GI g3355468 BLAST score 222 1.0e-18 E value Match length 64 77 % identity

(AC004218) putative ribosomal protein L35 [Arabidopsis NCBI Description

thaliana]

137213 Seq. No.

Seq. ID ARABL1-047-Q1-B1-D2

Method BLASTN NCBI GI g4741959 BLAST score 172 E value 4.0e-92 Match length 202



% identity 96
NCBI Description Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete

cds

Seq. No. 137214

Seq. ID ARABL1-047-Q1-B1-D3

Method BLASTN
NCBI GI g2760170
BLAST score 97
E value 2.0e-47
Match length 202

Match length 202 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MIO24, complete sequence [Arabidopsis thaliana]

Seq. No. 137215

Seq. ID ARABL1-047-Q1-B1-E1

Method BLASTX
NCBI GI g115767
BLAST score 405
E value 5.0e-40
Match length 79
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 137216

Seq. ID ARABL1-047-Q1-B1-E3

Method BLASTX
NCBI GI g3063472
BLAST score 307
E value 2.0e-28
Match length 59
% identity 100

NCBI Description (AC003981) F22013.34 [Arabidopsis thaliana]

Seq. No. 137217

Seq. ID ARABL1-047-Q1-B1-E4

Method BLASTX
NCBI GI g421826
BLAST score 261
E value 4.0e-23
Match length 73
% identity 67

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis

thaliana]

Seq. No. 137218

Seq. ID ARABL1-047-Q1-B1-E6

Method BLASTN NCBI GI g259446



BLAST score 1.0e-111 E value 208 Match length 72 % identity

glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana, NCBI Description

C24, mRNA, 680 nt]

Seq. No. Seq. ID 137219

ARABL1-047-Q1-B1-E9

Method BLASTX NCBI GI g2129672 BLAST score 202 4.0e-16 E value Match length 61

% identity 69

photosystem II reaction center protein, 6.1K - Arabidopsis NCBI Description

thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1 kDa polypeptide of photosystem II reaction center

[Arabidopsis thaliana]

Seq. No. 137220

Seq. ID ARABL1-047-Q1-B1-F11

Method BLASTN NCBI GI q4584841 BLAST score 170 7.0e-91 E value Match length 259 100 % identity

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T23E23,

complete sequence

137221 Seq. No.

Seq. ID ARABL1-047-Q1-B1-F2

Method BLASTN NCBI GI q2618601 BLAST score 240 1.0e-132 E value Match length 240 % identity 100

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No. 137222

Seq. ID ARABL1-047-Q1-B1-F6

 ${\tt BLASTX}$ Method NCBI GI g2338712 BLAST score 268 6.0e-24 E value Match length 50 100 % identity

(AF013959) metallothionein-like protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 137223

Seq. ID ARABL1-047-Q1-B1-G1

Method BLASTX NCBI GI g729479



```
BLAST score
E value
                  5.0e-21
Match length
                  71
% identity
                  66
                  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi 551131
NCBI Description
                  (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]
Seq. No.
                  137224
                  ARABL1-047-Q1-B1-G10
Seq. ID
Method
                  BLASTX
                  g16374
NCBI GI
BLAST score
                  447
E value
                  7.0e-45
Match length
                  86
% identity
                  100
                  (X03908) chlorophyll a/b binding protein (LHCP AB 180)
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  137225
Seq. ID
                  ARABL1-047-Q1-B1-G11
Method
                  BLASTX
NCBI GI
                  g132939
BLAST score
                  338
E value
                  4.0e-32
Match length
                  73
                  88
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal
NCBI Description
                  protein L3 (ARP1) - Arabidopsis thaliana >gi 166858
                   (M32654) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                  137226
Seq. ID
                  ARABL1-047-Q1-B1-G12
Method
                  BLASTX
NCBI GI
                  g3337367
BLAST score
                  237
E value
                  3.0e-20
Match length
                  86
% identity
                  60
                  (AC004481) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  137227
Seq. ID
                  ARABL1-047-Q1-B1-G2
Method
                  BLASTN
NCBI GI
                  g3763915
BLAST score
                  52
E value
                  2.0e-20
Match length
                  76
                  92
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F14B2 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```

Seq. No. 137228

Seq. ID ARABL1-047-Q1-B1-G3

Method BLASTX
NCBI GI g1399349
BLAST score 205
E value 1.0e-16



Match length % identity 75

(U43412) 3'-phosphoadenosine 5'-phosphosulfate reductase NCBI Description

[Arabidopsis thaliana]

137229 Seq. No.

Seq. ID ARABL1-047-Q1-B1-G4

Method BLASTN q1399348 NCBI GI BLAST score 112 E value 2.0e-56 Match length 136 % identity

Arabidopsis thaliana 3'-phosphoadenosine 5'-phosphosulfate NCBI Description

reductase mRNA, complete cds

137230 Seq. No.

Seq. ID ARABL1-047-Q1-B1-G6

Method BLASTX g549010 NCBI GI BLAST score 370 5.0e-36 E value Match length 75 % identity 100

EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) NCBI Description

(OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi_322554_pir__S31328 omnipotent suppressor protein SUP1

homolog (clone G18) - Arabidopsis thaliana

>gi_16514_emb_CAA49172_ (X69375) similar to yeast omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis

thaliana] >gi 1495249 emb CAA66118 (X97486) eRF1-3

[Arabidopsis thaliana]

Seq. No. 137231

ARABL1-047-Q1-B1-G7 Seq. ID

Method BLASTX NCBI GI g115783 258 BLAST score 8.0e-23 E value Match length 52 % identity 96

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

137232 Seq. No.

ARABL1-047-Q1-B1-H11 Seq. ID

BLASTX Method q541858 NCBI GI BLAST score 459 3.0e-46 E value 85 Match length 100 % identity

NCBI Description endoxyloglucan transferase - Arabidopsis thaliana

E value

Match length % identity

211

76





>gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

137233 Seq. No. ARABL1-047-Q1-B1-H2 Seq. ID Method BLASTN q4757414 NCBI GI 242 BLAST score 1.0e-134 E value Match length 242 100 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence Seq. No. 137234 ARABL1-047-Q1-B1-H4 Seq. ID Method BLASTN q2696018 NCBI GI 134 BLAST score 2.0e-69 E value 243 Match length % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana] 137235 Seq. No. ARABL1-047-Q1-B1-H6 Seq. ID Method BLASTX q2160158 NCBI GI BLAST score 254 2.0e-22 E value Match length 50 % identity 100 NCBI Description (AC000132) Similar to elongation factor 1-gamma (qb EF1G XENLA). ESTs qb T20564, gb T45940, gb T04527 come from this gene. [Arabidopsis thaliana] Seq. No. 137236 Seq. ID ARABL1-047-Q1-B1-H8 Method BLASTX g4585882 NCBI GI BLAST score 165 7.0e-12 E value Match length 34 100 % identity (AC005850) PSI type III chlorophyll a/b-binding protein NCBI Description [Arabidopsis thaliana] 137237 Seq. No. Seq. ID ARABL1-047-Q1-E1-A12 BLASTN Method NCBI GI g4063735 BLAST score 104 2.0e-51



NCBI Description Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No. 137238

Seq. ID ARABL1-047-Q1-E1-B11

Method BLASTN
NCBI GI g4689466
BLAST score 25
E value 6.0e-05
Match length 80
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T23015 genomic

sequence, complete sequence

Seq. No. 137239

Seq. ID ARABL1-047-Q1-E1-C7

Method BLASTN
NCBI GI g2760166
BLAST score 262
E value 1.0e-146
Match length 262
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBK20, complete sequence [Arabidopsis thaliana]

Seq. No. 137240

Seq. ID ARABL1-047-Q1-E1-G6

Method BLASTX
NCBI GI g322525
BLAST score 370
E value 4.0e-36
Match length 75
% identity 100

NCBI Description omnipotent suppressor protein SUP1 homolog (clone A18) -

Arabidopsis thaliana (fragment) >gi_16512_emb_CAA49171_ (X69374) similar to yeast omnipotent suppressor protein

SUP1 (SUP45); ORF [Arabidopsis thaliana]

Seq. No. 137241

Seq. ID ARABL1-047-Q1-E1-H2

Method BLASTN
NCBI GI g4757414
BLAST score 246
E value 1.0e-136
Match length 280
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYF24, complete sequence

Seq. No. 137242

Seq. ID ARABL1-047-Q1-E1-H4

Method BLASTN
NCBI GI g2696018
BLAST score 242
E value 1.0e-134
Match length 327
% identity 100



```
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   137243
                  ARABL1-05-Q1-B1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2749918
                  119
BLAST score
                   9.0e-61
E value
                  140
Match length
                   95
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F3I6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                   137244
Seq. No.
                  ARABL1-05-Q1-B1-A4
Seq. ID
                  BLASTN
Method
                   g3335331
NCBI GI
BLAST score
                   132
                   2.0e-68
E value
Match length
                   153
                   94
% identity
                  Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                   137245
                  ARABL1-05-Q1-B1-B2
Seq. ID
Method
                  BLASTX
                   q586079
NCBI GI
BLAST score
                   516
E value
                   8.0e-53
Match length
                   103
                   100
% identity
                   TUBULIN GAMMA-1 CHAIN >gi 460089 (U02069) g1-tubulin
NCBI Description
                   [Arabidopsis thaliana]
                   137246
Seq. No.
Seq. ID
                   ARABL1-05-Q1-B1-B3
Method
                   BLASTN
                   g3193282
NCBI GI
BLAST score
                   118
                   7.0e-60
E value
                   225
Match length
% identity
                   86
NCBI Description Arabidopsis thaliana BAC T14P8
                   137247
Seq. No.
Seq. ID
                   ARABL1-05-Q1-B1-C12
Method
                   BLASTX
NCBI GI
                   g4335724
BLAST score
                   527
```

NCBI GI g4335724
BLAST score 527
E value 4.0e-54
Match length 93
% identity 100

NCBI Description (AC006248) putative RING-H2 finger protein [Arabidopsis thaliana]



Seq. No. 137248 Seq. ID ARABL1-05-Q1-B1-C6 Method BLASTN NCBI GI q3873174 BLAST score 381 0.0e+00E value Match length 384 % identity 100 Genomic sequence for Arabidopsis thaliana BAC F14N23, NCBI Description complete sequence [Arabidopsis thaliana] 137249 Seq. No. Seq. ID ARABL1-05-Q1-B1-D7 Method BLASTX NCBI GI g4741952 BLAST score 265 9.0e-24 E value Match length 50 % identity 100 NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana] Seq. No. 137250 ARABL1-05-Q1-B1-E5 Seq. ID Method BLASTX g2275217 NCBI GI BLAST score 379 E value 3.0e-41Match length 112 % identity 82 NCBI Description (AC002337) chloroplast protein CP12 isolog [Arabidopsis thaliana] Seq. No. 137251 Seq. ID ARABL1-05-Q1-B1-E9 Method BLASTX g3021266 NCBI GI BLAST score 303 9.0e-28 E value Match length 95 % identity 60 NCBI Description (AL022347) serine/threonine kinase - like protein [Arabidopsis thaliana] >gi_3292840_emb_CAA19830_ (AL031018) serine/threonine kinase - like protein [Arabidopsis thaliana] Seq. No. 137252 Seq. ID ARABL1-05-Q1-B1-F10

Method BLASTX
NCBI GI g602076
BLAST score 500
E value 8.0e-51
Match length 101
% identity 23

NCBI Description (X77456) pentameric polyubiquitin [Nicotiana tabacum]

Seq. No. 137253

Seq. ID ARABL1-05-Q1-B1-F4



Method BLASTN NCBI GI q4538895 BLAST score 176 2.0e-94 E value Match length 334 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8

(ESSA project)

Seq. No. 137254

Seq. ID ARABL1-05-Q1-B1-F6

Method BLASTN NCBI GI g4741184 BLAST score 304 E value 1.0e-171 Match length 304 100 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7

(ESSA project)

Seq. No. 137255

Seq. ID ARABL1-05-Q1-B1-F8

Method BLASTN g2618602 NCBI GI BLAST score 289 E value 1.0e-162 Match length 329 % identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 137256

Seq. ID ARABL1-05-Q1-B1-H9

Method BLASTN NCBI GI g3327922 BLAST score 195 E value 1.0e-106 Match length 195 % identity 72

NCBI Description Arabidopsis thaliana chromosome II BAC T31E10 genomic

sequence, complete sequence [Arabidopsis thaliana]

137257

Seq. No. Seq. ID ARABL1-06-Q1-B1-A6

Method BLASTX NCBI GI g2827714 BLAST score 258 E value 2.0e-22 Match length 112 % identity

NCBI Description (AL021684) receptor protein kinase - like protein

[Arabidopsis thaliana]

Seq. No. 137258

Seq. ID ARABL1-06-Q1-B1-C3

Method BLASTX NCBI GI g1173245



```
BLAST score
                  273
                  2.0e-24
E value
                  69
Match length
                  74
% identity
                  40S RIBOSOMAL PROTEIN RP10 >gi 2130267 pir S62431
NCBI Description
                  hypothetical protein SPAC13G6.02c - fission yeast
                  (Schizosaccharomyces pombe) >gi_1008987_emb_CAA91095
                  (Z54308) 40S ribosomal protein subunit [Schizosaccharomyces
                  pombe]
                  137259
Seq. No.
                  ARABL1-06-Q1-B1-E1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4581161
BLAST score
                  129
                  2.0e-66
E value
                  319
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T20G20 genomic
NCBI Description
                  sequence, complete sequence
                  137260
Seq. No.
                  ARABL1-06-Q1-B1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1345594
                  409
BLAST score
E value
                  4.0e-40
                  85
Match length
                  98
% identity
                  14-3-3-LIKE PROTEIN GF14 KAPPA >gi 1022780 (U36447) GF14
NCBI Description
                  Kappa isoform [Arabidopsis thaliana]
                  137261
Seq. No.
                  ARABL1-06-Q1-B1-F6
Seq. ID
Method
                  BLASTN
                  g16300
NCBI GI
BLAST score
                  169
E value
                  2.0e-90
Match length
                  227
                  97
% identity
NCBI Description
                  A.thaliana mRNA for glycine rich protein
                  >gi 166836 gb L00648 ATHRBPA Arabidopsis thaliana
                  RNA-binding protein mRNA, complete cds
Seq. No.
                  137262
Seq. ID
                  ARABL1-06-Q1-B1-G2
Method
                  BLASTN
NCBI GI
                  g2828180
BLAST score
                  361
                  0.0e + 00
E value
Match length
                  364
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

Seq. No. 137263

Seq. ID ARABL1-06-Q1-B1-G3

MDK4, complete sequence [Arabidopsis thaliana]



```
Method BLASTX
NCBI GI g4586256
BLAST score 422
E value 8.0e-42
Match length 102
% identity 82
```

NCBI Description (AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No. 137264

Seq. ID ARABL1-06-Q1-B1-G7

Method BLASTN
NCBI GI g2696018
BLAST score 191
E value 1.0e-103
Match length 191
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXC9, complete sequence [Arabidopsis thaliana]

Seq. No. 137265

Seq. ID ARABL1-07-Q1-B1-A2

Method BLASTN
NCBI GI g16375
BLAST score 67
E value 2.0e-29
Match length 143
% identity 97

NCBI Description A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding

protein

Seq. No. 137266

Seq. ID ARABL1-07-Q1-B1-G11

Method BLASTN
NCBI GI g2853071
BLAST score 132
E value 4.0e-68
Match length 295
% identity 94

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7

(ESSA project)

> Seq. No. 137267

Seq. ID ARABL1-07-Q1-B1-G3

Method BLASTX
NCBI GI g131398
BLAST score 434
E value 4.0e-43
Match length 105
% identity 85

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,



gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No. 137268

Seq. ID ARABL1-08-Q1-B1-A6

Method BLASTX
NCBI GI g3287696
BLAST score 420
E value 1.0e-41
Match length 90
% identity 92

NCBI Description (AC003979) Strong similarity to phosphoribosylanthranilate

transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region.

[Arabidopsis thaliana]

Seq. No. 137269

Seq. ID ARABL1-08-Q1-B1-C2

Method BLASTN
NCBI GI g4584841
BLAST score 130
E value 6.0e-67
Match length 291
% identity 39

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T23E23,

complete sequence

Seq. No. 137270

Seq. ID ARABL1-08-Q1-B1-C9

Method BLASTN
NCBI GI g2738247
BLAST score 100
E value 2.0e-49
Match length 144
% identity 92

NCBI Description Arabidopsis thaliana cobalamin-independent methionine

synthase (ATCIMS) mRNA, complete cds

Seq. No. 137271

Seq. ID ARABL1-08-Q1-B1-D6

Method BLASTN
NCBI GI g4589410
BLAST score 128
E value 5.0e-66
Match length 164
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F2015, complete sequence

Seq. No. 137272

Seq. ID ARABL1-08-Q1-B1-D9

Method BLASTN
NCBI GI 94567300
BLAST score 138
E value 5.0e-72
Match length 159
% identity 96



NCBI Description Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

137273 Seq. No.

ARABL1-08-Q1-B1-E5 Seq. ID

Method BLASTX NCBI GI g3128205 BLAST score 345 1.0e-32 E value Match length 87 83 % identity

(AC004077) putative pyruvate dehydrogenase complex E1 beta NCBI Description

subunit [Arabidopsis thaliana]

Seq. No. 137274

ARABL1-08-Q1-B1-F2 Seq. ID

Method BLASTX NCBI GI q2119848 BLAST score 94 8.0e-21 E value Match length 53 79 % identity

chlorophyll a/b-binding protein type I precursor Lhb1B1 -NCBI Description

Arabidopsis thaliana >gi 16366 emb CAA45789 (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]

Seq. No. 137275

Seq. ID ARABL1-08-Q1-B1-F9

Method BLASTX NCBI GI g2338712 BLAST score 262 7.0e-23 E value Match length 69 % identity

NCBI Description (AF013959) metallothionein-like protein [Arabidopsis

thaliana]

Seq. No. 137276

Seq. ID ARABL1-08-Q1-B1-G8

Method BLASTX NCBI GI q464621 BLAST score 196 E value 2.0e-15 Match length 47 79 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586

ribosomal protein ML16 - common ice plant >gi_19539 emb_CAA49175_ (X69378) ribosomal protein YL16

[Mesembryanthemum crystallinum]

137277 Seq. No.

Seq. ID ARABL1-08-Q1-B1-H10

Seq. ID

Method



```
Method
                  BLASTN
NCBI GI
                  q2583106
BLAST score
                  94
E value
                  1.0e-45
                  189
Match length
                  61
% identity
                  Arabidopsis thaliana chromosome II BAC F4L23 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  137278
Seq. ID
                  ARABL1-16-Q1-B1-E12
Method
                  BLASTX
NCBI GI
                  q16374
BLAST score
                  355
E value
                  7.0e - 34
Match length
                  68
                  100
% identity
                  (X03908) chlorophyll a/b binding protein (LHCP AB 180)
NCBI Description
                  [Arabidopsis thaliana]
                  137279
Seq. No.
Seq. ID
                  ARABL1-16-Q1-B1-E9
Method
                  BLASTX
NCBI GI
                  q1943945
BLAST score
                  159
                  6.0e-11
E value
Match length
                  42
                  69
% identity
NCBI Description
                  (U85780) Spinacia oleracea Spinach choline monooxygenase
                  TRANSLATE of cmoll17.gcg from: 57 to: 1376 [Spinacia
                  oleracea]
                  137280
Seq. No.
Seq. ID
                  ARABL1-16-Q1-B1-F12
Method
                  BLASTN
NCBI GI
                  g11802
BLAST score
                  189
E value
                  1.0e-102
Match length
                  341
% identity
                   90
                  Tobacco chloropast DNA homologous to ribosomal protein S12
NCBI Description
                  gene
Seq. No.
                  137281
                  ARABL1-16-Q1-B1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2351061
BLAST score
                  53
                   6.0e-21
E value
Match length
                  334
% identity
                   63
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAF19, complete sequence [Arabidopsis thaliana]
                  137282
Seq. No.
```

16436

ARABL1-17-Q1-B1-A12

BLASTN



NCBI GI g4454585
BLAST score 187
E value 1.0e-101
Match length 350
% identity 100
NCBI Description Arabidopsi

NCBI Description Arabidopsis thaliana BAC T13D4 from chromosome IV near 21.5

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cM, complete sequence

Seq. No. 137283

Seq. ID ARABL1-17-Q1-B1-E10

Method BLASTN
NCBI GI g3176695
BLAST score 238
E value 1.0e-131
Match length 281
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F14J9 genomic

sequence contains phyA marker, complete sequence

[Arabidopsis thaliana]

Seq. No. 137284

Seq. ID ARABL1-18-Q1-B1-D11

Method BLASTN
NCBI GI g2252823
BLAST score 23
E value 4.0e-03
Match length 257
% identity 91

NCBI Description Arabidopsis thaliana BAC IG005I10

Seq. No. 137285

Seq. ID ARABL1-18-Q1-B1-G3

Method BLASTX
NCBI GI g421826
BLAST score 197
E value 2.0e-15
Match length 92
% identity 64

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi_298036_emb_CAA50712 (X71878) CP29 [Arabidopsis

thaliana]

Seq. No. 137286

Seq. ID ARABL1-18-Q1-B1-H12

Method BLASTX
NCBI GI g2894574
BLAST score 502
E value 4.0e-51
Match length 95
% identity 100

NCBI Description (AL021890) peroxidase prxrl [Arabidopsis thaliana]

>gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1

[Arabidopsis thaliana]

Seq. No. 137287

Seq. ID ARABLI-04-Q1-B1-D12

Method BLASTN



```
NCBI GI
                  q2435510
BLAST score
                  208
E value
                  1.0e-113
                  323
Match length
% identity
                  100
NCBI Description Arabidopsis thaliana BAC TM017A05
Seq. No.
                  137288
                  ARABLI-06-Q1-B1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2809232
BLAST score
                  530
E value
                  2.0e-54
Match length
                  114
                  88
% identity
NCBI Description
                  (AC002560) F21B7.1 [Arabidopsis thaliana]
                  137289
Seq. No.
Seq. ID
                  ARABLI-06-Q1-B1-C12
Method
                  BLASTX
NCBI GI
                  g2317913
BLAST score
                  541
E value
                  2.0e-55
Match length
                  106
% identity
                  100
                  (U89959) cathepsin B-like cysteine proteinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  137290
                  ARABLI-06-Q1-B1-D10
Seq. ID
Method
                  BLASTX
                  q4262236
NCBI GI
BLAST score
                  383
E value
                  4.0e-37
Match length
                  110
% identity
                  75
NCBI Description
                  (AC006200) putative ribose 5-phosphate isomerase
                  [Arabidopsis thaliana]
Seq. No.
                  137291
Seq. ID
                  ARABLI-06-Q1-B1-E9
Method
                  BLASTX
NCBI GI
                  g4587527
BLAST score
                  287
E value
                  7.0e-26
                  106
Match length
% identity
                  52
                  (AC007060) Strong similarity to F19I3.2 gi 3033375 putative
NCBI Description
                  berberine bridge enzyme from Arabidopsis thaliana BAC
                  gb_AC004238
                  137292
Seq. No.
Seq. ID
                  ARABLI-09-Q1-B1-A10
```

Method BLASTX

NCBI GI g3123327 BLAST score 223 E value 2.0e-18



Match length % identity 97 (AJ005927) squalene epoxidase homologue [Arabidopsis NCBI Description thaliana] 137293 Seq. No. Seq. ID ARABLI-09-Q1-B1-B1 Method BLASTN NCBI GI g1871173 BLAST score 56 E value 1.0e-23 Match length 56 % identity 100 NCBI Description Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence Seq. No. 137294 Seq. ID ARABLI-09-Q1-B1-D12 Method BLASTX NCBI GI g3738316 BLAST score 343 2.0e-32 E value 80 Match length 80 % identity NCBI Description (AC005170) unknown protein [Arabidopsis thaliana] 137295 Seq. No. ARABLI-09-Q1-B1-D3 Seq. ID Method BLASTX q135406 NCBI GI BLAST score 406 7.0e-40 E value Match length 76 % identity 99 TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin NCBI Description alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi 166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana] 137296 Seq. No. Seq. ID ARABLI-09-Q1-B1-D5 Method BLASTN NCBI GI g457715 BLAST score 225 E value 1.0e-123 Match length 333 % identity 99 NCBI Description A.thaliana CXc750 gene

Seq. No. 137297

Seq. ID ARABLI-09-Q1-B1-F2

Method BLASTX g3386569 NCBI GI BLAST score 251 E value 1.0e-21 48 Match length 96 % identity



NCBI Description (AF079590) photosystem II type II chlorophyll a/b binding protein [Sorghum bicolor]

137298 Seq. No.

ARABLI-09-Q1-B1-G1 Seq. ID

Method BLASTN NCBI GI g4572664 80 BLAST score 3.0e-37 E value Match length 253

% identity NCBI Description Arabidopsis thaliana chromosome II BAC F25P17 genomic

sequence, complete sequence

137299 Seq. No.

ARABLI-09-Q1-B1-G4 Seq. ID

97

Method BLASTN NCBI GI g2894557 BLAST score 91 E value 3.0e-44Match length 91 100 % identity

Arabidopsis thaliana DNA chromosome 4, BAC clone T805 NCBI Description

(ESSAII project)

Seq. No. 137300

ARABLI-09-Q1-B1-H2 Seq. ID

Method BLASTN NCBI GI q4454447 BLAST score 218 1.0e-119 E value 322 Match length 100 % identity

Arabidopsis thaliana chromosome II BAC F5H14 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137301

Seq. ID ARABLI-10-Q1-B1-B2

Method BLASTN NCBI GI g3492855 BLAST score 46 E value 7.0e-17 Match length 130 90 % identity

Genomic sequence for Arabidopsis thaliana BAC F20N2, NCBI Description

complete sequence [Arabidopsis thaliana]

Seq. No. 137302

Seq. ID ARABLI-10-Q1-B1-C3

Method BLASTX q4741954 NCBI GI BLAST score 618 1.0e-64 E value Match length 129 % identity 91

(AF134127) Lhcb4.2 protein [Arabidopsis thaliana] NCBI Description



```
Seq. No.
                    137303
Seq. ID
                    ARABLI-10-Q1-B1-C7
Method
                    BLASTX
NCBI GI
                    a1170089
BLAST score
                    661
E value
                    1.0e-69
Match length
                    130
% identity
                    100
                    GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)
NCBI Description
                    >gi_481822_pir__S39542 probable glutathione transferase (EC
                    2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789 dbj_BAA04554_ (D17673) glutathione S-transferase
                    [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione
                    S-transferase [Arabidopsis thaliana]
```

Seq. No. 137304 Seq. ID ARABLI-10-Q1-B1-D10 Method BLASTX NCBI GI q4512689 BLAST score 155 2.0e-10

137305

E value Match length 82 % identity 41

Seq. No.

(AC006931) hypothetical protein [Arabidopsis thaliana] NCBI Description

ARABLI-10-Q1-B1-D9 Seq. ID Method BLASTX NCBI GI q1351271 BLAST score 518 5.0e-53 E value Match length 111 % identity

NCBI Description TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi_1084309_pir__S52032 triose-phosphate isomerase (EC

5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme

[Spinacia oleracea]

Seq. No. 137306

Seq. ID ARABLI-10-Q1-B1-E5

Method BLASTX NCBI GI g4454481 BLAST score 523 2.0e-53 E value Match length 122 % identity

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

>gi 4512647 gb AAD21702.1 (AC007048) unknown protein

[Arabidopsis thaliana]

137307 Seq. No.

Seq. ID ARABLI-10-Q1-B1-F11

Method BLASTX NCBI GI g115767 BLAST score 166 E value 4.0e-12



Match length 30 % identity 100 NCBI Description CHL

ction CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 137308

Seq. ID ARABLI-10-Q1-B1-F7

Method BLASTN
NCBI GI g3176701
BLAST score 173
E value 1.0e-92
Match length 250
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC T20K24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137309

Seq. ID ARABLI-10-Q1-B1-G2

Method BLASTX
NCBI GI g4741952
BLAST score 279
E value 2.0e-25
Match length 53
% identity 100

NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No. 137310

Seq. ID ARABLI-10-Q1-B1-G5

Method BLASTN
NCBI GI g3688798
BLAST score 61
E value 2.0e-26
Match length 61
% identity 100

NCBI Description Arabidopsis thaliana gamma tonoplast intrinsic protein 2

(TIP2) mRNA, complete cds

Seq. No. 137311

Seq. ID ARABLI-10-Q1-B1-H11

Method BLASTN
NCBI GI g4262221
BLAST score 176
E value 2.0e-94
Match length 338
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F10A8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137312

Seq. ID ARABLI-11-Q1-B1-B4

Method BLASTX NCBI GI g444790

% identity

100



```
BLAST score
E value
                  3.0e-54
Match length
                  122
                  88
% identity
NCBI Description nucleotide translocator [Arabidopsis thaliana]
                  137313
Seq. No.
                  ARABLI-11-Q1-B1-B5
Seq. ID
                  BLASTX
Method
                  g2853084
NCBI GI
BLAST score
                  206
                  3.0e-16
E value
                  68
Match length
% identity
                  54
NCBI Description (AL021768) putative protein [Arabidopsis thaliana]
                  137314
Seq. No.
                  ARABLI-11-Q1-B1-B6
Seq. ID
Method
                  BLASTX
                  g4580393
NCBI GI
                  263
BLAST score
                  6.0e-23
E value
                  111
Match length
% identity
                  50
                  (AC007171) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  137315
                  ARABLI-11-Q1-B1-D7
Seq. ID
                  BLASTX
Method
                  g1076345
NCBI GI
BLAST score
                   129
                   2.0e-07
E value
                  71
Match length
                   9
% identity
                  cold acclimation protein 1ti30 - Arabidopsis thaliana
NCBI Description
                   (fragment)
                   137316
Seq. No.
                   ARABLI-11-Q1-B1-E7
Seq. ID
Method
                   BLASTN
                   q4454587
NCBI GI
                   346
BLAST score
                   0.0e + 00
E value
                   362
Match length
% identity
                   99
                  Arabidopsis thaliana BAC F21A20 from chromosome V near 61
NCBI Description
                   cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                   137317
                   ARABLI-12-Q1-B1-A3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3366536
BLAST score
                   342
E value
                   0.0e+00
Match length
                   342
```

16443

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T25N2O,





complete sequence [Arabidopsis thaliana]

```
137318
Seq. No.
                  ARABLI-12-Q1-B1-B11
Seq. ID
                  BLASTN
Method
                  g3901293
NCBI GI
                  182
BLAST score
                  3.0e-98
E value
                  190
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana rpp8 gene, complete cds
                  137319
Seq. No.
                  ARABLI-12-Q1-B1-B2
Seq. ID
                  BLASTN
Method
                  g870791
NCBI GI
                  60
BLAST score
                  2.0e-25
E value
Match length
                  111
                  95
% identity
                  Arabidopsis thaliana polyubiquitin (ubq10) mRNA, complete
NCBI Description
                  137320
Seq. No.
                  ARABLI-12-Q1-B1-B8
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4581161
                  347
BLAST score
                  0.0e + 00
E value
Match length
                  354
                   65
% identity
                 Arabidopsis thaliana chromosome II BAC T20G20 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  137321
                  ARABLI-12-Q1-B1-C4
Seq. ID
Method
                  BLASTN
                   q4159704
NCBI GI
BLAST score
                   201
E value
                   1.0e-109
                   343
Match length
                   66
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MCB17, complete sequence
                   137322
Seq. No.
                   ARABLI-12-Q1-B1-D8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3420008
BLAST score
                   233
                   2.0e-19
E value
Match length
                   113
% identity
                   39
                  (AF000307) steroid sulfotransferase 3 [Brassica napus]
NCBI Description
```

ARABLI-12-Q1-B1-E5

137323

Seq. No.

Seq. ID



Method BLASTX
NCBI GI g2244949
BLAST score 200
E value 2.0e-15
Match length 104
% identity 45

NCBI Description (Z97339) similarity to ORF - Lilium longiflorum

[Arabidopsis thaliana]

Seq. No. 137324

Seq. ID ARABLI-12-Q1-B1-G1

Method BLASTX
NCBI GI g2894574
BLAST score 529
E value 3.0e-54
Match length 110
% identity 100

NCBI Description (AL021890) peroxidase prxr1 [Arabidopsis thaliana]

>gi 2961341 emb CAA18099.1 (AL022140) peroxidase prxr1

[Arabidopsis thaliana]

Seq. No. 137325

Seq. ID ARABLI-13-Q1-B1-A2

Method BLASTN
NCBI GI g4581161
BLAST score 148
E value 5.0e-78
Match length 148
% identity 65

NCBI Description Arabidopsis thaliana chromosome II BAC T20G20 genomic

sequence, complete sequence

Seq. No. 137326

Seq. ID ARABLI-13-Q1-B1-B7

Method BLASTX
NCBI GI g2842615
BLAST score 337
E value 1.0e-31
Match length 128
% identity 55

NCBI Description ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (ASA DEHYDROGENASE)

>gi 1359593 emb CAA66607 (X97964) aspartate-semialdehyde

dehydrogenase [Campylobacter jejuni]

Seq. No. 137327

Seq. ID ARABLI-13-Q1-B1-B8

Method BLASTX
NCBI GI g2213592
BLAST score 264
E value 5.0e-23
Match length 110
% identity 26

NCBI Description (ACO00348) T7N9.12 [Arabidopsis thaliana]

Seq. No. 137328

Seq. ID ARABLI-13-Q1-B1-E5

Method BLASTN



NCBI GI g2244788
BLAST score 315
E value 1.0e-177
Match length 336
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 137329

Seq. ID ARABLI-13-Q1-B1-H4

Method BLASTX
NCBI GI g4741923
BLAST score 305
E value 7.0e-28
Match length 92
% identity 63

NCBI Description (AF130849) PIT1 [Arabidopsis thaliana]

Seq. No. 137330

Seq. ID ARABLI-14-Q1-B1-A2

Method BLASTX
NCBI GI 94587564
BLAST score 443
E value 3.0e-44
Match length 89
% identity 100

NCBI Description (AC006550) Strong similarity to gb_X14017 photosystem I

reaction centre subunit II precursor (psaD) from Spinacia oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133,

gb N65521, gb T42498, gb T41918, gb N38024

Seq. No. 137331

Seq. ID ARABLI-14-Q1-B1-B11

Method BLASTN
NCBI GI g4757662
BLAST score 279
E value 1.0e-156
Match length 392
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10B6 from

chromosome I, complete sequence

Seq. No. 137332

Seq. ID ARABLI-14-Q1-B1-C12

Method BLASTX
NCBI GI g2498731
BLAST score 373
E value 4.0e-36
Match length 83
% identity 84

NCBI Description PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1

>gi_1362013_pir__S57611 zeta-crystallin homolog Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)

zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No. 137333

Seq. ID ARABLI-14-Q1-B1-D8



Method BLASTX
NCBI GI g1175012
BLAST score 439
E value 1.0e-43
Match length 98
% identity 89

NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN

B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane

protein TMP-B [Arabidopsis thaliana]

Seq. No. 137334

Seq. ID ARABLI-14-Q1-B1-E7

Method BLASTX
NCBI GI g4538963
BLAST score 492
E value 8.0e-50
Match length 94
% identity 72

NCBI Description (AL049488) chlorophyll a/b-binding protein-like

[Arabidopsis thaliana] >qi 4741958 gb AAD28776.1 AF134129 1

(AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No. 137335

Seq. ID ARABLI-14-Q1-B1-F1

Method BLASTX
NCBI GI g4741940
BLAST score 467
E value 7.0e-47
Match length 85
% identity 61

NCBI Description (AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No. 137336

Seq. ID ARABLI-14-Q1-B1-F10

Method BLASTX
NCBI GI g629511
BLAST score 440
E value 7.0e-44
Match length 90
% identity 100

NCBI Description cold-regulated protein cor15b precursor - Arabidopsis

thaliana >gi_4559338_gb_AAD23000.1_AC007087_19 (AC007087)

cold-regulated protein cor15b precursor [Arabidopsis

thaliana]

Seq. No. 137337

Seq. ID ARABLI-14-Q1-B1-F11

Method BLASTN
NCBI GI g4581138
BLAST score 238
E value 1.0e-131
Match length 315
% identity 66

NCBI Description Arabidopsis thaliana chromosome II BAC F1011 genomic

sequence, complete sequence

Seq. No. 137338



ARABLI-14-01-B1-F9 Seq. ID BLASTX Method q602076 NCBI GI 500 BLAST score 8.0e-51 E value 101 Match length 23 % identity (X77456) pentameric polyubiquitin [Nicotiana tabacum] NCBI Description 137339 Seq. No. ARABLI-14-Q1-B1-H7 Seq. ID BLASTN Method g3046850 NCBI GI BLAST score 198 E value 1.0e-107 Match length 397 100 % identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K24G6, complete sequence [Arabidopsis thaliana] 137340 Seq. No. ARABLI-15-Q1-B1-A8 Seq. ID BLASTX Method g3668080 NCBI GI 365 BLAST score 3.0e-35 E value 88 Match length 78 % identity (AC004667) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 137341 ARABLI-15-Q1-B1-B11 Seq. ID BLASTN Method g166679 NCBI GI BLAST score 119 1.0e-60 E value 166 Match length 99 % identity Arabidopsis thaliana negative regulator of the ethylene NCBI Description response pathway (CTR1) mRNA, complete cds. >gi_996469_gb_I14046_I14046 Sequence 1 from patent US 5444166 >gi_2087615_gb_I35764_I35764 Sequence 1 from patent 137342 Seq. No. ARABLI-15-Q1-B1-C10 Seq. ID BLASTX Method q2493144 NCBI GI

BLAST score 331 3.0e-31 E value Match length 82 52 % identity

VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE NCBI Description

16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132

H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis



thaliana]

 Seq. No.
 137343

 Seq. ID
 ARABLI-15-Q1-B1-D1

 Method
 BLASTN

NCBI GI g4206762
BLAST score 96
E value 1.0e-46
Match length 169
% identity 83

NCBI Description Arabidopsis thaliana cell wall-plasma membrane linker

protein homolog (CWLP) mRNA, complete cds

Seq. No. 137344

Seq. ID ARABLI-15-Q1-B1-G2

Method BLASTX
NCBI GI g2982452
BLAST score 588
E value 4.0e-61
Match length 125
% identity 92

NCBI Description (AL022223) receptor protein kinase-like protein

[Arabidopsis thaliana]

Seq. No. 137345

Seq. ID ARABLI-15-Q1-B1-G6

Method BLASTX
NCBI GI g115767
BLAST score 632
E value 3.0e-66
Match length 135
% identity 96

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 137346

Seq. ID ARABLI-15-Q1-B1-G7

Method BLASTN
NCBI GI 94589433
BLAST score 287
E value 1.0e-160
Match length 287
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNI5, complete sequence

Seq. No. 137347

Seq. ID ARABLI-15-Q1-B1-H8

Method BLASTN
NCBI GI g16260
BLAST score 345
E value 0.0e+00



Match length 360 % identity 99

NCBI Description Arabisdopsis thaliana EF-1 alpha Al gene for elongation

factor 1-alpha

Seq. No. 137348

Seq. ID ARABLI-16-Q1-B1-B7

Method BLASTN
NCBI GI g3128142
BLAST score 290
E value 1.0e-162
Match length 290
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQN23, complete sequence [Arabidopsis thaliana]

Seq. No. 137349

Seq. ID ARABLI-16-Q1-B1-B8

Method BLASTN
NCBI GI g4581161
BLAST score 278
E value 1.0e-155
Match length 278
% identity 66

NCBI Description Arabidopsis thaliana chromosome II BAC T20G20 genomic

sequence, complete sequence

Seq. No. 137350

Seq. ID ARABLI-16-Q1-B1-D6

Method BLASTX
NCBI GI g282865
BLAST score 490
E value 1.0e-49
Match length 108
% identity 86

NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana

>gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
protein [Arabidopsis thaliana] >gi_166644 (M85150)
chlorophyll a/b-binding protein [Arabidopsis thaliana]
>gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 137351

Seq. ID ARABLI-16-Q1-B1-E3

Method BLASTX
NCBI GI g1495366
BLAST score 213
E value 3.0e-17
Match length 93
% identity 51

NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

Seq. No. 137352

Seq. ID ARABLI-16-Q1-B1-E7

Method BLASTN
NCBI GI g4539290
BLAST score 356



```
0.0e + 00
E value
Match length
                  416
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19
                  (ESSA project)
Seq. No.
                  137353
Seq. ID
                  ARABLI-16-Q1-B1-F6
Method
                  BLASTX
NCBI GI
                  q2578823
BLAST score
                  289
E value
                  5.0e-26
Match length
                  56
                  98
% identity
NCBI Description
                  (AB000835) similar to YGR200c [Arabidopsis thaliana]
Seq. No.
                  137354
```

ARABLI-16-Q1-B1-F8 Seq. ID Method BLASTX NCBI GI g544424 BLAST score 240 1.0e-20 E value

Match length 47 % identity 100

NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN 7 >qi 419755 pir S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana

>gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >qi 166837 (L00648) RNA-binding

protein [Arabidopsis thaliana]

>gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)

glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No. 137355

Seq. ID ARABLI-16-Q1-B1-G1

Method BLASTX NCBI GI g1170555 BLAST score 187 E value 5.0e-14 Match length 88 % identity 51

NCBI Description MYO-INOSITOL 4-O-METHYLTRANSFERASE >gi 282822_pir__S22696 methyltransferase - common ice plant >gi 167262 (M87340)

myo-inositol O-methyl transferase [Mesembryanthemum

crystallinum] >gi_1488237 (U63634) inositol

methyltransferase [Mesembryanthemum crystallinum]

Seq. No. 137356

Seq. ID ARABLI-17-Q1-B1-B7

Method BLASTN NCBI GI q4510360 BLAST score 33 5.0e-09 E value Match length 65 % identity

Arabidopsis thaliana chromosome II BAC F11F19 genomic NCBI Description

sequence, complete sequence



```
Seq. No.
                  137357
                  ARABLI-17-Q1-B1-D3
Seq. ID
Method
                  BLASTN
                  g2828183
NCBI GI
BLAST score
                  318
E value
                  1.0e-179
Match length
                  318
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MPL12, complete sequence [Arabidopsis thaliana]
                  137358
Seq. No.
                  ARABLI-17-Q1-B1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3600039
BLAST score
                  355
                  5.0e-34
E value
Match length
                  85
                  95
% identity
NCBI Description
                  (AF080119) similar to Schizosaccharomyces pombe isp4
                  protein (GB:D14061) [Arabidopsis thaliana]
                  137359
Seq. No.
                  ARABLI-17-Q1-B1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  410
                  2.0e-40
E value
Match length
                  96
% identity
                  83
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  137360
Seq. ID
                  ARABLI-17-Q1-B1-G8
Method
                  BLASTN
                  g3492855
NCBI GI
BLAST score
                  89
E value
                  8.0e-43
Match length
                  132
% identity
                  100
                  Genomic sequence for Arabidopsis thaliana BAC F20N2,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  137361
Seq. ID
                  ARABLI-17-Q1-B1-H2
Method
                  BLASTX
NCBI GI
                  q231700
BLAST score
                  240
E value
                  8.0e-21
Match length
                  47
% identity
                  100
NCBI Description
                  22 KD CALMODULIN-LIKE CALCIUM-BINDING PROTEIN (CABP-22)
```

>gi_479694_pir__S35188 calmodulin-related protein (clone CaBP-22) - Arabidopsis thaliana >gi_16209 emb_CAA78124



(Z12136) calcium binding protein [Arabidopsis thaliana] >gi_3402708 (AC004261) calcium binding protein [Arabidopsis thaliana]

Seq. No. 137362

Seq. ID LIB146-001-Q1-E1-A1

Method BLASTX
NCBI GI g4559369
BLAST score 581
E value 2.0e-60
Match length 106
% identity 96

NCBI Description (AC006585) putative Rieske iron-sulfur protein [Arabidopsis

thaliana]

Seq. No. 137363

Seq. ID LIB146-001-Q1-E1-A9

Method BLASTX
NCBI GI g4581108
BLAST score 534
E value 7.0e-55
Match length 105
% identity 100

NCBI Description (AC005825) putative chloroplast outer membrane protein

86, also very similar to GTP-inding protein from pea

(GB:L36857) [Arabidopsis thaliana]

Seq. No. 137364

Seq. ID LIB146-001-Q1-E1-B6

Method BLASTX
NCBI GI g112741
BLAST score 530
E value 2.0e-54
Match length 99
% identity 99

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir_ NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 137365

Seq. ID LIB146-001-Q1-E1-B7

Method BLASTX
NCBI GI g1628583
BLAST score 545
E value 4.0e-56
Match length 105
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137366

Seq. ID LIB146-001-Q1-E1-C11



```
Method
                  BLASTX
NCBI GI
                  q2623306
BLAST score
                  332
                  5.0e-31
E value
                  84
Match length
                  76
% identity
NCBI Description
                 (AC002409) unknown protein [Arabidopsis thaliana]
Seq. No.
                  137367
                  LIB146-001-Q1-E1-C5
Seq. ID
Method
                  BLASTX
                  g112737
NCBI GI
BLAST score
                  456
E value
                  5.0e-50
                  130
Match length
                  72
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  137368
                  LIB146-001-Q1-E1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4056489
BLAST score
                  303
E value
                  1.0e-27
                  129
Match length
                  60
% identity
                  (AC005896) putative white protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  137369
                  LIB146-001-Q1-E1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112739
BLAST score
                  421
E value
                  2.0e-41
Match length
                  120
                  71
% identity
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  137370
Seq. ID
                  LIB146-001-Q1-E1-D8
Method
                  BLASTN
```

q4757399 NCBI GI BLAST score 38 E value 5.0e-12 Match length 346



% identity 28
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
MEE13, complete sequence

Seq. No. 137371

Seq. ID LIB146-001-Q1-E1-D9

Method BLASTX
NCBI GI g112682
BLAST score 538
E value 3.0e-55
Match length 115
% identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 137372

Seq. ID LIB146-001-Q1-E1-E2

Method BLASTX
NCBI GI g1628583
BLAST score 545
E value 4.0e-56
Match length 105
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137373

Seq. ID LIB146-001-Q1-E1-E9

Method BLASTX
NCBI GI g4204299
BLAST score 706
E value 7.0e-75
Match length 133
% identity 100

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 137374

Seq. ID LIB146-001-Q1-E1-F12

Method BLASTN
NCBI GI g2264304
BLAST score 280
E value 1.0e-156
Match length 310
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBG8, complete sequence [Arabidopsis thaliana]

Seq. No. 137375

Seq. ID LIB146-001-Q1-E1-F3

Method BLASTX
NCBI GI g3075398
BLAST score 164

2.0e-11 E value Match length 84 % identity 48 (AC004484) unknown protein [Arabidopsis thaliana] NCBI Description 137376 Seq. No. LIB146-001-Q1-E1-F8 Seq. ID Method BLASTX q3860247 NCBI GI BLAST score 506 E value 2.0e-51 Match length 102 % identity 90 (AC005824) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 137377 Seq. ID LIB146-001-Q1-E1-H7 Method BLASTX NCBI GI q3004546 BLAST score 175 E value 9.0e-13 Match length 61 % identity (AC003673) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi 4185149 (AC005724) hypothetical protein [Arabidopsis

thaliana]

137378 Seq. No.

Seq. ID LIB146-001-Q1-E1-H9

Method BLASTX q3269286 NCBI GI BLAST score 375 4.0e-36 E value 94 Match length 87 % identity

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

137379 Seq. No.

LIB146-002-Q1-E1-A3 Seq. ID

Method BLASTN g3241917 NCBI GI 316 BLAST score 1.0e-178 E value Match length 324 99 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19B1, complete sequence [Arabidopsis thaliana]

137380 Seq. No.

Seq. ID LIB146-002-Q1-E1-B10

Method BLASTX q1628583 NCBI GI BLAST score 528 E value 4.0e-54 104 Match length % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis



thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137381 Seq. ID LIB146-002-Q1-E1-B2 Method BLASTX NCBI GI g112741 BLAST score 581 E value 2.0e-60 Match length 110 % identity 97 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

 Seq. No.
 137382

 Seq. ID
 LIB146-002-Q1-E1-C11

 Method
 BLASTX

 NCBI GI
 g266693

 BLAST score
 357

 F walke
 5.0e-34

E value 5.0e-34
Match length 66
% identity 100

NCBI Description OLEOSIN >gi_282875_pir_S22538 oleosin - Arabidopsis

thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_ (AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No. 137383

Seq. ID LIB146-002-Q1-E1-D12

Method BLASTX
NCBI GI g1628583
BLAST score 668
E value 2.0e-70
Match length 128
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137384

Seq. ID LIB146-002-Q1-E1-D7

Method BLASTX
NCBI GI g112737
BLAST score 501
E value 7.0e-51
Match length 124
% identity 79

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]



>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
precursor [Arabidopsis thaliana]

Seq. No. 137385

Seq. ID LIB146-002-Q1-E1-E1

Method BLASTX
NCBI GI g135858
BLAST score 316
E value 2.0e-29
Match length 53
% identity 100

NCBI Description TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)

>gi_99760_pir__S22201 tonoplast intrinsic protein alpha Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551)
tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
[Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast

intrinsic protein alpha [Arabidopsis thaliana]

Seq. No. 137386

Seq. ID LIB146-002-Q1-E1-E11

Method BLASTX
NCBI GI g1628583
BLAST score 545
E value 4.0e-56
Match length 105
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137387

Seq. ID LIB146-002-Q1-E1-E5

Method BLASTX
NCBI GI g1628583
BLAST score 493
E value 6.0e-50
Match length 129
% identity 77

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137388

Seq. ID LIB146-002-Q1-E1-E6

Method BLASTN
NCBI GI 94454004
BLAST score 187
E value 1.0e-101
Match length 219
% identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6

(ESSAII project)

Seq. No. 137389

Seq. ID LIB146-002-Q1-E1-F4

Method BLASTX



NCBI GI g1628583 BLAST score 663 E value 7.0e-70 Match length 127 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137390

Seq. ID LIB146-002-Q1-E1-F9

Method BLASTX
NCBI GI 94455208
BLAST score 652
E value 1.0e-68
Match length 135
% identity 93

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 137391

Seq. ID LIB146-002-Q1-E1-G11

Method BLASTX
NCBI GI g3882273
BLAST score 155
E value 2.0e-10
Match length 88
% identity 40

NCBI Description (AB018319) KIAA0776 protein [Homo sapiens]

Seq. No. 137392

Seq. ID LIB146-002-Q1-E1-G12

Method BLASTX
NCBI GI g1174864
BLAST score 525
E value 7.0e-54
Match length 99
% identity 100

NCBI Description UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN I

PRECURSOR >gi_1076200_pir__JX0300 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) chain I precursor - Euglena gracilis mitochondrion >gi_464153_dbj_BAA04079_ (D16671) complex III subunit I precursor [Euglena gracilis]

Sea. No. 137393

Seq. No. 137393 Seq. ID LIB146-002-Q1-E1-H2

Method BLASTN
NCBI GI g3046852
BLAST score 88
E value 4.0e-42
Match length 179
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQJ16, complete sequence [Arabidopsis thaliana]

Seq. No. 137394

Seq. ID LIB146-003-Q1-E1-A6

Method BLASTN



NCBI GI g4220632 BLAST score 218 E value 1.0e-119 Match length 397 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K6M13, complete sequence [Arabidopsis thaliana]

Seq. No. 137395

Seq. ID LIB146-003-Q1-E1-B10

Method BLASTX
NCBI GI g3820564
BLAST score 162
E value 4.0e-11
Match length 122
% identity 34

NCBI Description (AF080002) ATP-dependent zinc metallopeptidase FtsH

[Heliobacillus mobilis]

Seq. No. 137396

Seq. ID LIB146-003-Q1-E1-C10

Method BLASTX
NCBI GI g3608412
BLAST score 304
E value 1.0e-27
Match length 137
% identity 50

NCBI Description (AF079355) protein phosphatase-2c [Mesembryanthemum

crystallinum]

Seq. No. 137397

Seq. ID LIB146-003-Q1-E1-C3

Method BLASTX
NCBI GI g2982431
BLAST score 128
E value 4.0e-07
Match length 127
% identity 4

NCBI Description (AL022224) leucine rich repeat-like protein [Arabidopsis

thaliana]

Seq. No. 137398

Seq. ID LIB146-003-Q1-E1-E2

Method BLASTN
NCBI GI g4006885
BLAST score 430
E value 0.0e+00
Match length 430
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 137399

Seq. ID LIB146-003-Q1-E1-E6

Method BLASTX
NCBI GI g3075390
BLAST score 583



```
2.0e-60
E value
                  140
Match length
% identity
                  77
NCBI Description
                  (AC004484) protein kinase ARSK1 [Arabidopsis thaliana]
                  137400
Seq. No.
                  LIB146-003-Q1-E1-F10
Seq. ID
Method
                  BLASTN
                  q2264305
NCBI GI
BLAST score
                  34
                  1.0e-09
E value
Match length
                  78
% identity
                  86
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBK23, complete sequence [Arabidopsis thaliana]
                  137401
Seq. No.
                  LIB146-003-Q1-E1-G8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2182286
BLAST score
                  412
E value
                  0.0e+00
Match length
                  420
% identity
                  100
                  Sequence of BAC F20P5 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  137402
Seq. ID
                  LIB146-003-Q1-E1-H8
Method
                  BLASTN
                  g4589445
NCBI GI
BLAST score
                  392
                  0.0e+00
E value
Match length
                  416
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWL2, complete sequence
Seq. No.
                  137403
                  LIB146-004-Q1-E1-A7
Seq. ID
Method
                  BLASTN
                  g4454447
NCBI GI
BLAST score
                  170
                  9.0e-91
E value
Match length
                  338
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F5H14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
```

Seq. No. 137404

Seq. ID LIB146-004-Q1-E1-B4

Method BLASTN
NCBI GI 94558586
BLAST score 227
E value 1.0e-125
Match length 296
% identity 95



NCBI Description Arabidopsis thaliana chromosome 1 BAC T518 sequence, complete sequence

Seq. No. 137405
Seq. ID LIB146-004-Q1-E1-B9

Method BLASTN
NCBI GI g3135250
BLAST score 128
E value 1.0e-65
Match length 336
% identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137406

Seq. ID LIB146-004-Q1-E1-C1

Method BLASTN
NCBI GI g4757414
BLAST score 167
E value 6.0e-89
Match length 219
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYF24, complete sequence

Seq. No. 137407

Seq. ID LIB146-004-Q1-E1-C6

Method BLASTX
NCBI GI g1628583
BLAST score 490
E value 1.0e-49
Match length 93
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137408

Seq. ID LIB146-004-Q1-E1-D12

Method BLASTX
NCBI GI g3738315
BLAST score 217
E value 1.0e-17
Match length 118
% identity 47

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 137409

Seq. ID LIB146-004-Q1-E1-E5

Method BLASTX
NCBI GI g2586081
BLAST score 178
E value 4.0e-13
Match length 110
% identity 7

NCBI Description (U72725) receptor kinase-like protein [Oryza

longistaminata]

% identity

NCBI Description

86



```
Seq. No.
                  137410
Seq. ID
                  LIB146-004-Q1-E1-F12
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  263
E value
                  2.0e-23
Match length
                  53
                  100
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  137411
Seq. ID
                  LIB146-004-Q1-E1-G12
Method
                  BLASTN
NCBI GI
                  g4454585
BLAST score
                  53
                  2.0e-21
E value
                  92
Match length
% identity
                  Arabidopsis thaliana BAC T13D4 from chromosome IV near 21.5
NCBI Description
                  cM, complete sequence
Seq. No.
                  137412
Seq. ID
                  LIB146-004-Q1-E1-H1
Method
                  BLASTN
NCBI GI
                  q2494106
BLAST score
                  93
E value
                  7.0e-45
Match length
                  326
% identity
                  100
                  Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  137413
Seq. ID
                  LIB146-004-Q1-E1-H11
Method
                  BLASTX
                  g3927836
NCBI GI
BLAST score
                  233
                  2.0e-19
E value
Match length
                  70
% identity
                  (AC005727) unknown protein [Arabidopsis thaliana]
NCBI Description
                  137414
Seq. No.
                  LIB146-004-Q1-E1-H9
Seq. ID
Method
                  BLASTX
                  g266693
NCBI GI
BLAST score
                  581
E value
                  3.0e-60
Match length
                  137
```

16463

OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis

thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_ (AL035523) oleosin, 18.5K [Arabidopsis thaliana]



```
137415
Seq. No.
Seq. ID
                  LIB146-005-Q1-E1-A6
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  654
                  8.0e-69
E value
Match length
                  127
% identity
                  99
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495 emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  137416
Seq. ID
                  LIB146-005-Q1-E1-B10
Method
                  BLASTN
NCBI GI
                  q4510338
BLAST score
                  211
E value
                  1.0e-115
Match length
                  399
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC F2H17 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  137417
Seq. ID
                  LIB146-005-Q1-E1-C8
Method
                  BLASTX
NCBI GI
                  g4263543
BLAST score
                  610
E value
                  1.0e-63
                  129
Match length
% identity
                  88
                  (ACO06250) putative Athila retroelement ORF1 protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  137418
                  LIB146-005-Q1-E1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4559391
BLAST score
                  471
                  2.0e-47
E value
Match length
                  89
                  100
% identity
                  (AC006526) putative auxin response factor 1 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  137419
                  LIB146-005-Q1-E1-F11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4586241
```

Method BLASTN
NCBI GI g458624
BLAST score 332
E value 0.0e+00
Match length 397
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18

(ESSA project)



Seq. No. 137420 Seq. ID LIB146-

LIB146-005-Q1-E1-F7

Method BLASTX
NCBI GI g112681
BLAST score 474
E value 1.0e-47
Match length 115
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 137421

Seq. ID LIB146-005-Q1-E1-F9

Method BLASTX
NCBI GI g266693
BLAST score 493
E value 7.0e-50
Match length 119
% identity 84

NCBI Description OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis

thaliana >gi 16405 emb CAA44225 (X62353) oleosin [Arabidopsis thaliana] >gi 4455257 emb CAB36756.1 (AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No. 137422

Seq. ID LIB146-005-Q1-E1-G12

Method BLASTN
NCBI GI g4519193
BLAST score 299
E value 1.0e-167
Match length 363
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC11, complete sequence

Seq. No. 137423

Seq. ID LIB146-005-Q1-E1-G8

Method BLASTN
NCBI GI g4467131
BLAST score 364
E value 0.0e+00
Match length 372
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13

(ESSA project)

Seq. No. 137424

Seq. ID LIB146-005-Q1-E1-G9

Method BLASTN
NCBI GI g3510339
BLAST score 259
E value 1.0e-144
Match length 401
% identity 98



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No. 137425

Seq. ID LIB146-005-Q1-E1-H6

Method BLASTX
NCBI GI g4103987
BLAST score 246
E value 5.0e-21
Match length 61
% identity 75

NCBI Description (AF030516) 5,10-methylenetetrahydrofolate

dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase

[Pisum sativum]

Seq. No. 137426

Seq. ID LIB146-006-Q1-E1-A10

Method BLASTX
NCBI GI g4038045
BLAST score 268
E value 2.0e-23
Match length 96
% identity 59

NCBI Description (AC005936) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No. 137427

Seq. ID LIB146-006-Q1-E1-A6

Method BLASTX
NCBI GI g4544399
BLAST score 367
E value 4.0e-35
Match length 106
% identity 65

NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 137428

Seq. ID LIB146-006-Q1-E1-C11

Method BLASTX
NCBI GI g1628583
BLAST score 475
E value 4.0e-48
Match length 92
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137429

Seq. ID LIB146-006-Q1-E1-C3

Method BLASTX
NCBI GI 94406051
BLAST score 236
E value 5.0e-20
Match length 93
% identity 59



(AF067605) linalool synthase-like protein [Arabidopsis thaliana]

Seq. No. 137430

NCBI Description

Seq. ID LIB146-006-Q1-E1-C4

Method BLASTN NCBI GI q4757414 BLAST score 340 E value 0.0e + 00Match length 340 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYF24, complete sequence

Seq. No. 137431

Seq. ID LIB146-006-Q1-E1-C8

Method BLASTN NCBI GI g3582315 BLAST score 181 E value 3.0e-97 Match length 343 % identity 97

Arabidopsis thaliana chromosome II BAC T27A16 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137432

Seq. ID LIB146-006-Q1-E1-D10

Method BLASTX NCBI GI q1628583 BLAST score 540 E value 1.0e-55 Match length 105 % identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137433

LIB146-006-Q1-E1-D12 Seq. ID

Method BLASTX NCBI GI q4567295 BLAST score 574 2.0e-59 E value 133 Match length % identity 77

NCBI Description (AC006918) putative pol polyprotein [Arabidopsis thaliana]

137434 Seq. No.

LIB146-006-Q1-E1-D6 Seq. ID

Method BLASTX NCBI GI g2583120 BLAST score 550 E value 1.0e-56 Match length 130 % identity 86

NCBI Description (AC002387) putative receptor-like protein kinase

[Arabidopsis thaliana]



```
Seq. No.
                   137435
Seq. ID
                   LIB146-006-Q1-E1-D8
Method
                  BLASTX
NCBI GI
                   g3763936
BLAST score
                   643
E value
                   1.0e-67
Match length
                   122
                   100
% identity
NCBI Description
                   (AC004450) putative myb-related transcription factor
                   [Arabidopsis thaliana]
Seq. No.
                   137436
Seq. ID
                   LIB146-006-Q1-E1-G12
Method
                   BLASTX
NCBI GI
                   q4467129
BLAST score
                   572
E value
                   3.0e-59
Match length
                   111
                   99
% identity
NCBI Description
                   (AL035538) calcium-dependent protein kinase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   137437
Seq. ID
                   LIB146-006-Q1-E1-G6
Method
                   BLASTX
NCBI GI
                   g3176665
BLAST score
                   689
E value
                   7.0e-73
Match length
                   128
% identity
                   98
NCBI Description
                  (AC004393) T1F15.9 [Arabidopsis thaliana]
                   137438
Seq. No.
                   LIB146-007-Q1-E1-A4
Seq. ID
Method
                   BLASTN
                   g3449322
NCBI GI
                   112
BLAST score
                   3.0e-56
E value
Match length
                   302
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MXC17, complete sequence [Arabidopsis thaliana]
                   137439
Seq. No.
Seq. ID
                   LIB146-007-Q1-E1-B3
Method
                   BLASTN
                   g3510342
                   35
```

NCBI GI BLAST score E value 3.0e-10 Match length 87 % identity 85

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MGN6, complete sequence [Arabidopsis thaliana]

Seq. No. 137440

Seq. ID LIB146-007-Q1-E1-B7



Method BLASTX
NCBI GI g1628583
BLAST score 249
E value 2.0e-21
Match length 48
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137441

Seq. ID LIB146-007-Q1-E1-C6

Method BLASTX
NCBI GI g4454027
BLAST score 178
E value 3.0e-13
Match length 63
% identity 62

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 137442

Seg. ID LIB146-007-Q1-E1-G1

Method BLASTN
NCBI GI g4406752
BLAST score 314
E value 1.0e-176
Match length 339
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F19B11 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137443

Seq. ID LIB146-007-Q1-E1-G10

Method BLASTX
NCBI GI g112741
BLAST score 588
E value 4.0e-61
Match length 108
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 137444

Seq. ID LIB146-007-Q1-E1-G6

Method BLASTX
NCBI GI g1628583
BLAST score 541
E value 1.0e-55
Match length 104
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

% identity

NCBI Description

55





cruciferin seed storage protein [Arabidopsis thaliana]

```
Seq. No.
                  137445
Seq. ID
                  LIB146-008-Q1-E1-B11
Method
                  BLASTX
                  q4567296
NCBI GI
BLAST score
                  341
                  4.0e-32
E value
                  94
Match length
                  73
% identity
                   (ACOO6918) putative Athila retroelement ORF1 protein
NCBI Description
                   [Arabidopsis thaliana]
                  137446
Seq. No.
Seq. ID
                  LIB146-008-Q1-E1-C4
Method
                  BLASTN
                  g4510360
NCBI GI
BLAST score
                  281
                  1.0e-157
E value
                  325
Match length
% identity
                   96
                  Arabidopsis thaliana chromosome II BAC F11F19 genomic
NCBI Description
                  sequence, complete sequence
                  137447
Seq. No.
                  LIB146-008-Q1-E1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1628583
                   489
BLAST score
                   2.0e-49
E value
                   127
Match length
                   77
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   137448
Seq. No.
                  LIB146-008-Q1-E1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   a4512651
                   289
BLAST score
                   6.0e-26
E value
                   128
Match length
% identity
                   45
NCBI Description
                   (AC007048) putative tyrosine transaminase [Arabidopsis
                   thaliana]
Seq. No.
                   137449
Seq. ID
                   LIB146-008-Q1-E1-G4
Method
                   BLASTX
NCBI GI
                   q4567216
BLAST score
                   274
                   2.0e-24
E value
Match length
                   110
```

(AC007113) hypothetical protein [Arabidopsis thaliana]



```
137450
Seq. No.
                  LIB146-008-Q1-E1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  580
E value
                  5.0e-60
Match length
                  135
                  84
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  137451
Seq. ID
                  LIB146-008-Q1-E1-H10
Method
                  BLASTN
NCBI GI
                  g2924733
BLAST score
                  423
                  0.0e + 00
E value
Match length
                  423
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUF9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  137452
Seq. ID
                  LIB146-008-Q1-E1-H3
Method
                  BLASTN
NCBI GI
                  g3449318
BLAST score
                  230
                  1.0e-126
E value
Match length
                  242
                  85
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLF18, complete sequence [Arabidopsis thaliana]
Seq. No.
                  137453
                  LIB146-008-Q1-E1-H6
Seq. ID
Method
                  BLASTX
                  g4773887
NCBI GI
BLAST score
                  363
E value
                  6.0e-35
Match length
                  90
                  87
% identity
                  (AF076243) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  137454
Seq. No.
                  LIB146-009-Q1-E1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2924651
```

Method BLASTN
NCBI GI g292465
BLAST score 382
E value 0.0e+00
Match length 382
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K2A18, complete sequence [Arabidopsis thaliana]

```
137455
Seq. No.
                  LIB146-009-Q1-E1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3080406
BLAST score
                   19
E value
                   1.3e+00
Match length
                   103
                   90
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12
NCBI Description
                   (ESSA project)
Seq. No.
                   137456
                  LIB146-009-Q1-E1-C6
Seq. ID
```

Method BLASTN

NCBI GI g2656028 BLAST score 136 E value 2.0e-70 Match length 323 98 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MNF13

Seq. No. 137457 LIB146-009-Q1-E1-D12 Seq. ID Method BLASTN NCBI GI g2264321 BLAST score 75

5.0e-34 E value Match length 236 % identity 92

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MXM12, complete sequence [Arabidopsis thaliana]

137458 Seq. No.

LIB146-009-Q1-E1-F10 Seq. ID

Method BLASTN NCBI GI g2264319 BLAST score 268 E value 1.0e-149 Match length 341 99 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MXA21, complete sequence [Arabidopsis thaliana]

137459 Seq. No.

Seq. ID LIB146-009-Q1-E1-F4

Method BLASTX NCBI GI g1628583 BLAST score 535 E value 5.0e-55 Match length 104 % identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137460



```
LIB146-009-Q1-E1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  483
E value
                  6.0e-49
Match length
                  91
% identity
                  99
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >qi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  137461
                  LIB146-009-Q1-E1-G2
Seq. ID
Method
                  BLASTN
                  g2656031
NCBI GI
BLAST score
                  356
                  0.0e + 00
E value
Match length
                  364
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC20
Seq. No.
                  137462
Seq. ID
                  LIB146-009-Q1-E1-G3
Method
                  BLASTN
NCBI GI
                  g2264303
BLAST score
                  214
E value
                  1.0e-117
Match length
                  218
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBB18, complete sequence [Arabidopsis thaliana]
                  137463
Seq. No.
                  LIB146-009-Q1-E1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4580365
BLAST score
                  188
                  1.0e-101
E value
Match length
                  235
% identity
                  94
                  Arabidopsis thaliana chromosome I BAC F3F20 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  137464
                  LIB146-009-Q1-E1-H7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3292807
BLAST score
                  415
                  0.0e+00
E value
Match length
                  415
```

16473

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19

100

% identity



(ESSAII project)

```
Seq. No.
                  137465
Seq. ID
                  LIB146-010-Q1-E1-A1
Method
                  BLASTX
                  g2494144
NCBI GI
                  143
BLAST score
                  2.0e-09
E value
                  45
Match length
                  69
% identity
                   (AC002329) predicted leucine-rich protein [Arabidopsis
NCBI Description
                  thaliana]
                  137466
Seq. No.
Seq. ID
                  LIB146-010-Q1-E1-A12
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  625
                  2.0e-65
E value
                  120
Match length
% identity
                   100
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   137467
                   LIB146-010-Q1-E1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4510401
                   486
BLAST score
                   4.0e-49
E value
                   114
Match length
                   74
% identity
                   (AC006587) putative general negative regulator of
NCBI Description
                   transcription [Arabidopsis thaliana]
                   137468
Seq. No.
                   LIB146-010-Q1-E1-A8
Seq. ID
                   BLASTN
Method
                   g4757404
NCBI GI
BLAST score
                   38
                   6.0e-12
E value
Match length
                   369
                   36
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MLJ15, complete sequence
                   137469
Seq. No.
Seq. ID
                   LIB146-010-Q1-E1-B4
Method
                   BLASTN
NCBI GI
                   q3335331
                   366
BLAST score
                   0.0e + 00
E value
                   370
Match length
                   100
% identity
                   Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
NCBI Description
```

16474

complete sequence [Arabidopsis thaliana]

E value Match length

% identity



```
137470
Seq. No.
Seq. ID
                  LIB146-010-Q1-E1-C3
Method
                  BLASTX
NCBI GI
                  g2129659
BLAST score
                  337
E value
                  1.0e-31
Match length
                  66
                  97
% identity
NCBI Description
                  oleosin, isoform 21K - Arabidopsis thaliana >gi_725260
                  (L40954) oleosin [Arabidopsis thaliana]
Seq. No.
                  137471
Seq. ID
                  LIB146-010-Q1-E1-D2
Method
                  BLASTX
NCBI GI
                  q4033365
BLAST score
                  86
E value
                  1.0e-69
Match length
                  135
% identity
                  97
NCBI Description
                  (AJ223499) ATP sulfurylase [Brassica juncea]
Seq. No.
                  137472
Seq. ID
                  LIB146-010-Q1-E1-D3
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  618
E value
                  1.0e-64
Match length
                  114
% identity
                  100
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) > gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >qi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  137473
Seq. ID
                  LIB146-010-Q1-E1-D7
Method
                  BLASTN
NCBI GI
                  g4757414
                  205
BLAST score
                  1.0e-111
E value
Match length
                  361
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MYF24, complete sequence
                  137474
Seq. No.
Seq. ID
                  LIB146-010-Q1-E1-F11
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  607
```

16475

3.0e-63

116



(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb_CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137475

NCBI Description

Seq. ID LIB146-010-Q1-E1-F3

Method BLASTX
NCBI GI g1628583
BLAST score 663
E value 7.0e-70
Match length 127
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137476

Seq. ID LIB146-010-Q1-E1-G5

Method BLASTX
NCBI GI g3805763
BLAST score 149
E value 8.0e-10
Match length 83
% identity 45

NCBI Description (AC005693) hypothetical protein [Arabidopsis thaliana]

Seq. No. 137477

Seq. ID LIB146-011-Q1-E1-A12

Method BLASTN
NCBI GI g2828182
BLAST score 225
E value 1.0e-123
Match length 246
% identity 51

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No. 137478

Seq. ID LIB146-011-Q1-E1-A3

Method BLASTN
NCBI GI g3510343
BLAST score 293
E value 1.0e-164
Match length 348
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJC20, complete sequence [Arabidopsis thaliana]

Seq. No. 137479

Seq. ID LIB146-011-Q1-E1-A8

Method BLASTN
NCBI GI 94678315
BLAST score 285
E value 1.0e-159
Match length 363
% identity 49

NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15



(ESSA project)

```
Seq. No.
                   137480
Seq. ID
                   LIB146-011-Q1-E1-A9
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   545
E value
                   4.0e-56
Match length
                   105
% identity
                   100
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   137481
Seq. ID
                   LIB146-011-Q1-E1-B8
Method
                   BLASTN
NCBI GI
                   g4589445
BLAST score
                   128
E value
                   1.0e-65
Match length
                   345
% identity
                   91
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWL2, complete sequence
Seq. No.
                   137482
Seq. ID
                  LIB146-011-Q1-E1-D12
Method
                  BLASTX
NCBI GI
                  g4753655
BLAST score
                  312
E value
                  7.0e-29
Match length
                  88
% identity
                  77
NCBI Description
                  (AL049751) pectate lyase like protein [Arabidopsis
                  thaliana]
Seq. No.
                  137483
Seq. ID
                  LIB146-011-Q1-E1-E7
Method
                  BLASTN
NCBI GI
                  g4584841
BLAST score
                  187
E value
                  1.0e-101
Match length
                  255
% identity
                  99
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T23E23,
                  complete sequence
Seq. No.
                  137484
Seq. ID
                  LIB146-011-Q1-E1-F1
Method
                  BLASTX
NCBI GI
                  g3157930
BLAST score
                  583
E value
                  2.0e-60
Match length
                  109
% identity
NCBI Description
                  (AC002131) Strong similarity to
                  amino-cyclopropane-carboxylic acid oxidase gb_L27664 from
```



Brassica napus. ESTs gb Z48548 and gb Z48549 come from this gene. [Arabidopsis thaliana]

137485 Seq. No.

Seq. ID LIB146-011-Q1-E1-G4

Method BLASTX q1628583 NCBI GI 473 BLAST score 7.0e-48 E value 92 Match length % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

137486 Seq. No.

Seq. ID LIB146-011-Q1-E1-G7

Method BLASTX NCBI GI g534982 192 BLAST score 4.0e-15 E value 79 Match length % identity

NCBI Description (X75898) phosphoglucomutase [Spinacia oleracea]

137487 Seq. No.

Seq. ID LIB146-012-Q1-E1-A2

Method BLASTX NCBI GI g1628583 BLAST score 541 E value 1.0e-55 Match length 104 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

> thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137488

LIB146-012-Q1-E1-C12 Seq. ID

Method BLASTN NCBI GI g2842474 BLAST score 158 E value 6.0e-84 Match length 162 % identity 99

Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 NCBI Description

(ESSAII project)

Seq. No. 137489

LIB146-012-Q1-E1-D1 Seq. ID

Method BLASTX NCBI GI g4678361 BLAST score 561 E value 5.0e-58 Match length 112 96 % identity

(AL049659) cytochrome P450-like protein [Arabidopsis NCBI Description

% identity

NCBI Description



thaliana]

Seq. No. 137490 Seq. ID LÍB146-012-Q1-E1-D9 Method BLASTN NCBI GI g4432793 BLAST score 280 E value 1.0e-156 Match length 360 46 % identity Arabidopsis thaliana chromosome II BAC T19K21 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 137491 Seq. No. Seq. ID LIB146-012-Q1-E1-E6 Method BLASTN NCBI GI q16231 BLAST score 130 E value 3.0e-67 150 Match length 97 % identity NCBI Description Arabidopsis CRA1 gene for 12S seed storage protein >qi 166675 qb M37247 ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4 Seq. No. 137492 Seq. ID LIB146-012-Q1-E1-F11 Method BLASTN NCBI GI g3426033 BLAST score 233 E value 1.0e-128 Match length 257 % identity 97 Arabidopsis thaliana chromosome II BAC F12C20 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 137493 LIB146-012-Q1-E1-F4 Seq. ID Method BLASTN NCBI GI g3522932 BLAST score 242 E value 1.0e-133 331 Match length 95 % identity Arabidopsis thaliana chromosome II BAC F14M4 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 137494 Seq. No. LIB146-012-Q1-E1-F8 Seq. ID Method BLASTX g112741 NCBI GI BLAST score 566 E value 1.0e-58 Match length 105 100

16479

2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -



Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No. 137495 LIB146-012-Q1-E1-G1 Seq. ID Method BLASTN NCBI GI g2828278 BLAST score 170 E value 9.0e-91 327 Match length 99 % identity Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 NCBI Description (ESSAII project) Seq. No. 137496 Seq. ID LIB146-012-Q1-E1-G11 Method BLASTX NCBI GI q2642448 BLAST score 353

1.0e-33

thaliana]

Match length 114
% identity 34
NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]
>qi 3169187 (AC004401) hypothetical protein [Arabidopsis

Seq. No. 137497

E value

Seq. ID LIB146-012-Q1-E1-G12

Method BLASTN
NCBI GI g4699904
BLAST score 25
E value 3.0e-04
Match length 412
% identity 79

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F1E22,

complete sequence

Seq. No. 137498

Seq. ID LIB146-012-Q1-E1-G4

Method BLASTN
NCBI GI g2058505
BLAST score 39
E value 1.0e-12
Match length 39
% identity 100

NCBI Description Brassica rapa zinc-finger protein BcZFP1 (BcAFP1(3-2z))

gene, complete cds

Seq. No. 137499

Seq. ID LIB146-012-Q1-E1-H8

MethodBLASTXNCBI GIg4467126BLAST score525E value8.0e-54



Match length % identity 99 (AL035538) guanine nucleotide-exchange protein-like NCBI Description [Arabidopsis thaliana] Seq. No. 137500 Seq. ID LIB146-012-Q1-E1-H9 Method BLASTX NCBI GI q2274993 BLAST score 385 E value 2.0e-37 Match length 95 72 % identity NCBI Description (AJ000230) unnamed protein product [Hordeum vulgare] Seq. No. 137501 Seq. ID LIB146-013-Q1-E1-A12 Method BLASTN NCBI GI q2104523 BLAST score 278 E value 1.0e-155 Match length 369 % identity 94 Arabidopsis thaliana BAC T10M13 from chromosome IV, from NCBI Description 10.8 cM to 11.6 cM, complete sequence Seq. No. 137502 Seq. ID LIB146-013-Q1-E1-A5 Method BLASTX NCBI GI g2529229 BLAST score 439 E value 1.0e-43 Match length 102 85 % identity (AB007907) 6-phosphogluconate dehydrogenase [Glycine max] NCBI Description Seq. No. 137503 LIB146-013-Q1-E1-B10 Seq. ID Method BLASTN NCBI GI g3608126 BLAST score 200 1.0e-108 E value Match length 305 100 % identity NCBI Description Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 137504

LIB146-013-Q1-E1-C10 Seq. ID

Method BLASTX NCBI GI g729775 BLAST score 152 E value 6.0e-10 Match length 105 33 % identity

NCBI Description HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR)



>gi_100264_pir__S25481 heat shock transcription factor 8 Peruvian tomato >gi_19492_emb_CAA47869_ (X67600) heat shock
transcription factor 8 [Lycopersicon peruvianum]

 Seq. No.
 137505

 Seq. ID
 LIB146-013-Q1-E1-C4

 Method
 BLASTN

 NCBI GI
 q4454022

NCBI GI g4454022 BLAST score 187 E value 1.0e-101 Match length 361 % identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16

(ESSAII project)

Seq. No. 137506

Seq. ID LIB146-013-Q1-E1-C7

Method BLASTN
NCBI GI g2358139
BLAST score 215
E value 1.0e-118
Match length 223
% identity 99

NCBI Description Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete

sequence [Arabidopsis thaliana]

Seq. No. 137507

Seq. ID LIB146-013-Q1-E1-C8

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137508

Seq. ID LIB146-013-Q1-E1-D5

Method BLASTX
NCBI GI g131360
BLAST score 241
E value 2.0e-20
Match length 61
% identity 82

NCBI Description PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR

>gi 81727_pir__S02115 photosystem II protein psbK precursor

- white mustard chloroplast >gi_12209 emb_CAA31909_ (X13558) K preprotein (AA -24 to 37) [Sinapis alba]

Seq. No. 137509

Seq. ID LIB146-013-Q1-E1-D6

MethodBLASTXNCBI GIg4467126BLAST score690E value5.0e-73



Match length 136 % identity 99

NCBI Description (AL035538) guanine nucleotide-exchange protein-like

[Arabidopsis thaliana]

Seq. No. 137510

Seq. ID LIB146-013-Q1-E1-D7

Method BLASTX
NCBI GI g112681
BLAST score 710
E value 2.0e-75
Match length 134
% identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 137511

Seq. ID LIB146-013-Q1-E1-E1

Method BLASTN
NCBI GI g4757415
BLAST score 365
E value 0.0e+00
Match length 393
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MYN21, complete sequence

Seq. No. 137512

Seq. ID LIB146-013-Q1-E1-E12

Method BLASTX
NCBI GI g2129738
BLAST score 643
E value 1.0e-67
Match length 124
% identity 100

NCBI Description shaggy-like kinase dzeta - Arabidopsis thaliana

>gi_1225913_emb_CAA64408_ (X94938) shaggy-like kinase dzeta
[Arabidopsis thaliana] >gi_1669653_emb_CAA70483_ (Y09300)

serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 137513

Seq. ID LIB146-013-Q1-E1-F10

Method BLASTX
NCBI GI g4325282
BLAST score 306
E value 5.0e-28
Match length 59
% identity 93

NCBI Description (AF123310) NAC domain protein NAM [Arabidopsis thaliana]

>gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM

[Arabidopsis thaliana]

Seq. No. 137514

Seq. ID LIB146-013-Q1-E1-F9

E value

2.0e-23



```
BLASTX
Method
                  g4512666
NCBI GI
BLAST score
                  378
E value
                  2.0e-36
Match length
                  122
% identity
                  38
                  (AC006931) putative mei2 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  137515
                  LIB146-013-Q1-E1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406821
BLAST score
                  586
E value
                  8.0e-61
Match length
                  106
% identity
                  100
                  (AC006201) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  137516
                  LIB146-014-Q1-E1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3152576
BLAST score
                  189
                  1.0e-14
E value
Match length
                   64
% identity
                   59
                  (AC002986) Similar to liver-specific transport protein
NCBI Description
                  gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]
                   137517
Seq. No.
                  LIB146-014-Q1-E1-C1
Seq. ID
Method
                  BLASTN
                   q4539309
NCBI GI
BLAST score
                   126
                   1.0e-64
E value
Match length
                   302
                   93
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22
NCBI Description
                   (ESSA project)
                   137518
Seq. No.
                   LIB146-014-Q1-E1-C3
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2264309
BLAST score
                   183
E value
                   1.0e-98
                   217
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MJJ3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   137519
                   LIB146-014-Q1-E1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4587526
BLAST score
                   267
```



Match length 112 % identity 48

NCBI Description (AC007060) Strong similarity to F19I3.2 gi_3033375 putative

berberine bridge enzyme from Arabidopsis thaliana BAC gb AC004238. ESTs gb F19886, gb Z30784 and gb Z30785 come

from this gene

Seq. No. 137520

Seq. ID LIB146-014-Q1-E1-D11

Method BLASTN
NCBI GI g4539290
BLAST score 349
E value 0.0e+00
Match length 373
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19

(ESSA project)

Seq. No. 137521

Seq. ID LIB146-014-Q1-E1-D12

Method BLASTX
NCBI GI g112681
BLAST score 564
E value 3.0e-58
Match length 132
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 137522

Seq. ID LIB146-014-Q1-E1-E9

Method BLASTX
NCBI GI g112741
BLAST score 484
E value 4.0e-49
Match length 90
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 137523

Seq. ID LIB146-014-Q1-E1-F6

Method BLASTX
NCBI GI 94539452
BLAST score 372
E value 7.0e-36
Match length 100
% identity 70

NCBI Description (AL049500) putative phosphoribosylanthranilate transferase



[Arabidopsis thaliana]

```
Seq. No.
                  137524
Seq. ID
                  LIB146-014-Q1-E1-H1
Method
                  BLASTN
                  q2842474
NCBI GI
BLAST score
                  228
E value
                  1.0e-125
Match length
                  260
% identity
                  96
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
NCBI Description
                   (ESSAII project)
Seq. No.
                  137525
Seq. ID
                  LIB146-014-Q1-E1-H12
Method
                  BLASTX
NCBI GI
                  g2829892
BLAST score
                  365
E value
                   6.0e-35
Match length
                  121
% identity
                  59
                  (AC002311) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  137526
Seq. ID
                  LIB146-014-Q1-E1-H3
Method
                  BLASTX
NCBI GI
                  g4510418
BLAST score
                  415
E value
                   4.0e-41
Match length
                  85
% identity
                  98
                  (AC006929) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  137527
                  LIB146-015-Q1-E1-A2
Seq. ID
Method
                  BLASTX
                  g1619602
NCBI GI
BLAST score
                  313
E value
                   6.0e-29
Match length
                  73
                  82
% identity
NCBI Description
                  (Y08726) MtN3 [Medicago truncatula]
                  137528
Seq. No.
                  LIB146-015-Q1-E1-B5
Seq. ID
Method
                  BLASTX
                  g112741
NCBI GI
BLAST score
                   595
                   6.0e-62
E value
Match length
                   109
% identity
                   100
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
```

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3



precursor [Arabidopsis thaliana]

```
137529
Seq. No.
                  LIB146-015-Q1-E1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2660672
BLAST score
                  534
E value
                  8.0e-55
Match length
                  115
% identity
                  41
                  (AC002342) similar to pMS10 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  137530
Seq. ID
                  LIB146-015-Q1-E1-E10
Method
                  BLASTX
NCBI GI
                  q4559380
BLAST score
                  648
E value
                  4.0e-68
Match length
                  123
                                                              ,5°3,
                  100
% identity
                   (AC006526) putative auxin-responsive GH3 protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  137531
Seq. ID
                  LIB146-015-Q1-E1-E11
Method
                  BLASTN
NCBI GI
                  q2760172
BLAST score
                  185
E value
                   1.0e-99
Match length
                   356
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUB3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  137532
Seq. ID
                  LIB146-015-Q1-E1-F1
Method
                  BLASTN
                  q3617740
NCBI GI
                   87
BLAST score
                   3.0e-41
E value
                   99
Match length
                   97
% identity
                  Arabidopsis thaliana BAC F1I21 from chromosome 1, near 59
NCBI Description
                   cM, complete sequence [Arabidopsis thaliana]
                   137533
Seq. No.
Seq. ID
                  LIB146-015-Q1-E1-G11
Method
                  BLASTX
NCBI GI
                   g2760830
BLAST score
                   607
                   2.0e-63
E value
                   117
Match length
                   100
% identity
                   (ACO03105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana]
```

16487

137534

Seq. No.



Seq. ID LIB146-015-Q1-E1-G4

Method BLASTX
NCBI GI g3341684
BLAST score 153
E value 4.0e-10
Match length 91
% identity 41

NCBI Description (AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No. 137535

Seq. ID LIB146-015-Q1-E1-H3

Method BLASTN
NCBI GI g2098816
BLAST score 333
E value 0.0e+00
Match length 337
% identity 100

NCBI Description Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No. 137536

Seq. ID LIB146-015-Q1-E1-H6

Method BLASTX
NCBI GI g112741
BLAST score 618
E value 1.0e-64
Match length 114
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 137537

Seq. ID LIB146-016-Q1-E1-A6

Method BLASTX
NCBI GI g112737
BLAST score 464
E value 1.0e-46
Match length 116
% identity 78

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 137538

Seq. ID LIB146-016-Q1-E1-B12

Method BLASTX
NCBI GI g3860272
BLAST score 209
E value 1.0e-16



```
Match length
                  100
% identity
                  (AC005824) putative suppressor protein [Arabidopsis
NCBI Description
                  thaliana] >gi 4314399 gb_AAD15609_ (AC006232) putative skdl
                  protein [Arabidopsis thaliana]
                  137539
Seq. No.
                  LIB146-016-Q1-E1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3510331
BLAST score
                  401
                  0.0e + 00
E value
                  405
Match length
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K13P22, complete sequence [Arabidopsis thaliana]
                  137540
Seq. No.
                  LIB146-016-Q1-E1-C10
Seq. ID
Method
                  BLASTX
                  g4689479
NCBI GI
BLAST score
                  245
                  8.0e-21
E value
                  85
Match length
                  64
% identity
                  (AC007213) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  137541
Seq. No.
                  LIB146-016-Q1-E1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  663
E value
                  7.0e-70
Match length
                  127
% identity
                   100
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis -
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   137542
                  LIB146-016-Q1-E1-F1
Seq. ID
Method
                  BLASTX
                   q3721856
NCBI GI
                   318
BLAST score
E value
                   1.0e-29
                  89
Match length
% identity
                   62
NCBI Description
                  (AB014057) beta-Amyrin Synthase [Panax ginseng]
                   137543
Seq. No.
Seq. ID
                   LIB146-017-Q1-E1-A1
Method
                  BLASTN
```

Method BLASTN
NCBI GI g4733984
BLAST score 340
E value 0.0e+00
Match length 356
% identity 49



nosome II BAC F1404 genomic

NCBI Description Arabidopsis thaliana chromosome II BAC F1404 genomic sequence, complete sequence

Seq. No. 137544

Seq. ID LIB146-017-Q1-E1-A11

Method BLASTN
NCBI GI g4732164
BLAST score 109
E value 2.0e-54
Match length 231
% identity 43

NCBI Description Arabidopsis thaliana BAC F10A2

Seq. No. 137545

Seq. ID LIB146-017-Q1-E1-B8

Method BLASTN
NCBI GI g3811319
BLAST score 134
E value 2.0e-69
Match length 212
% identity 98

NCBI Description Arabidopsis thaliana ROOT HAIRLESS 1 (RHL1) gene, complete

cds

Seq. No. 137546

Seq. ID LIB146-017-Q1-E1-C2

Method BLASTN
NCBI GI g3763915
BLAST score 256
E value 1.0e-142
Match length 300
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC F14B2 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137547

Seq. ID LIB146-017-Q1-E1-C3

Method BLASTX
NCBI GI g1628583
BLAST score 460
E value 2.0e-46
Match length 86
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137548

Seq. ID LIB146-017-Q1-E1-C7

Method BLASTX
NCBI GI g112741
BLAST score 691
E value 4.0e-73
Match length 128
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -



Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

137549 Seq. No. Seq. ID LIB146-017-Q1-E1-D6 Method BLASTX NCBI GI g3860250 BLAST score 268 E value 1.0e-23 Match length 103 61 % identity NCBI Description (AC005824) putative chloroplast prephenate dehydratase [Arabidopsis thaliana] Seq. No. 137550 Seq. ID LIB146-017-Q1-E1-E1 Method BLASTX

Method BLASTX
NCBI GI g2245048
BLAST score 446
E value 2.0e-44
Match length 124
% identity 74

NCBI Description (Z97342) resistance gene homolog [Arabidopsis thaliana]

Seq. No. 137551

Seq. ID LIB146-017-Q1-E1-E6

Method BLASTN
NCBI GI g3451055
BLAST score 271
E value 1.0e-151
Match length 371
% identity 94

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20

(ESSAII project)

Seq. No. 137552

Seq. ID LIB146-017-Q1-E1-E7

Method BLASTX
NCBI GI g112737
BLAST score 536
E value 6.0e-55
Match length 130
% identity 80

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 137553

Seq. ID LIB146-017-Q1-E1-F1

Method BLASTN



NCBI GI g4725940
BLAST score 395
E value 0.0e+00
Match length 395
% identity 100
NCBI Description Arabidop

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T1P17

(ESSA project)

Seq. No. 137554

Seq. ID LIB146-017-Q1-E1-G11

Method BLASTX
NCBI GI g1628583
BLAST score 480
E value 1.0e-48
Match length 95
% identity 96

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137555

Seq. ID LIB146-017-Q1-E1-G7

Method BLASTN
NCBI GI g2656026
BLAST score 207
E value 1.0e-113
Match length 379
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

MDF20

Seq. No. 137556

Seq. ID LIB146-017-Q1-E1-H1

Method BLASTN
NCBI GI g3785992
BLAST score 291
E value 1.0e-163
Match length 345
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC T6A23 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137557

Seq. ID LIB146-017-Q1-E1-H2

Method BLASTN
NCBI GI g3046852
BLAST score 351
E value 0.0e+00
Match length 351
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQJ16, complete sequence [Arabidopsis thaliana]

Seq. No. 137558

Seq. ID LIB146-017-Q1-E1-H4

Method BLASTX NCBI GI g3128192



BLAST score 271 E value 6.0e-24 Match length 87 % identity 63

NCBI Description (AC004521) axi 1-like protein [Arabidopsis thaliana]

Seq. No. 137559

Seq. ID LIB146-018-Q1-E1-A1

Method BLASTN
NCBI GI g4454587
BLAST score 336
E value 0.0e+00
Match length 336
% identity 100

NCBI Description Arabidopsis thaliana BAC F21A20 from chromosome V near 61

cM, complete sequence [Arabidopsis thaliana]

Seq. No. 137560

Seq. ID LIB146-018-Q1-E1-A11

Method BLASTN
NCBI GI g4732168
BLAST score 25
E value 4.0e-04
Match length 355
% identity 45

NCBI Description Arabidopsis thaliana BAC T1J24

Seq. No. 137561

Seq. ID LIB146-018-Q1-E1-A5

Method BLASTX
NCBI GI g4033735
BLAST score 281
E value 1.0e-25
Match length 75
% identity 67

NCBI Description (AF054284) spliceosomal protein SAP 155 [Homo sapiens]

Seq. No. 137562

Seq. ID LIB146-018-Q1-E1-B10

Method BLASTX
NCBI GI g2160169
BLAST score 269
E value 1.0e-23
Match length 96
% identity 54

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 137563

Seq. ID LIB146-018-Q1-E1-B11

Method BLASTN
NCBI GI g4454447
BLAST score 207
E value 1.0e-113
Match length 328
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]



Seq. No. 137564

Seq. ID LIB146-018-Q1-E1-B2

Method BLASTX
NCBI GI g4558671
BLAST score 199
E value 2.0e-15
Match length 48
% identity 71

NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]

>gi_4726111_gb_AAD28311.1_AC006436_2 (AC006436)
hypothetical protein [Arabidopsis thaliana]

Seq. No. 137565

Seq. ID LIB146-018-Q1-E1-B4

Method BLASTX
NCBI GI g3337361
BLAST score 443
E value 3.0e-44
Match length 96
% identity 79

NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 137566

Seq. ID LIB146-018-Q1-E1-B6

Method BLASTX
NCBI GI g3819699
BLAST score 218
E value 1.0e-17
Match length 55
% identity 82

NCBI Description (AJ009609) BnMAP4K alpha2 [Brassica napus]

Seq. No. 137567

Seq. ID LIB146-018-Q1-E1-C1

Method BLASTX
NCBI GI g1628583
BLAST score 535
E value 6.0e-55
Match length 103
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137568

Seq. ID LIB146-018-Q1-E1-C11

Method BLASTN
NCBI GI g3080430
BLAST score 238
E value 1.0e-131
Match length 238
% identity 64

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19

(ESSAII project)

Seq. No. 137569



```
Seq. ID
                   LIB146-018-Q1-E1-C9
Method
                  BLASTX
NCBI GI
                  q4726114
BLAST score
                   498
E value
                   2.0e-50
Match length
                   123
% identity
NCBI Description
                  (AC006436) putative retrotransposon Athila [Arabidopsis
                  thaliana]
Seq. No.
                  137570
                  LIB146-018-Q1-E1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4185738
BLAST score
                   366
E value
                  4.0e-35
Match length
                  116
% identity
                  59
NCBI Description
                  (AF079998) putative glutamate receptor [Arabidopsis
                  thaliana]
Seq. No.
                  137571
                  LIB146-018-Q1-E1-D12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4512656
BLAST score
                  304
E value
                  1.0e-171
Match length
                  304
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
                  sequence, complete sequence
Seq. No.
                  137572
Seq. ID
                  LIB146-018-Q1-E1-D2
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  472
                  2.0e-47
E value
Match length
                  89
% identity
                  99
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  137573
Seq. ID
                  LIB146-018-Q1-E1-F6
Method
                  BLASTX
                  q3687228
                  675
                  3.0e-71
```

NCBI GI BLAST score E value Match length 136 98 % identity

NCBI Description (AC005169) putative malate dehydrogenase [Arabidopsis

thaliana]

Seq. No. 137574

Seq. ID LIB146-018-Q1-E1-G4



Method BLASTX
NCBI GI g1628583
BLAST score 663
E value 7.0e-70
Match length 127
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137575

Seq. ID LIB146-018-Q1-E1-H3

Method BLASTX
NCBI GI g112681
BLAST score 527
E value 6.0e-54
Match length 125
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 137576

Seq. ID LIB146-019-Q1-E1-A10

Method BLASTX
NCBI GI g2832620
BLAST score 467
E value 6.0e-47
Match length 111
% identity 77

NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]

Seq. No. 137577

Seq. ID LIB146-019-Q1-E1-A3

Method BLASTN
NCBI GI 94204173
BLAST score 346
E value 0.0e+00
Match length 358
% identity 99

NCBI Description Arabidopsis thaliana chromosome 1 BAC T2K10 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 137578

Seq. ID LIB146-019-Q1-E1-A9

Method BLASTX
NCBI GI g1628583
BLAST score 265
E value 2.0e-23
Match length 85
% identity 66

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Match length

NCBI Description

% identity

310

(ESSAII project)

94



```
Seq. No.
                  137579
Seq. ID
                  LIB146-019-Q1-E1-B5
Method
                  BLASTX
                  g4773906
NCBI GI
BLAST score
                  319
E value
                  2.0e-29
Match length
                  71
% identity
                  86
NCBI Description
                  (AF074021) putative symbiosis-related protein [Arabidopsis
Seq. No.
                  137580
Seq. ID
                  LIB146-019-Q1-E1-C12
Method
                  BLASTX
NCBI GI
                  q1769568
BLAST score
                  213
E value
                  3.0e-17
Match length
                  64
                  73
% identity
NCBI Description
                  (U82202) fumarase; fumarate hydratase [Arabidopsis
                  thaliana]
Seq. No.
                  137581
Seq. ID
                  LIB146-019-Q1-E1-C3
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  661
E value
                  1.0e-69
Match length
                  132
% identity
                  98
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  137582
Seq. ID
                  LIB146-019-Q1-E1-D3
Method
                  BLASTX
NCBI GI
                  g3184281
BLAST score
                  540
                  2.0e-55
E value
Match length
                  132
% identity
                  77
NCBI Description
                 (AC004136) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  137583
Seq. ID
                  LIB146-019-Q1-E1-D9
Method
                  BLASTN
NCBI GI
                  g4455321
BLAST score
                  242
                  1.0e-134
E value
```

16497

Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10



Seq. No. 137584

Seq. ID LIB146-019-Q1-E1-E12

Method BLASTX
NCBI GI g133320
BLAST score 304
E value 7.0e-28
Match length 101
% identity 57

NCBI Description DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (A135)

(RNA POLYMERASE I SUBUNIT 2) >gi_101446_pir__A39607 DNA-directed RNA polymerase (EC 2.7.7.6) I 135K chain yeast (Saccharomyces cerevisiae) >gi_172464 (M62804) RNA polymerase I (second largest subunit) [Saccharomyces cerevisiae] >gi_887587_emb_CAA90154_ (Z49919) Rpa2p [Saccharomyces cerevisiae] >gi_939744 (U31900) Rpa135p [Saccharomyces cerevisiae] >gi_1314085_emb_CAA95050_

(Z71255) Rpa2p [Saccharomyces cerevisiae]

Seq. No. 137585

Seq. ID LIB146-019-Q1-E1-E5

Method BLASTX
NCBI GI g1628583
BLAST score 663
E value 7.0e-70
Match length 127
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137586

Seq. ID LIB146-019-Q1-E1-F1

Method BLASTN
NCBI GI g2828187
BLAST score 34
E value 2.0e-09
Match length 50
% identity 44

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21C13, complete sequence [Arabidopsis thaliana]

Seq. No. 137587

Seq. ID LIB146-019-Q1-E1-F3

Method BLASTX
NCBI GI g4544426
BLAST score 344
E value 2.0e-32
Match length 128
% identity 53

NCBI Description (AC006955) putative transposase [Arabidopsis thaliana]

Seq. No. 137588

Seq. ID LIB146-019-Q1-E1-G5

Method BLASTX
NCBI GI g112681
BLAST score 538
E value 3.0e-55



Match length 127 % identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 137589

Seq. ID LIB146-019-Q1-E1-G9

Method BLASTN
NCBI GI g2656032
BLAST score 246
E value 1.0e-136
Match length 280
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MZF18

Seq. No. 137590

Seq. ID LIB146-019-Q1-E1-H2

Method BLASTN
NCBI GI g4587986
BLAST score 362
E value 0.0e+00
Match length 362
% identity 100

NCBI Description Arabidopsis thaliana ABA-regulated gene cluster, complete

sequence

Seq. No. 137591

Seq. ID LIB146-020-Q1-E1-A7

Method BLASTX
NCBI GI g3169059
BLAST score 183
E value 1.0e-13
Match length 63
% identity 54

NCBI Description (AL023704) weak similarity to B. subtilis spore outgrowth f

actor B [Schizosaccharomyces pombe]

Seq. No. 137592

Seq. ID LIB146-020-Q1-E1-B5

Method BLASTN
NCBI GI g2351061
BLAST score 344
E value 0.0e+00
Match length 344
dentity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAF19, complete sequence [Arabidopsis thaliana]

Seq. No. 137593

Seq. ID LIB146-020-Q1-E1-C4

Method BLASTN NCBI GI g4581161 BLAST score 324



E value 0.0e+00 Match length 332 % identity 14

NCBI Description Arabidopsis thaliana chromosome II BAC T20G20 genomic

sequence, complete sequence

Seq. No. 137594

Seq. ID LIB146-020-Q1-E1-E3

Method BLASTN
NCBI GI g3335356
BLAST score 298
E value 1.0e-167
Match length 336
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC F16M14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137595

Seq. ID LIB146-020-Q1-E1-G3

Method BLASTX
NCBI GI g112681
BLAST score 489
E value 2.0e-49
Match length 119
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 137596

Seq. ID LIB146-020-Q1-E1-G4

Method BLASTX
NCBI GI g3152605
BLAST score 369
E value 2.0e-35
Match length 71
% identity 100

NCBI Description (AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 137597

Seq. ID LIB146-020-Q1-E1-H2

Method BLASTX
NCBI GI g112741
BLAST score 622
E value 4.0e-65
Match length 115
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir_ NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712 emb_CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No.

Seq. ID Method

137603

BLASTN

LIB146-021-Q1-E1-C11



```
137598
Seq. No.
                  LIB146-020-Q1-E1-H3
Seq. ID
                  BLASTX
Method
                  g2245017
NCBI GI
                  491
BLAST score
                  8.0e-50
E value
                  114
Match length
                  90
% identity
                  (Z97341) membrane protein homolog [Arabidopsis thaliana]
NCBI Description
                  137599
Seq. No.
                  LIB146-021-Q1-E1-A7
Seq. ID
                  BLASTN
Method
                   g4490717
NCBI GI
BLAST score
                   400
                  0.0e + 00
E value
                   400
Match length
                   100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone
NCBI Description
                  project)
                   137600
Seq. No.
                  LIB146-021-Q1-E1-B1
Seq. ID
                  BLASTN
Method
NCBI GI
                   g4589415
                   23
BLAST score
                   6.0e-03
E value
Match length
                   365
                   55
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K14A3, complete sequence
                   137601
Seq. No.
                   LIB146-021-Q1-E1-B10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3831448
BLAST score
                   319
                   1.0e-179
E value
                   360
Match length
                   96
% identity
                   Arabidopsis thaliana chromosome II BAC T32F6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   137602
Seq. No.
Seq. ID
                   LIB146-021-Q1-E1-B6
Method
                   BLASTX
                   q3184283
NCBI GI
                   544
BLAST score
E value
                   6.0e-56
                   108
Match length
% identity
                   (AC004136) putative TBP-binding protein [Arabidopsis
NCBI Description
                   thaliana]
```



```
q2182285
NCBI GI
                   154
BLAST score
                   3.0e-81
E value
                   298
Match length
                   100
% identity
                   Sequence of BAC F5I14 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
                   137604
Seq. No.
                   LIB146-021-Q1-E1-D12
Seq. ID
                   BLASTN
Method
                   g4027862
NCBI GI
                   342
BLAST score
                   0.0e+00
E value
Match length
                   342
                   100
% identity
                   Arabidopsis thaliana chromosome 1 BAC T7A14 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   137605
Seq. No.
                   LIB146-021-Q1-E1-E8
Seq. ID
                   BLASTX
Method
                   g112682
NCBI GI
                   583
BLAST score
                   2.0e-60
E value
                   123
Match length
                   89
% identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
                   137606
Seq. No.
                   LIB146-021-Q1-E1-F3
Seq. ID
                   BLASTX
Method
                   g112682
NCBI GI
BLAST score
                   550
                   1.0e-56
E value
                   117
Match length
                   88
% identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81605_pir__S08510
NCBI Description
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
                   137607
Seq. No.
                   LIB146-021-Q1-E1-F4
Seq. ID
```

Method BLASTX NCBI GI q112681 534 BLAST score 9.0e-55 E value 125 Match length 83 % identity

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604 pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana

16502



>qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 137608

Seq. ID LIB146-021-Q1-E1-F6

Method BLASTN NCBI GI q3738275 BLAST score 327 E value 0.0e + 00Match length 384 % identity 96

Arabidopsis thaliana chromosome II BAC F17A22 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137609

Seq. ID LIB146-021-Q1-E1-F8

Method BLASTX NCBI GI q2335108 BLAST score 436 E value 9.0e-49112 Match length % identity

NCBI Description (AC002339) putative isulinase [Arabidopsis thaliana]

137610 Seq. No.

LIB146-021-Q1-E1-F9 Seq. ID

Method BLASTX NCBI GI g112741 BLAST score 575 E value 1.0e-59 Match length 106 % identity 100

2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 137611

Seq. ID LIB146-021-Q1-E1-G10

Method BLASTN NCBI GI g3449334 BLAST score 41 E value 9.0e-14Match length 53 % identity 94

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MYH9, complete sequence [Arabidopsis thaliana]

137612 Seq. No.

Seq. ID LIB146-021-Q1-E1-G11

Method BLASTN NCBI GI g2337888 BLAST score 227



1.0e-124 E value 361 Match length 100 % identity Genomic sequence for Arabidopsis thaliana BAC F14J16, NCBI Description complete sequence [Arabidopsis thaliana] 137613 Seq. No. LIB146-021-Q1-E1-G12 Seq. ID Method BLASTN g2264316 NCBI GI BLAST score 115 6.0e-58 E value 247 Match length % identity 97 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana] 137614 Seq. No. Seq. ID LIB146-022-Q1-E1-A5 13. 1 Method BLASTN g2262097 NCBI GI 348 BLAST score 0.0e+00E value Match length 373 % identity 98 Arabidopsis thaliana chromosome IV BAC T19F6 genomic NCBI Description sequence, complete sequence 137615 Seq. No. LIB146-022-Q1-E1-B11 Seq. ID Method BLASTN g3297806 NCBI GI 313 BLAST score E value 1.0e-176 Match length 342 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 (ESSA project) Seq. No. 137616 LIB146-022-Q1-E1-C10 Seq. ID Method BLASTN NCBI GI q16472 BLAST score 163 E value 2.0e-86 Match length 308 17 % identity NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type Seq. No. 137617 LIB146-022-Q1-E1-C11 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g112681
BLAST score 508
E value 1.0e-51
Match length 107
% identity 91



12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 137618 Seq. ID LIB146-022-Q1-E1-C2 Method BLASTN NCBI GI q2702261 BLAST score 181 E value 2.0e-97 Match length 230 % identity Arabidopsis thaliana chromosome II BAC T21L14 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 137619 LIB146-022-Q1-E1-C4 Seq. ID Method BLASTN NCBI GI q3859610 126 BLAST score E value 6.0e-65 Match length 138 % identity NCBI Description Arabidopsis thaliana BAC T9E19 137620 Seq. No. Seq. ID LIB146-022-Q1-E1-E12 Method BLASTX NCBI GI g2275201 BLAST score 365 E value 6.0e-35 Match length 81 % identity 88 NCBI Description (AC002337) unknown protein [Arabidopsis thaliana] Seq. No. 137621 Seq. ID LIB146-022-Q1-E1-E5 Method BLASTX q3738297 NCBI GI BLAST score 176 4.0e-13 E value Match length 41 % identity 16 (AC005309) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 137622 Seq. ID LIB146-022-Q1-E1-F5

Method BLASTX g2618701 NCBI GI BLAST score 182 1.0e-13 E value Match length 61 59 % identity

(AC002510) hypothetical protein [Arabidopsis thaliana] NCBI Description



```
Seq. No.
                  137623
Seq. ID
                  LIB146-022-Q1-E1-H4
Method
                  BLASTX
                  q3695382
NCBI GI
BLAST score
                  335
                  2.0e-31
E value
                  127
Match length
                  58
% identity
                  (AF096370) contains similarity to Arabidopsis thaliana
NCBI Description
                  retrotransposon Tall-1 (GB:L47193) [Arabidopsis thaliana]
Seq. No.
                  137624
                  LIB146-023-Q1-E1-C1
Seq. ID
Method
                  BLASTX
                  g4102600
NCBI GI
BLAST score
                  201
                  5.0e-16
E value
                  54
Match length
                  74
% identity
                  (AF013467) ARF6 [Arabidopsis thaliana]
NCBI Description
                  137625
Seq. No.
                  LIB146-023-Q1-E1-D1
Seq. ID
Method
                  BLASTX
                  g3249105
NCBI GI
BLAST score
                  161
                  3.0e-11
E value
Match length
                  51
                  59
% identity
                   (AC003114) Contains similarity to protein phosphatase 2C
NCBI Description
                   (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
                  137626
Seq. No.
Seq. ID
                  LIB146-023-Q1-E1-D7
Method
                  BLASTN
NCBI GI
                  g3128136
BLAST score
                   143
                  8.0e-75
E value
                  207
Match length
% identity
                   92
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K1F13, complete sequence [Arabidopsis thaliana]
                   137627
Seq. No.
Seq. ID
                  LIB146-023-Q1-E1-H8
Method
                  BLASTN
NCBI GI
                   q4220645
BLAST score
                   114
E value
                   9.0e-58
Match length
                   145
```

% identity 95

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MYA6, complete sequence [Arabidopsis thaliana]

Seq. No. 137628

Seq. ID LIB146-024-Q1-E1-A3

Method BLASTX



NCBI GI BLAST score 232 7.0e-20 E value 55 Match length 78 % identity 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana] Seq. No. 137629 LIB146-024-Q1-E1-A7 Seq. ID Method BLASTN NCBI GI q12212 BLAST score 116 9.0e-59 E value Match length 164 93 % identity S.alba chloroplast rp123 and rp12 genes for ribosomal NCBI Description proteins L23 and L2 Seq. No. 137630 LIB146-024-Q1-E1-A8 Seq. ID Method BLASTN q4220643 NCBI GI BLAST score 123 5.0e-63 E value 191 Match length 91 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MWD22, complete sequence [Arabidopsis thaliana] Seq. No. 137631 Seq. ID LIB146-024-Q1-E1-C7 Method BLASTN NCBI GI g2264305 BLAST score 96 6.0e-47 E value Match length 180 88 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MBK23, complete sequence [Arabidopsis thaliana] Seq. No. 137632 Seq. ID LIB146-024-Q1-E1-G7 Method BLASTN NCBI GI q4388816 BLAST score 43

4.0e-15 E value Match length 149 90 % identity

Arabidopsis thaliana chromosome II BAC F9B22 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                  137633
                  LIB146-024-Q1-E1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3420042
BLAST score
                  258
                  1.0e-143
E value
                  310
Match length
                  96
% identity
                  Arabidopsis thaliana chromosome II BAC T13E15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  137634
Seq. No.
                  LIB146-025-Q1-E1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2351073
BLAST score
                  368
                  0.0e + 00
E value
Match length
                  376
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYJ24, complete sequence [Arabidopsis thaliana]
                  137635
Seq. No.
                  LIB146-025-Q1-E1-C1
Seq. ID
Method
                  BLASTN
                  g4589434
NCBI GI
BLAST score
                   273
                   1.0e-152
E value
Match length
                   293
% identity
                   98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNJ7, complete sequence
Seq. No.
                   137636
                   LIB146-025-Q1-E1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3335216
BLAST score
                   256
                   4.0e-22
E value
                   62
Match length
% identity
                   82
                   (AF074928) 1-aminocyclopropane-1-carboxylate synthase 2
NCBI Description
                   [Sinapis arvensis]
Seq. No.
                   137637
                   LIB146-025-Q1-E1-C3
Seq. ID
```

Method BLASTX NCBI GI q2642450 BLAST score 355 8.0e-34 E value Match length 106 % identity 68

(AC002391) putative metal ion transporter (Nramp) NCBI Description [Arabidopsis thaliana] >gi 3169188 (AC004401) putative

metal ion transporter (Nramp) [Arabidopsis thaliana]

Seq. No. 137638



```
LIB146-025-Q1-E1-D4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2760170
                  336
                                        * 7×6-
BLAST score
                  0.0e+00
E value
                  356
Match length
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIO24, complete sequence [Arabidopsis thaliana]
                  137639
Seq. No.
                  LIB146-025-Q1-E1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128169
BLAST score
                  83
                  1.0e-09
E value
Match length
                  82
                  50
% identity
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]
                  137640
Seq. No.
                  LIB146-025-Q1-E1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4558590
BLAST score
                  408
E value
                  0.0e + 00
Match length
                  412
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T17C22 genomic
                  sequence, complete sequence
Seq. No.
                  137641
                  LIB146-025-Q1-E1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  578
E value
                  8.0e-60
Match length
                  139
                  81
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                  137642
```

Seq. ID LIB146-025-Q1-E1-H11

Method BLASTX NCBI GI g4377180 BLAST score 276 8.0e-25 E value Match length 84 % identity

(AE001667) Phosphoglycerate Mutase [Chlamydia pneumoniae] NCBI Description

137643 Seq. No.

Seq. ID LIB146-025-Q1-E1-H12



Method BLASTX
NCBI GI g2924784
BLAST score 645
E value 1.0e-67
Match length 123
% identity 100

NCBI Description (AC002334) similar to jasmonate inducible protein

[Arabidopsis thaliana]

Seq. No. 137644

Seq. ID LIB146-025-Q1-E1-H2

Method BLASTN
NCBI GI 94757662
BLAST score 356
E value 0.0e+00
Match length 360
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10B6 from

chromosome I, complete sequence

Seq. No. 137645

Seq. ID LIB146-025-Q1-E1-H7

Method BLASTX
NCBI GI g2244868
BLAST score 93
E value 1.0e-13
Match length 104
% identity 43

NCBI Description (Z97337) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 137646

Seq. ID LIB146-026-Q1-K1-A10

Method BLASTN
NCBI GI g3805839
BLAST score 80
E value 5.0e-37
Match length 374
% identity 43

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14

(ESSAII project)

Seq. No. 137647

Seq. ID LIB146-026-Q1-K1-A11

Method BLASTN
NCBI GI g3176693
BLAST score 142
E value 4.0e-74
Match length 333
% identity 98

NCBI Description Arabidopsis thaliana chromosome I BAC T27I1 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137648

Seq. ID LIB146-026-Q1-K1-A12

Method BLASTN
NCBI GI g3643588
BLAST score 361



E value 0.0e+00 Match length 373 % identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137649

Seq. ID LIB146-026-Q1-K1-A2

Method BLASTX
NCBI GI g1076529
BLAST score 382
E value 7.0e-37
Match length 77
% identity 95

NCBI Description heat shock protein HSP71.2 - garden pea >gi_562006 (U08848)

PsHSP71.2 [Pisum sativum] >gi_1771479 emb_CAA67867_ (X99515) heat shock protein hsp70 [Pisum sativum]

Seq. No. 137650

Seq. ID LIB146-026-Q1-K1-A4

Method BLASTN
NCBI GI g3659491
BLAST score 370
E value 0.0e+00
Match length 434
% identity 100

NCBI Description Sequence of BAC T22H22 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 137651

Seq. ID LIB146-026-Q1-K1-B11

Method BLASTX
NCBI GI g2642158
BLAST score 125
E value 1.0e-09
Match length 68
% identity 50

NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No. 137652

Seq. ID LIB146-026-Q1-K1-B3

Method BLASTN
NCBI GI g4757417
BLAST score 209
E value 1.0e-114
Match length 420
% identity 57

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

T30G6, complete sequence

Seq. No. 137653

Seq. ID LIB146-026-Q1-K1-B5

Method BLASTN
NCBI GI g4589950
BLAST score 230
E value 1.0e-126
Match length 418

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The American of
```

% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T28P16 genomic

sequence, complete sequence

Seq. No. 137654

Seq. ID LIB146-026-Q1-K1-B7

Method BLASTN
NCBI GI g11571
BLAST score 116
E value 7.0e-59
Match length 168
% identity 92

NCBI Description Soybean chloroplast rps12 and rps7 genes

Seq. No. 137655

Seq. ID LIB146-026-Q1-K1-B8

Method BLASTX
NCBI GI g4206210
BLAST score 714
E value 9.0e-76
Match length 142
% identity 63

NCBI Description (AF071527) putative calcium channel [Arabidopsis thaliana]

>gi 4263043 gb AAD15312 (AC005142) putative calcium

channel [Arabidopsis thaliana]

Seq. No. 137656

Seq. ID LIB146-026-Q1-K1-C12

Method BLASTN
NCBI GI g4581161
BLAST score 123
E value 1.0e-62
Match length 209
% identity 87

NCBI Description Arabidopsis thaliana chromosome II BAC T20G20 genomic

sequence, complete sequence

Seq. No. 137657

Seq. ID LIB146-026-Q1-K1-C2

Method BLASTX
NCBI GI g3056598
BLAST score 293
E value 2.0e-26
Match length 60
% identity 93

NCBI Description (AC004255) T1F9.19 [Arabidopsis thaliana]

Seq. No. 137658

Seq. ID LIB146-026-Q1-K1-C9

Method BLASTN
NCBI GI g3985949
BLAST score 210
E value 1.0e-114
Match length 358
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MOB24, complete sequence [Arabidopsis thaliana]

Seq. ID

Method



```
137659
Seq. No.
                  LIB146-026-Q1-K1-D1
Seq. ID
                  BLASTN
Method
                  g2760172
NCBI GI
                  388
BLAST score
                  0.0e+00
E value
Match length
                  400
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUB3, complete sequence [Arabidopsis thaliana]
                  137660
Seq. No.
                  LIB146-026-Q1-K1-E1
Seq. ID
                  BLASTX
Method
                  g3860247
NCBI GI
                   720
BLAST score
                  2.0e-76
E value
                  140
Match length
                   96
% identity
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
                  137661
Seq. No.
                  LIB146-026-Q1-K1-E5
Seq. ID
Method
                  BLASTX
                   g3328240
NCBI GI
BLAST score
                   307
                   4.0e-28
E value
                   106
Match length
% identity
                   51
                   (AF064775) early nodule-specific protein [Medicago
NCBI Description
                   truncatula]
                   137662
Seq. No.
                   LIB146-026-Q1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2529229
                   549
BLAST score
                   2.0e-56
E value
Match length
                   117
                   90
% identity
                  (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
NCBI Description
                   137663
Seq. No.
                   LIB146-026-Q1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2980771
BLAST score
                   486
                   4.0e-49
E value
Match length
                   111
                   87
% identity
                   (AL022198) chloroplast omega-6 fatty acid desaturase (fad6)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   137664
```

16513

LIB146-026-Q1-K1-E9

BLASTN



NCBI GI g2570223

BLAST score 75

E value 1.0e-34
Match length 120
% identity 89

NCBI Description Arabidopsis thaliana chromosome 1 BAC F20D22 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 137665

Seq. ID LIB146-026-Q1-K1-F12

Method BLASTN
NCBI GI g2832639
BLAST score 56
E value 8.0e-23
Match length 128
% identity 86

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12

(ESSAII project)

Seq. No. 137666

Seq. ID LIB146-026-Q1-K1-F7

Method BLASTX
NCBI GI g2062169
BLAST score 106
E value 1.0e-15
Match length 72
% identity 57

NCBI Description (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis

thaliana]

Seq. No. 137667

Seq. ID LIB146-026-Q1-K1-G7

Method BLASTX
NCBI GI g4529972
BLAST score 581
E value 3.0e-60
Match length 140
% identity 86

NCBI Description (AC002330) putative chloroplast outer envelope 86-like

protein [Arabidopsis thaliana]

Seq. No. 137668

Seq. ID LIB146-026-Q1-K1-H1

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 137669

Seq. ID LIB146-026-Q1-K1-H2

Method BLASTX NCBI GI g4262216



BLAST score 658 E value 3.0e-69 Match length 128 % identity 98

NCBI Description (AC006161) putative DNA binding protein [Arabidopsis

thaliana]

Seq. No. 137670

Seq. ID LIB146-026-Q1-K1-H6

Method BLASTN
NCBI GI g3243214
BLAST score 319
E value 1.0e-179
Match length 327
% identity 99

NCBI Description Arabidopsis thaliana BAC T19B17 from chromsome IV, near

19.3 cM, complete sequence [Arabidopsis thaliana]

Seq. No. 137671

Seq. ID LIB146-027-Q1-K1-A2

Method BLASTN
NCBI GI g3928074
BLAST score 184
E value 5.0e-99
Match length 406
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC T7F6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137672

Seq. ID LIB146-027-Q1-K1-B5

Method BLASTX
NCBI GI g267055
BLAST score 387
E value 5.0e-38
Match length 75
% identity 99

NCBI Description SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)

>gi_66572_pir__YUMU sucrose synthase (EC 2.4.1.13) Arabidopsis thaliana >gi_16526_emb_CAA43303_ (X60987)

sucrose synthase [Arabidopsis thaliana]

Seq. No. 137673

Seq. ID LIB146-027-Q1-K1-D2

Method BLASTX
NCBI GI g4115379
BLAST score 141
E value 8.0e-09
Match length 42
% identity 69

NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis

thaliana]

Seq. No. 137674

Seq. ID LIB146-027-Q1-K1-D8

Method BLASTX NCBI GI g1173151



BLAST score 300 E value 9.0e-28 Match length 65 % identity 89

NCBI Description DNA-DIRECTED RNA POLYMERASE BETA CHAIN

>gi 629607 pir S48842 DNA-directed RNA polymerase (EC

2.7.7.6) beta chain - white mustard chloroplast

>gi_563343_emb_CAA57814_ (X82417) RNA polymerase subunit

beta [Sinapis alba]

Seq. No. 137675

Seq. ID LIB146-027-Q1-K1-G3

Method BLASTX
NCBI GI g3080389
BLAST score 234
E value 2.0e-19
Match length 116
% identity 47

NCBI Description (AL022603) putative membrane associated protein

[Arabidopsis thaliana]

Seq. No. 137676

Seq. ID LIB146-027-Q1-K1-G4

Method BLASTX
NCBI GI g4678299
BLAST score 560
E value 6.0e-58
Match length 110
% identity 96

NCBI Description (AL049655) cysteine proteinase precursor-like protein

[Arabidopsis thaliana]

Seq. No. 137677

Seq. ID LIB146-027-Q1-K1-H3

Method BLASTN
NCBI GI 94455262
BLAST score 190
E value 1.0e-102
Match length 356
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22

(ESSAII project)

Seq. No. 137678

Seq. ID LIB146-027-Q1-K1-H5

Method BLASTN
NCBI GI g3299824
BLAST score 324
E value 0.0e+00
Match length 352
% identity 97

NCBI Description Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,

near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No. 137679

Seq. ID LIB146-029-Q1-K1-A3

Method BLASTX



```
NCBI GI
                  q4559342
BLAST score
                  181
                  2.0e-13
E value
                  37
Match length
% identity
                  92
                   (AC007087) putative copper methylamine oxidase [Arabidopsis
NCBI Description
                  thaliana]
                  137680
Seq. No.
                  LIB146-029-Q1-K1-A8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4432793
BLAST score
                  314
                  1.0e-176
E value
Match length
                  370
                  88
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T19K21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  137681
Seq. ID
                  LIB146-029-Q1-K1-B2
Method
                  BLASTN
NCBI GI
                  g3135250
BLAST score
                  121
                  5.0e-62
E value
Match length
                  121
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC F27F23 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No. Seq. ID
                  137682
                  LIB146-029-Q1-K1-D11
Method
                  BLASTN
NCBI GI
                   q4539331
BLAST score
                   157
E value
                   5.0e-83
Match length
                   306
% identity
                   99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13
                   (ESSA project)
Seq. No.
                  137683
Seq. ID
                  LIB146-029-Q1-K1-D7
Method
                  BLASTN
NCBI GI
                  g4432793
BLAST score
                  165
E value
                  7.0e-88
Match length
                  277
                  75
% identity
                  Arabidopsis thaliana chromosome II BAC T19K21 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
```

Seq. No. 137684

Seq. ID LIB146-029-Q1-K1-E1

Method BLASTX NCBI GI g4580462 BLAST score 237



```
E value
                  5.0e-20
Match length
                  109
% identity
                  55
NCBI Description
                  (AC006081) hypothetical protein [Arabidopsis thaliana]
                  137685
Seq. No.
                  LIB146-029-Q1-K1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4678291
BLAST score
                  272
                  1.0e-151
E value
                  299
Match length
                  98
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10
                  (ESSA project)
                  137686
Seq. No.
                  LIB146-029-Q1-K1-E3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2815519
BLAST score
                  157
                  3.0e-83
E value
Match length
                  178
                  77
% identity
NCBI Description Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  137687
Seq. ID
                  LIB146-029-Q1-K1-E6
Method
                  BLASTX
                  g1170247
NCBI GI
BLAST score
                  199
E value
                  2.0e-15
Match length
                  43
% identity
                  91
NCBI Description
                  HEVEIN-LIKE PROTEIN PRECURSOR >gi 407248 (U01880)
                  pre-hevein-like protein [Arabidopsis thaliana]
Seq. No.
                  137688
Seq. ID
                  LIB146-029-Q1-K1-E7
Method
                  BLASTN
NCBI GI
                  q4512656
BLAST score
                  204
E value
                  1.0e-111
Match length
                  204
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
                  sequence, complete sequence
```

Seq. No. 137689

Seq. ID LIB146-029-Q1-K1-F11

Method BLASTX NCBI GI q3548806 BLAST score 150 E value 3.0e-10 Match length 63 % identity 52



NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 137690

Seq. ID LIB146-029-Q1-K1-F4

Method BLASTX
NCBI GI g1723643
BLAST score 155
E value 4.0e-17
Match length 109
% identity 43

NCBI Description HYPOTHETICAL 44.9 KD PROTEIN IN SEC9-MSB2 INTERGENIC REGION

>gi_2132582_pir___S64299 probable membrane protein YGR010w yeast (Saccharomyces cerevisiae) >gi_1322971_emb_CAA96993_

(Z72795) ORF YGR010w [Saccharomyces cerevisiae]

Seq. No. 137691

Seq. ID LIB146-029-Q1-K1-G1

Method BLASTN
NCBI GI g3869072
BLAST score 256
E value 1.0e-142
Match length 346
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJB24, complete sequence [Arabidopsis thaliana]

Seq. No. 137692

Seq. ID LIB146-029-Q1-K1-G12

Method BLASTN
NCBI GI g3193305
BLAST score 126
E value 6.0e-65
Match length 134
% identity 99

NCBI Description Arabidopsis thaliana BAC F3D13

Seq. No. 137693

Seq. ID LIB146-029-Q1-K1-H5

Method BLASTX
NCBI GI g3033400
BLAST score 430
E value 1.0e-42
Match length 118
% identity 71

NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 137694

Seq. ID LIB146-029-Q1-K1-H7

Method BLASTN
NCBI GI g4699904
BLAST score 131
E value 1.0e-67
Match length 261
% identity 99

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F1E22,

complete sequence



Seq. No. 137695 Seq. ID LIB146-0 Method BLASTN

LIB146-030-Q1-K1-A5 BLASTN

NCBI GI g4335744
BLAST score 353
E value 0.0e+00
Match length 426
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC T4M8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137696

Seq. ID LIB146-030-Q1-K1-A8

Method BLASTX
NCBI GI g3172044
BLAST score 241
E value 6.0e-21
Match length 54
% identity 91

NCBI Description (AB010080) aldehyde oxidase [Arabidopsis thaliana]

Seq. No. 137697

Seq. ID LIB146-030-Q1-K1-B4

Method BLASTN
NCBI GI g432445
BLAST score 346
E value 0.0e+00
Match length 374
% identity 98

NCBI Description Arabidopsis thaliana (FUS6) gene, complete cds

Seq. No. 137698

Seq. ID LIB146-030-Q1-K1-B6

Method BLASTX
NCBI GI g3335378
BLAST score 277
E value 1.0e-24
Match length 109
% identity 51

NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis

thaliana]

Seq. No. 137699

Seq. ID LIB146-030-Q1-K1-C5

Method BLASTN
NCBI GI 94388714
BLAST score 292
E value 1.0e-163
Match length 392
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F5K7 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137700

Seq. ID LIB146-030-Q1-K1-C7

Method BLASTX



NCBI GI a3695399 BLAST score 486 4.0e-49 E value Match length 96 % identity 94

NCBI Description (AF096372) contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]

Seq. No. 137701

Seq. ID LIB146-030-Q1-K1-D10

Method BLASTN NCBI GI q4063735 BLAST score 84 E value 1.0e-39 159

Match length % identity 93

Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 NCBI Description

cM, complete sequence [Arabidopsis thaliana]

137702 Seq. No.

Seq. ID LIB146-030-Q1-K1-D11

Method BLASTX NCBI GI g4309698 BLAST score 474 E value 9.0e-48 Match length 118 % identity 81

(AC006266) putative glucosyltransferase [Arabidopsis NCBI Description

thaliana]

Seq. No. 137703

Seq. ID LIB146-030-Q1-K1-E1

Method BLASTX NCBI GI g3184275 BLAST score 222 E value 1.0e-18 Match length 42 % identity 98

NCBI Description (AC004136) hypothetical protein [Arabidopsis thaliana]

Seq. No. 137704

Seq. ID LIB146-030-Q1-K1-E8

Method BLASTN NCBI GI g4191771 BLAST score 404 E value 0.0e + 00Match length 412 % identity 100

Arabidopsis thaliana chromosome II BAC F3P11 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137705

Seq. ID LIB146-030-Q1-K1-F1

Method BLASTN NCBI GI g2760172 BLAST score 328 E value 0.0e + 00

Match length % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MUB3, complete sequence [Arabidopsis thaliana] 137706 Seq. No. LIB146-030-Q1-K1-G10 Seq. ID Method BLASTN g3004543 NCBI GI 168 BLAST score 2.0e-89 E value 415 Match length 99 % identity Arabidopsis thaliana chromosome II BAC F19F24 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 137707 Seq. No. LIB146-030-Q1-K1-G3 Seq. ID Method BLASTN NCBI GI g3831437 BLAST score 337 0.0e + 00E value 365 Match length 98 % identity Arabidopsis thaliana chromosome II BAC T3A4 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 137708 Seq. No. LIB146-030-Q1-K1-G8 Seq. ID Method BLASTN NCBI GI g4755185 BLAST score 206 1.0e-112 E value Match length 234 % identity Arabidopsis thaliana chromosome II BAC F5G3 genomic NCBI Description sequence, complete sequence

137709

Seq. No. Seq. ID LIB146-030-Q1-K1-H11

Method BLASTN NCBI GI g3241916 BLAST score 305 E value 1.0e-171 Match length 402 92 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K15N18, complete sequence [Arabidopsis thaliana]

Seq. No. 137710

LIB146-030-Q1-K1-H7 Seq. ID

Method BLASTX q3738316 NCBI GI BLAST score 368 E value 3.0e-35 102 Match length 69 % identity





```
(AC005170) unknown protein [Arabidopsis thaliana]
NCBI Description
                  137711
Seq. No.
                  LIB22-001-Q1-E1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2047324
BLAST score
                   485
E value
                   4.0e-49
Match length
                   92
                   100
% identity
                  (U80192) HAL3 homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   137712
                   LIB22-001-Q1-E1-C6
Seq. ID
Method
                   BLASTN
NCBI GI
                   a3985955
BLAST score
                   347
E value
                   0.0e + 00
                   384
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MTH16, complete sequence [Arabidopsis thaliana]
Seq. No.
                   137713
                   LIB22-001-Q1-E1-C8
Seq. ID
                   BLASTN
Method
                   g2827140
NCBI GI
BLAST score
                   170
E value
                   1.0e-90
                   170
Match length
                   100
% identity
                   Arabidopsis thaliana cellulose synthase catalytic subunit
NCBI Description
                   (Ath-A) mRNA, complete cds
Seq. No.
                   137714
                   LIB22-001-Q1-E1-D7
Seq. ID
Method
                   BLASTN
                   q3821780
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   137715
Seq. No.
                   LIB22-001-Q1-E1-E6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2160155
BLAST score
                   397
                   0.0e + 00
E value
                   397
Match length
```

100 % identity

Sequence of BAC F21M12 from Arabidopsis thaliana chromosome NCBI Description

1, complete sequence [Arabidopsis thaliana]

137716 Seq. No.

Seq. ID LIB22-001-Q1-E1-F2



Method BLASTX
NCBI GI g1491615
BLAST score 459
E value 5.0e-46
Match length 121
% identity 69

NCBI Description (X99923) male sterility 2-like protein [Arabidopsis

thaliana]

Seq. No. 137717

Seq. ID LIB22-001-Q1-E1-G1

Method BLASTX
NCBI GI g4033469
BLAST score 170
E value 3.0e-12
Match length 36
% identity 86

NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP41

>gi_1707370_emb_CAA67799_ (X99436) splicing factor

[Arabidopsis thaliana]

Seq. No. 137718

Seq. ID LIB22-001-Q1-E1-G3

Method BLASTN
NCBI GI g2760168
BLAST score 350
E value 0.0e+00
Match length 350
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MEE6, complete sequence [Arabidopsis thaliana]

Seq. No. 137719

Seq. ID LIB22-001-Q1-E1-G6

Method BLASTN
NCBI GI 94587582
BLAST score 431
E value 0.0e+00
Match length 431
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T16B14 genomic

sequence, complete sequence

Seq. No. 137720

Seq. ID LIB22-001-Q1-E1-G7

Method BLASTX
NCBI GI 94757762
BLAST score 184
E value 1.0e-13
Match length 126
% identity 29

NCBI Description androgen receptor associated protein 54

>gi_4530066_gb_AAD21842.1_ (AF060544) androgen receptor

associated protein 54 [Homo sapiens]

Seq. No. 137721

Seq. ID LIB22-002-Q1-E1-A10



```
Method
NCBI GI
                  q4210330
BLAST score
                  595
E value
                  7.0e-62
                  126
Match length
                  87
% identity
NCBI Description
                   (AJ223802) 2-oxoglutarate dehydrogenase, El subunit
                   [Arabidopsis thaliana]
                  137722
Seq. No.
Seq. ID
                  LIB22-002-Q1-E1-B2
Method
                  BLASTN
NCBI GI
                  g4589433
                  379
BLAST score
                  0.0e + 00
E value
                  379
Match length
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNI5, complete sequence
Seq. No.
                  137723
Seq. ID
                  LIB22-002-Q1-E1-B9
Method
                  BLASTX
NCBI GI
                  g2245060
BLAST score
                   368
                  2.0e-35
E value
                  76
Match length
                  99
% identity
NCBI Description
                  (Z97342) allergen homolog [Arabidopsis thaliana]
Seq. No.
                  137724
Seq. ID
                  LIB22-002-Q1-E1-C5
Method
                  BLASTN
NCBI GI
                  g3702731
BLAST score
                   34
                   7.0e-10
E value
Match length
                   170
% identity
                   80
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFC19, complete sequence [Arabidopsis thaliana]
                   137725
Seq. No.
Seq. ID
                  LIB22-002-Q1-E1-D1
Method
                  BLASTN
NCBI GI
                  g4732164
BLAST score
                  82
E value
                   3.0e-38
Match length
                  175
                   91
% identity
                  Arabidopsis thaliana BAC F10A2
NCBI Description
Seq. No.
                   137726
```

Seq. ID LIB22-002-Q1-E1-D3

Method BLASTX
NCBI GI g401213
BLAST score 585
E value 8.0e-61



Match length 116
% identity 100
NCBI Description ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE PRECURSOR >gi_166792
(M96073) phosphoribosylanthranilate transferase
[Arabidopsis thaliana] >gi_445600_prf__1909347A
phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No. 137727
Seq. ID LIB22-002-Q1-E1-D4
Method BLASTX

Method BLASTX
NCBI GI g4371296
BLAST score 460
E value 3.0e-46
Match length 90
% identity 99

NCBI Description (AC006260) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 137728

Seq. ID LIB22-002-Q1-E1-D6

Method BLASTX
NCBI GI g1279640
BLAST score 338
E value 1.0e-31
Match length 88
% identity 73

NCBI Description (X92204) NAM [Petunia x hybrida]

Seq. No. 137729

Seq. ID LIB22-002-Q1-E1-E10

Method BLASTX
NCBI GI g2244910
BLAST score 159
E value 7.0e-11
Match length 108
% identity 35

NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No. 137730

Seq. ID LIB22-002-Q1-E1-E12

Method BLASTN
NCBI GI g2832639
BLAST score 303
E value 1.0e-170
Match length 401
% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12

(ESSAII project)

Seq. No. 137731

Seq. ID LIB22-002-Q1-E1-E2

Method BLASTN
NCBI GI g3869071
BLAST score 134
E value 1.0e-69
Match length 190



% identity 93
NCBI Description Arabidopsis thaliana genomic DNA, chromosome

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIL23, complete sequence [Arabidopsis thaliana]

Seq. No. 137732

Seq. ID LIB22-002-Q1-E1-E5

Method BLASTX
NCBI GI g603074
BLAST score 360
E value 2.0e-34
Match length 110
% identity 60

NCBI Description (U18197) ATP:citrate lyase [Homo sapiens]

Seq. No. 137733

Seq. ID LIB22-002-Q1-E1-E9

Method BLASTX
NCBI GI g3258573
BLAST score 245
E value 7.0e-21
Match length 92
% identity 53

NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 137734

Seq. ID LIB22-002-Q1-E1-F12

Method BLASTN
NCBI GI g3869066
BLAST score 79
E value 1.0e-36
Match length 246
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBM17, complete sequence [Arabidopsis thaliana]

Seq. No. 137735

Seq. ID LIB22-002-Q1-E1-F5

Method BLASTN
NCBI GI g4314374
BLAST score 398
E value 0.0e+00
Match length 398
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F10A12 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137736

Seq. ID LIB22-002-Q1-E1-F6

Method BLASTX
NCBI GI g1684913
BLAST score 344
E value 1.0e-32
Match length 107
% identity 62

NCBI Description (U77888) receptor-like protein kinase [Ipomoea nil]

Seq. No. 137737



```
Seq. ID
                  LIB22-002-Q1-E1-G12
Method
                  BLASTX
NCBI GI
                  q681904
BLAST score
                  455
                  2.0e-45
E value
Match length
                  106
% identity
                  86
NCBI Description
                  (D31711) cp29 [Arabidopsis thaliana]
                  137738
Seq. No.
                  LIB22-002-Q1-E1-G8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2264311
BLAST score
                  189
                  1.0e-102
E value
Match length
                  322
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLN1, complete sequence [Arabidopsis thaliana]
                  137739
Seq. No.
                  LIB22-002-Q1-E1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832641
BLAST score
                  501
E value
                  5.0e-51
                  100
Match length
% identity
                  99
                  (AL021710) glycolate oxidase - like protein [Arabidopsis
NCBI Description
                  thaliana]
                  137740
Seq. No.
Seq. ID
                  LIB22-002-Q1-E1-H6
Method
                  BLASTN
NCBI GI
                  g4589438
BLAST score
                  387
E value
                  0.0e+00
Match length
                  391
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQJ2, complete sequence
Seq. No.
                  137741
Seq. ID
                  LIB22-002-Q1-E1-H7
Method
                  BLASTX
NCBI GI
                  g4138282
BLAST score
                  307
E value
                  5.0e-28
Match length
                  118
% identity
                  56
NCBI Description
                  (AJ011576) RNA-directed RNA polymerase [Nicotiana tabacum]
```

Seq. ID LIB22-003-Q1-E1-B11

Method BLASTX
NCBI GI g4006865
BLAST score 297



```
E value
 Match length
                    67
                    85
 % identity
                    (Z99707) putative protein [Arabidopsis thaliana]
 NCBI Description
                    137743
 Seq. No.
 Seq. ID
                    LIB22-003-Q1-E1-B12
                    BLASTN
 Method
 NCBI GI
                    g2252823
 BLAST score
                    127
 E value
                    3.0e-65
 Match length
                    230
 % identity
                    99
 NCBI Description Arabidopsis thaliana BAC IG005I10
                    137744
 Seq. No.
                    LIB22-003-Q1-E1-B5
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q2244863
 BLAST score
                    209
                    1.0e-16
 E value
 Match length
                    47
 % identity
                    81
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
· NCBI Description
 Seq. No.
                    137745
                    LIB22-003-Q1-E1-C3
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q3540207
 BLAST score
                    512
 E value
                    3.0e-52
 Match length
                    126
                    87
  % identity
 NCBI Description
                   (AC004260) Putative protein kinase [Arabidopsis thaliana]
  Seq. No.
                    137746
  Seq. ID
                    LIB22-003-Q1-E1-C4
  Method
                    BLASTN
  NCBI GI
                    g2182287
  BLAST score
                    200
                    1.0e-109
  E value
 Match length
                    227
                    97
  % identity
                   Genomic sequence for Arabidopsis thaliana BAC T7N9,
  NCBI Description
                    complete sequence [Arabidopsis thaliana]
  Seq. No.
                    137747
  Seq. ID
                    LIB22-003-Q1-E1-D11
  Method
                    BLASTX
  NCBI GI
                    q2738248
  BLAST score
                    158
```

E value 1.0e-10 Match length 101 % identity 75

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]



```
137748
Seq. No.
Seq. ID
                  LIB22-003-Q1-E1-F11
Method
                  BLASTX
NCBI GI
                  q2191131
BLAST score
                  445
                  1.0e-44
E value
Match length
                  93
% identity
                  86
                  (AF007269) A_IG002N01.8 gene product [Arabidopsis thaliana]
NCBI Description
                  137749
Seq. No.
                  LIB22-003-Q1-E1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4490291
BLAST score
                  270
E value
                  1.0e-150
Match length
                  273
                  100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5
                   (ESSA project)
Seq. No.
                  137750
                  LIB22-003-Q1-E1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169128
BLAST score
                  412
                  1.0e-40
E value
                  90
Match length
                  90
% identity
                  SERINE/THREONINE-PROTEIN KINASE CTR1 >gi_166680 (L08789)
NCBI Description
                  protein kinase [Arabidopsis thaliana] >gi 166682 (L08790)
                  protein kinase [Arabidopsis thaliana]
Seq. No.
                  137751
Seq. ID
                  LIB22-003-Q1-E1-G8
Method
                  BLASTN
NCBI GI
                  q4263694
BLAST score
                  241
E value
                   1.0e-133
Match length
                   241
                   100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F22D22 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  137752
Seq. ID
                  LIB22-003-Q1-E1-H3
Method
                  BLASTN
NCBI GI
                  g3241917
BLAST score
                  172
E value
                   4.0e-92
Match length
                   224
% identity
                   94
```

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K19B1, complete sequence [Arabidopsis thaliana]

137753 Seq. No.

LIB22-003-Q1-E1-H7 Seq. ID

NCBI GI BLAST score

E value



```
Method
NCBI GI
                  a4630748
BLAST score
                  388
                  5.0e-38
E value
Match length
                  81
                  93
% identity
                  (AC007236) putative anion exchange protein 3 [Arabidopsis
NCBI Description
                  thaliana]
                  137754
Seq. No.
Seq. ID
                  LIB22-004-Q1-E1-A10
Method
                  BLASTX
NCBI GI
                  q3184258
BLAST score
                  183
E value
                  1.0e-13
Match length
                  80
                  41
% identity
                  (U82130) tumor susceptibility protein [Homo sapiens]
NCBI Description
                  137755
Seq. No.
                  LIB22-004-Q1-E1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3299824
BLAST score
                  251
E value
                  1.0e-139
Match length
                  338
                  100
% identity
                  Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,
NCBI Description
                  near 17 cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  137756
Seq. ID
                  LIB22-004-Q1-E1-B8
Method
                  BLASTX
                  g2702281
NCBI GI
BLAST score
                  469
E value
                  3.0e-47
Match length
                  104
% identity
                  86
                   (AC003033) putative protein disulfide isomerase precursor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  137757
Seq. ID
                  LIB22-004-Q1-E1-B9
Method
                  BLASTX
NCBI GI
                  g3776005
BLAST score
                  614
E value
                  4.0e-64
Match length
                  135
% identity
                  90
NCBI Description
                  (AJ010466) RNA helicase [Arabidopsis thaliana]
                  137758
Seq. No.
Seq. ID
                  LIB22-004-Q1-E1-C11
                  BLASTN
Method
```

0.0e+00

g4589950

331



```
Match length
% identity
                  97
                  Arabidopsis thaliana chromosome II BAC T28P16 genomic
NCBI Description
                  sequence, complete sequence
                  137759
Seq. No.
Seq. ID
                  LIB22-004-Q1-E1-C2
Method
                  BLASTX
NCBI GI
                  g3193284
BLAST score
                  213
                  5.0e-17
E value
Match length
                  90
% identity
                  46
NCBI Description
                  (AF069298) No definition line found [Arabidopsis thaliana]
                  137760
Seq. No.
Seq. ID
                  LIB22-004-Q1-E1-C3
Method
                  BLASTX
NCBI GI
                  q4406780
BLAST score
                  407
E value
                  7.0e-40
Match length
                  116
% identity
                  69
NCBI Description
                  (AC006532) putative multispanning membrane protein
                  [Arabidopsis thaliana]
Seq. No.
                  137761
                  LIB22-004-Q1-E1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2961356
BLAST score
                  530
E value
                  3.0e-54
Match length
                  122
% identity
                  78
                   (AL022140) alcohol dehydrogenase like protein [Arabidopsis
NCBI Description
                  thaliana]
                  137762
Seq. No.
Seq. ID
                  LIB22-004-Q1-E1-C7
Method
                  BLASTX
NCBI GI
                  q3056594
BLAST score
                  693
E value
                  2.0e-73
Match length
                  124
% identity
                  100
NCBI Description
                  (AC004255) T1F9.15 [Arabidopsis thaliana]
Seq. No.
                  137763
Seq. ID
                  LIB22-004-Q1-E1-D10
Method
                  BLASTX
NCBI GI
                  q4580469
```

BLAST score 438 2.0e-43 E value

Match length 102 % identity 82

NCBI Description (AC006081) putative zinc finger protein [Arabidopsis

thaliana]



```
Seq. No.
                   137764
                  LIB22-004-Q1-E1-D12
Seq. ID
Method
                  BLASTN
                   q2281632
NCBI GI
BLAST score
                   46
E value
                  1.0e-16
Match length
                   46
                  100
% identity
NCBI Description
                  Arabidopsis thaliana AP2 domain containing protein RAP2.4
                  mRNA, partial cds
Seq. No.
                   137765
Seq. ID
                  LIB22-004-Q1-E1-E10
Method
                  BLASTX
NCBI GI
                   g1546698
BLAST score
                   697
E value
                   8.0e-74
Match length
                  136
                   100
% identity
                  (X98808) peroxidase ATP3a [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   137766
Seq. ID
                  LIB22-004-Q1-E1-F2
Method
                   BLASTN
NCBI GI
                   g2182287
BLAST score
                   407
E value
                   0.0e+00
Match length
                   407
% identity
                   100
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T7N9,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   137767
                   LIB22-004-Q1-E1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2688828
BLAST score
                   123
E value
                   7.0e-26
Match length
                   132
                   47
% identity
NCBI Description
                   (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus
                   armeniaca]
Seq. No.
                   137768
Seq. ID
                   LIB22-004-Q1-E1-G12
Method
                   BLASTN
NCBI GI
                   g3434972
BLAST score
                   159
E value
                   2.0e-84
Match length
                   197
% identity
                   100
```

NCBI Description

Seq. ID LIB22-005-Q1-E1-A7

16533

element binding factor 4, complete cds

Arabidopsis thaliana AtERF-4 mRNA for ethylene responsive



```
Method
                  BLASTX
NCBI GI
                  g1490554
BLAST score
                  636
                  1.0e-66
E value
                  141
Match length
                  91
% identity
                  (U63633) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
                  137770
Seq. No.
                  LIB22-005-Q1-E1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4454022
BLAST score
                  65
                  1.0e-28
E value
Match length
                  97
                  92
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16
NCBI Description
                  (ESSAII project)
                  137771
Seq. No.
                  LIB22-005-Q1-E1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4680659
BLAST score
                  222
                  4.0e-18
E value
Match length
                  104
% identity
                  41
                  (AF132944) CGI-10 protein [Homo sapiens]
NCBI Description
Seq. No.
                  137772
                  LIB22-005-Q1-E1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3600030
BLAST score
                  330
E value
                  9.0e-31
Match length
                  104
% identity
                  62
                  (AF080119) contains similarity to ankyrin repeats (Pfam:
NCBI Description
                  ank.hmm, score: 13.93, 14.93 and 27.78) [Arabidopsis
                  thaliana]
                  137773
Seq. No.
                  LIB22-005-Q1-E1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4432830
BLAST score
                  239
E value
                  1.0e-20
Match length
                  59
                  85
% identity
NCBI Description
                   (AC006283) similar to pheromone receptor deficient mutant
                   [Arabidopsis thaliana]
```

Seq. ID LIB22-005-Q1-E1-C9

Method BLASTN NCBI GI g2924729



BLAST score E value 0.0e + 00358 Match length 100 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No. 137775

LIB22-005-Q1-E1-D2 Seq. ID

Method BLASTN g2979540 NCBI GI BLAST score 148 E value 1.0e-77 Match length 357 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F17K2 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137776

Seq. ID LIB22-005-Q1-E1-D8

Method BLASTN NCBI GI g4757678 BLAST score 85 E value 3.0e-40 Match length 216 % identity 92

NCBI Description Arabidopsis thaliana chromosome I BAC F9H16 genomic

sequence, complete sequence

Seq. No. 137777

Seq. ID LIB22-005-Q1-E1-F4

Method BLASTN NCBI GI q4096078 BLAST score 245 E value 1.0e-135 Match length 378 % identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC T5A14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137778

Seq. ID LIB22-005-Q1-E1-G1

Method BLASTX NCBI GI g231586 BLAST score 210 E value 6.0e-17 Match length 101 % identity 54

ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description

>gi_82027_pir__S20504 H+-transporting ATP synthase (EC
3.6.1.34) beta chain, mitochondrial - Para rubber tree >gi 18831 emb CAA41401 (X58498) mitochondrial ATP synthase

beta-subunit [Hevea brasiliensis]

137779 Seq. No.

Seq. ID LIB22-005-Q1-E1-G12

Method BLASTX



```
NCBI GI
                  q4539452
BLAST score
                  364
                  8.0e-35
E value
Match length
                  125
% identity
                  54
                  (AL049500) putative phosphoribosylanthranilate transferase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  137780
Seq. ID
                  LIB22-005-Q1-E1-G3
Method
                  BLASTN
NCBI GI
                  g4586098
BLAST score
                  283
E value
                  1.0e-158
Match length
                  304
                  98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13
NCBI Description
                  (ESSA project)
Seq. No.
                  137781
                  LIB22-005-Q1-E1-G4
Seq. ID
                  BLASTX
                  g2244946
                  505
```

Method NCBI GI BLAST score E value 1.0e-51 Match length 99 100 % identity

(Z97339) unnamed protein product [Arabidopsis thaliana] NCBI Description >gi 2326344 emb CAA72072 (Y11187) G14587-6 [Arabidopsis

thaliana]

Seq. No. 137782

Seq. ID LIB22-005-Q1-E1-H6

Method BLASTN NCBI GI g2749918 BLAST score 268 E value 1.0e-149 Match length 343 % identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137783

Seq. ID LIB22-006-Q1-E1-A1

Method BLASTX NCBI GI q3337361 BLAST score 166 E value 7.0e-12Match length 59 % identity 49

(AC004481) ankyrin-like protein [Arabidopsis thaliana] NCBI Description

Seq. No. 137784

LIB22-006-Q1-E1-A7 Seq. ID

BLASTN Method NCBI GI g3766106

BLAST score 59



E value Match length 226 % identity

Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, NCBI Description

complete sequence [Arabidopsis thaliana]

137785 Seq. No.

LIB22-006-Q1-E1-B8 Seq. ID

Method BLASTN NCBI GI g3399678 BLAST score 137 2.0e-71 E value Match length 189 % identity 94

Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, NCBI Description

complete sequence [Arabidopsis thaliana]

137786 Seq. No.

LIB22-006-Q1-E1-C4 Seq. ID

Method BLASTN g2245126 NCBI GI BLAST score 300 E value 1.0e-168 Match length 338 % identity 100

Arabidopsis thaliana DNA chromosome 4, ESSA I contig NCBI Description

fragment No

Seq. No.

137787 LIB22-006-Q1-E1-C8 Seq. ID

Method BLASTX q4454043 NCBI GI BLAST score 171 E value 3.0e-12 Match length 70

% identity 44

(AL035394) putative receptor kinase [Arabidopsis thaliana] NCBI Description

Seq. No. 137788

LIB22-006-Q1-E1-D10 Seq. ID

Method BLASTX NCBI GI g3334441 BLAST score 343 E value 2.0e-32 116 Match length % identity 34

HYPOTHETICAL 47.9 KD PROTEIN T517.9 IN CHROMOSOME II NCBI Description

>qi 2642161 (AC003000) hypothetical protein [Arabidopsis

thaliana]

137789 Seq. No.

Seq. ID LIB22-006-Q1-E1-D2

 ${\tt BLASTX}$ Method g3377813 NCBI GI BLAST score 254 6.0e-22 E value 56 Match length

% identity

NCBI Description



```
% identity
                  (AF076275) No definition line found [Arabidopsis thaliana]
NCBI Description
                  137790
Seq. No.
                  LIB22-006-Q1-E1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2618683
                  281
BLAST score
                  1.0e-157
E value
                  410
Match length
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T32G6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  137791
                  LIB22-006-Q1-E1-F12
Seq. ID
                  BLASTN
Method
NCBI GI
                  q487790
BLAST score
                  138
                  1.0e-71
E value
                  178
Match length
                  94
% identity
                  Arabidopsis thaliana GF14omega isoform (GRF2) gene,
NCBI Description
                  complete cds
                  137792
Seq. No.
                  LIB22-006-Q1-E1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2811066
                  255
BLAST score
                  3.0e-22
E value
                  95
Match length
                  47
% identity
NCBI Description
                  PUTATIVE PROTEIN-TYROSINE PHOSPHATASE PTEN (MUTATED IN
                  MULTIPLE ADVANCED CANCERS 1) >gi 1916330 (U92437) MMAC1
                  [Mus musculus]
                  137793
Seq. No.
Seq. ID
                  LIB22-006-Q1-E1-G11
Method
                  BLASTX
NCBI GI
                  g2980773
BLAST score
                  623
E value
                  3.0e-65
Match length
                  129
% identity
                  73
                  (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  137794
Seq. ID
                  LIB22-006-Q1-E1-H4
Method
                  BLASTX
NCBI GI
                  q4581132
                  258
BLAST score
                  2.0e-22
E value
Match length
                  86
                  64
```

(AC005825) hypothetical protein [Arabidopsis thaliana]



```
Seq. No.
                   137795
Seq. ID
                   LIB22-007-Q1-E1-A12
Method
                   BLASTX
NCBI GI
                   g2911082
BLAST score
                   428
E value
                   2.0e-42
Match length
                   100
% identity
                   56
NCBI Description
                  (AL021960) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   137796
Seq. ID
                   LIB22-007-Q1-E1-A6
Method
                  BLASTX
NCBI GI
                   q4455750
BLAST score
                   175
E value
                   1.0e-12
Match length
                   111
% identity
                   36
NCBI Description
                  (AL035478) putative dehydrogenase [Streptomyces coelicolor]
Seq. No.
                   137797
Seq. ID
                  LIB22-007-Q1-E1-B2
Method
                  BLASTX
NCBI GI
                   q1335862
BLAST score
                   186
E value
                   2.0e-14
Match length
                   42
% identity
                   83
NCBI Description
                  (U42608) clathrin heavy chain [Glycine max]
Seq. No.
                   137798
Seq. ID
                   LIB22-007-Q1-E1-C12
Method
                  BLASTN
NCBI GI
                   g4586241
BLAST score
                   80
E value
                   3.0e-37
Match length
                   236
% identity
                   94
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18
                   (ESSA project)
Seq. No.
                   137799
Seq. ID
                  LIB22-007-Q1-E1-C3
Method
                  BLASTX
NCBI GI
                   g2062169
BLAST score
                  85
E value
                   4.4e-02
Match length
                  88
                  37
% identity
NCBI Description
                   (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis
                  thaliana]
Seq. No.
                  137800
```

Seq. ID LIB22-007-Q1-E1-C9

Method BLASTX NCBI GI g2244750 BLAST score 581



E value 3.0e-60 Match length 124 % identity 89

NCBI Description (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]

>gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase

[Arabidopsis thaliana]

Seq. No. 137801

Seq. ID LIB22-007-Q1-E1-E10

Method BLASTX
NCBI GI g2498731
BLAST score 448
E value 1.0e-44
Match length 126
% identity 67

NCBI Description PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1

>gi_1362013_pir__S57611 zeta-crystallin homolog Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)

zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No. 137802

Seq. ID LIB22-007-Q1-E1-F10

Method BLASTN
NCBI GI g4263586
BLAST score 342
E value 0.0e+00
Match length 342
% identity 100

NCBI Description Arabidopsis thaliana chromosome 1 BAC F28K20 sequence,

complete sequence

Seq. No. 137803

Seq. ID LIB22-007-Q1-E1-G12

Method BLASTN
NCBI GI g4539378
BLAST score 145
E value 4.0e-76
Match length 189
% identity 94

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21

(ESSA project)

Seq. No. 137804

Seq. ID LIB22-007-Q1-E1-G7

Method BLASTX
NCBI GI g3377517
BLAST score 235
E value 1.0e-19
Match length 116
% identity 39

NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No. 137805

Seq. ID LIB22-008-Q1-E1-B2

Method BLASTX NCBI GI g4586021 BLAST score 102



```
E value
                  3.0e-55
Match length
                  113
                  98
% identity
                   (AC007170) putative cytoplasmic aconitate hydratase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  137806
Seq. ID
                  LIB22-008-Q1-E1-C1
Method
                  BLASTN
NCBI GI
                  q2098816
BLAST score
                  38
E value
                  5.0e-12
Match length
                  94
                  85
% identity
NCBI Description Arabidopsis thaliana BAC F19G10, complete sequence
                  137807
Seq. No.
Seq. ID
                  LIB22-008-Q1-E1-C10
                  BLASTX
Method
                  q1563719
NCBI GI
                   303
BLAST score
                  1.0e-27
E value
Match length
                  88
% identity
                   68
NCBI Description (Y08320) cyclophylin [Digitalis lanata]
                   137808
Seq. No.
                  LIB22-008-Q1-E1-C11
Seq. ID
Method
                  BLASTN
                   g4589950
NCBI GI
BLAST score
                   230
                   1.0e-127
E value
                   230
Match length
% identity
                   100
NCBI Description Arabidopsis thaliana chromosome II BAC T28P16 genomic
                   sequence, complete sequence
                   137809
Seq. No.
Seq. ID
                   LIB22-008-Q1-E1-C5
Method
                   BLASTX
                   g2760844
NCBI GI
                   363
BLAST score
                   4.0e-35
E value
Match length
                   76
                   100
% identity
                  (AC003105) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   137810
Seq. No.
Seq. ID
                   LIB22-008-Q1-E1-D10
```

BLASTX Method g3915085 NCBI GI 541 BLAST score 1.0e-55 E value Match length 113 93 % identity

TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID NCBI Description 4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)



>gi_1773289 (U71081) cinnamate-4-hydroxylase [Arabidopsis
thaliana] >gi_1946370 (U93215) cinnamate-4-hydroxylase
[Arabidopsis thaliana]

Seq. No. 137811 LIB22-008-Q1-E1-E12 Seq. ID Method BLASTN NCBI GI q2583106 189 BLAST score 1.0e-102 E value Match length 333 89 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 137812 Seq. ID LIB22-008-Q1-E1-F11 Method BLASTX NCBI GI g2827143 BLAST score 200 E value 2.0e-15 Match length 139 77 % identity NCBI Description (AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana] Seq. No. 137813 LIB22-008-Q1-E1-F5 Seq. ID Method BLASTN NCBI GI q2832667 93 BLAST score 7.0e-45 E value 234 Match length % identity 100 Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 NCBI Description (ESSAII project) Seq. No. 137814 Seq. ID LIB22-008-Q1-E1-G3 Method BLASTX NCBI GI q3980378 BLAST score 656 E value 5.0e-69 Match length 119 % identity 97 NCBI Description (AC004561) putative RNA binding protein [Arabidopsis thaliana] Seq. No. 137815 Seq. ID LIB22-009-Q1-E1-A7 Method BLASTX NCBI GI g4191779

NCBI GI g4191779 BLAST score 499 E value 1.0e-50

Match length 100 % identity 100

NCBI Description (AC005917) putative recA protein [Arabidopsis thaliana]



```
137816
Seq. No.
                  LIB22-009-Q1-E1-B6
Seq. ID
Method
                  BLASTX
                  g1402912
NCBI GI
BLAST score
                  147
                  6.0e-10
E value
Match length
                  28
                  100
% identity
                  (X98317) peroxidase [Arabidopsis thaliana]
NCBI Description
                  137817
Seq. No.
Seq. ID
                  LIB22-009-Q1-E1-D10
Method
                  BLASTX
NCBI GI
                  g2245378
BLAST score
                  459
                  4.0e-46
E value
                  104
Match length
                  85
% identity
                  (U83245) auxin response factor 1 [Arabidopsis thaliana]
NCBI Description
                  137818
Seq. No.
                  LIB22-009-Q1-E1-D6
Seq. ID
Method
                  BLASTX
                  g2190558
NCBI GI
BLAST score
                  559
                  1.0e-57
E value
Match length
                  122
                  85
% identity
NCBI Description
                  (AC001229) F5I14.14 [Arabidopsis thaliana]
                  137819
Seq. No.
                  LIB22-009-Q1-E1-D7
Seq. ID
Method
                  BLASTX
                  g4220462
NCBI GI
BLAST score
                  461
E value
                  2.0e-46
Match length
                  91
% identity
                  100
NCBI Description
                   (AC006216) Strong similarity to gb Z50851 HD-zip (athb-8)
                  gene from Arabidopsis thaliana containing Homeobox PF 00046
                  and bZIP PF 00170 domains. [Arabidopsis thaliana]
Seq. No.
                  137820
Seq. ID
                  LIB22-009-Q1-E1-E9
Method
                  BLASTX
NCBI GI
                  g1361982
BLAST score
                  330
E value
                  3.0e-31
Match length
                  75
% identity
                  85
                  4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis
NCBI Description
                  thaliana >gi 609340 (U18675) 4-coumarate--coenzyme A ligase
                   [Arabidopsis thaliana]
```

Seq. ID LIB22-009-Q1-E1-F12



```
Method
                  BLASTN
NCBI GI
                  q4519192
BLAST score
                  304
E value
                  1.0e-171
Match length
                  311
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MBK21, complete sequence
Seq. No.
                  137822
Seq. ID
                  LIB22-009-Q1-E1-G6
Method
                  BLASTX
NCBI GI
                  g3582329
BLAST score
                  673
                  5.0e-71
E value
Match length
                  125
% identity
                  99
NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]
                  137823
Seq. No.
                  LIB22-009-Q1-E1-H8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4519182
BLAST score
                  83
E value
                  3.0e - 39
Match length
                  144
% identity
                  88
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K13H13, complete sequence
Seq. No.
                  137824
Seq. ID
                  LIB22-010-Q1-E1-B5
Method
                  BLASTN
NCBI GI
                  q1742964
BLAST score
                  424
E value
                  0.0e + 00
Match length
                  436
                  99
% identity
NCBI Description A.thaliana mRNA for HAPp48,5 protein
Seq. No.
                  137825
Seq. ID
                  LIB22-010-Q1-E1-B6
Method
                  BLASTX
NCBI GI
                  g3492806
BLAST score
                  264
E value
                  5.0e-23
Match length
                  101
% identity
                  51
                  (AJ225045) adventitious rooting related oxygenase [Malus
NCBI Description
                  domestica]
```

Seq. ID LIB22-010-Q1-E1-C2

Method BLASTX
NCBI GI g4056467
BLAST score 549
E value 2.0e-56



Match length 104 % identity 100

NCBI Description (AC005990) Strong similarity to gb_AB006693 spermidine synthase from Arabidopsis thaliana. ESTs gb_AA389822,

gb_T41794, gb_N38455, gb_AI100106, gb_F14442 and gb_F14256

come from this gene. [Arabidopsis thaliana]

Seq. No. 137827

Seq. ID LIB22-010-Q1-E1-C6

Method BLASTX
NCBI GI g2335096
BLAST score 337
E value 1.0e-31
Match length 147
% identity 47

NCBI Description (AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 137828

Seq. ID LIB22-010-Q1-E1-C9

Method BLASTN
NCBI GI g4586098
BLAST score 156
E value 2.0e-82
Match length 314
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13

(ESSA project)

Seq. No. 137829

Seq. ID LIB22-010-Q1-E1-D1

Method BLASTN
NCBI GI g4519195
BLAST score 298
E value 1.0e-167
Match length 308
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MQC12, complete sequence

Seq. No. 137830

Seq. ID LIB22-010-Q1-E1-E1

Method BLASTN
NCBI GI 94056476
BLAST score 169
E value 3.0e-90
Match length 190
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC F3G5 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137831

Seq. ID LIB22-010-Q1-E1-E4

Method BLASTN
NCBI GI g2833627
BLAST score 339
E value 0.0e+00
Match length 339

% identity Arabidopsis thaliana chromosome 1 BAC F1707 complete NCBI Description sequence [Arabidopsis thaliana] 137832 Seq. No. LIB22-010-Q1-E1-E5 Seq. ID Method BLASTN g2244870 NCBI GI 191 BLAST score 1.0e-103 E value Match length 337 100 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No 137833 Seq. No. LIB22-010-Q1-E1-E8 Seq. ID Method BLASTN g3522932 NCBI GI BLAST score 218 1.0e-119 E value 234 Match length 98 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 137834 LIB22-010-Q1-E1-F1 Seq. ID BLASTN Method g2980787 NCBI GI BLAST score 299 E value 1.0e-168 Match length 299 50 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project) Seq. No. 137835 LIB22-010-Q1-E1-G10 Seq. ID Method BLASTX q4455184 NCBI GI

Method BLASTX
NCBI GI g4455184
BLAST score 569
E value 5.0e-59
Match length 106
% identity 100

NCBI Description (AL035521) extra-large G-protein-like [Arabidopsis

thaliana]

Seq. No. 137836

Seq. ID LIB22-010-Q1-E1-G11

Method BLASTX
NCBI GI g4115377
BLAST score 405
E value 7.0e-40
Match length 95
% identity 81

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                  137837
Seq. ID
                  LIB22-010-Q1-E1-G4
Method
                  BLASTX
NCBI GI
                  q3426038
BLAST score
                  466
E value
                  8.0e-47
Match length
                  114
                  52
% identity
                  (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  137838
Seq. ID
                  LIB22-010-Q1-E1-H2
Method
                  BLASTX
NCBI GI
                  q3608155
BLAST score
                  461
                  6.0e-49
E value
Match length
                  130
% identity
                  81
                  (AC005314) putative RNA helicase [Arabidopsis thaliana]
NCBI Description
                  137839
Seq. No.
Seq. ID
                  LIB22-010-Q1-E1-H8
Method
                  BLASTN
NCBI GI
                  q2244788
BLAST score
                  263
E value
                   1.0e-146
Match length
                   368
% identity
                   100
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
Seq. No.
                   137840
Seq. ID
                   LIB22-011-Q1-E1-C11
Method
                   BLASTX
                   g3250696
NCBI GI
BLAST score
                   314
                   3.0e-29
E value
Match length
                   89
% identity
                   39
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]
                   137841
Seq. No.
Seq. ID
                   LIB22-011-Q1-E1-C5
Method
                   BLASTN
                   q2618683
NCBI GI
BLAST score
                   279
                   1.0e-156
E value
                   307
Match length
% identity
                   98
                  Arabidopsis thaliana chromosome II BAC T32G6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   137842
```

Seq. ID LIB22-011-Q1-E1-E6

Method BLASTN NCBI GI g2262155



BLAST score E value 3.0e-89 Match length 211 95 % identity DNA sequence of Arabidopsis thaliana BAC F5J6 from NCBI Description chromosome IV, complete sequence [Arabidopsis thaliana] Seq. No. 137843 LIB22-011-Q1-E1-F7 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g2854117
BLAST score 67
E value 6.4e+00
Match length 130
% identity 45

NCBI Description (AF045453) protein kinase YakA [Dictyostelium discoideum]

Seq. No. 137844

Seq. ID LIB22-011-Q1-E1-G12

Method BLASTX
NCBI GI g4572674
BLAST score 352
E value 2.0e-33
Match length 85
% identity 82

NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]

Seq. No. 137845

Seq. ID LIB22-011-Q1-E1-H11

Method BLASTX
NCBI GI g3869280
BLAST score 249
E value 1.0e-21
Match length 76
% identity 64

NCBI Description (AF064786) beta-galactosidase precursor [Carica papaya]

Seq. No. 137846

Seq. ID LIB22-011-Q1-K1-A12

Method BLASTN
NCBI GI g4206762
BLAST score 225
E value 1.0e-123
Match length 335
% identity 96

NCBI Description Arabidopsis thaliana cell wall-plasma membrane linker

protein homolog (CWLP) mRNA, complete cds

Seq. No. 137847

Seq. ID LIB22-011-Q1-K1-A6

Method BLASTX
NCBI GI g3046696
BLAST score 180
E value 4.0e-13
Match length 116
% identity 39

NCBI Description (AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. ID

137853

LIB22-012-Q1-E1-A6



```
Seq. No.
                  137848
                  LIB22-011-Q1-K1-D10
Seq. ID
Method
                  BLASTX
                  g1684855
NCBI GI
                  285
BLAST score
                  1.0e-25
E value
                  58
Match length
% identity
                  22
                  (U77939) ubiquitin-like protein [Phaseolus vulgaris]
NCBI Description
                  137849
Seq. No.
                  LIB22-011-Q1-K1-E9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3132469
                  239
BLAST score
                  1.0e-131
E value
                  542
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T29F13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  137850
Seq. No.
                  LIB22-011-Q1-K1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3831437
BLAST score
                  544
                  0.0e+00
E value
Match length
                  552
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T3A4 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  137851
Seq. No.
Seq. ID
                  LIB22-011-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  g3668097
BLAST score
                  210
                  1.0e-16
E value
Match length
                  118
% identity
                   44
                   (AC004667) putative glycine cleavage system protein H
NCBI Description
                  precursor [Arabidopsis thaliana]
Seq. No.
                  137852
                  LIB22-012-Q1-E1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3449312
BLAST score
                  179
                   4.0e-96
E value
Match length
                  332
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K16L22, complete sequence [Arabidopsis thaliana]
```



```
Method
                  g4512697
NCBI GI
                  258
BLAST score
                  3.0e-22
E value
                  98
Match length
                  57
% identity
                  (AC006569) unknown protein [Arabidopsis thaliana]
NCBI Description
                  137854
Seq. No.
                  LIB22-012-Q1-E1-B5
Seq. ID
                  BLASTN
Method
                  g4220641
NCBI GI
BLAST score
                  41
E value
                  7.0e-14
Match length
                  268
                  92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUL3, complete sequence [Arabidopsis thaliana]
                  137855
Seq. No.
                  LIB22-012-Q1-E1-D1
Seq. ID
                  BLASTX
Method
                  q4587602
NCBI GI
                  393
BLAST score
                   2.0e-38
E value
Match length
                   90
                   86
% identity
                   (AC006951) putative retrotransposon hopscotch polyprotein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   137856
                   LIB22-012-Q1-E1-D11
Seq. ID
Method
                  BLASTX
                   g3688173
NCBI GI
BLAST score
                   556
E value
                   2.0e-57
                   123
Match length
% identity
                   82
                  (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
                   137857
Seq. No.
                   LIB22-012-Q1-E1-E9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4159708
BLAST score
                   286
E value
                   1.0e-160
                   321
Match length
% identity
                   64
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MKP6, complete sequence
                   137858
Seq. No.
                   LIB22-012-Q1-E1-F11
```

Seq. ID

Method BLASTN NCBI GI g3702735 BLAST score 156 E value 2.0e-82



Match length 277 % identity 42

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQL5, complete sequence [Arabidopsis thaliana]

Seq. No. 137859

Seq. ID LIB22-012-Q1-E1-F4

Method BLASTN
NCBI GI g2828185
BLAST score 151
E value 9.0e-80
Match length 155
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUD21, complete sequence [Arabidopsis thaliana]

Seq. No. 137860

Seq. ID LIB22-012-Q1-E1-H4

Method BLASTN
NCBI GI g4056476
BLAST score 209
E value 1.0e-114
Match length 213
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F3G5 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137861

Seq. ID LIB22-012-Q1-E1-H5

Method BLASTN
NCBI GI g469113
BLAST score 108
E value 3.0e-54
Match length 108
% identity 100

NCBI Description A.thaliana (Columbia) Dr4 mRNA

Seq. No. 137862

Seq. ID LIB22-013-Q1-E1-B2

Method BLASTN
NCBI GI g4337186
BLAST score 145
E value 7.0e-76
Match length 310
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T28I24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137863

Seq. ID LIB22-013-Q1-E1-B5

Method BLASTX
NCBI GI g1531758
BLAST score 509
E value 5.0e-52
Match length 97
% identity 95

NCBI Description (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)

137869



unknown protein [Arabidopsis thaliana]

```
Seq. No.
                  137864
                  LIB22-013-Q1-E1-C8
Seq. ID
Method
                  BLASTN
                  g2494106
NCBI GI
BLAST score
                  345
E value
                  0.0e+00
                  357
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  137865
                  LIB22-013-Q1-E1-D12
Seq. ID
Method
                  BLASTN
                  g4567300
NCBI GI
BLAST score
                  293
E value
                  1.0e-164
                  329
Match length
                  89
% identity
                  Arabidopsis thaliana chromosome II P1 MHK10 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  137866
Seq. ID
                  LIB22-013-Q1-E1-D2
Method
                  BLASTN
NCBI GI
                  g2853071
BLAST score
                  89
E value
                  2.0e-42
Match length
                  263
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7
NCBI Description
                  (ESSA project)
                  137867
Seq. No.
Seq. ID
                  LIB22-013-Q1-E1-D6
Method
                  BLASTX
NCBI GI
                  q4454452
BLAST score
                  423
E value
                  7.0e-42
Match length
                  81
% identity
                  66
NCBI Description
                  (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                  137868
Seq. ID
                  LIB22-013-Q1-E1-D8
Method
                  BLASTN
                  g3386593
NCBI GI
BLAST score
                  341
                  0.0e + 00
E value
Match length
                  341
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC F4I18 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
```



```
LIB22-013-Q1-E1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g120675
                  526
BLAST score
                  9.0e-54
E value
                  121
Match length
% identity
                  84
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                  >gi 21143 emb CAA27844 (X04301) GAPDH (aa 1-338) [Sinapis
                  alba]
Seq. No.
                  137870
                  LIB22-013-Q1-E1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g549060
BLAST score
                  367
                  3.0e - 35
E value
                  96
Match length
                  75
% identity
                  T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)
NCBI Description
                  >gi_631656_pir__S43058 CCTeta protein eta chain - mouse
                  >gi_468504_emb_CAA83274_ (Z31399) CCTeta, eta subunit of
                  the chaperonin containing TCP-1 (CCT) [Mus musculus]
Seq. No.
                  137871
                  LIB22-013-Q1-E1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2924652
BLAST score
                  191
E value
                  1.0e-103
Match length
                  350
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K9L2, complete sequence [Arabidopsis thaliana]
Seq. No.
                   137872
Seq. ID
                  LIB22-013-Q1-E1-G3
Method
                  BLASTN
NCBI GI
                  q4733984
BLAST score
                   187
E value
                   1.0e-101
Match length
                   357
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F1404 genomic
                  sequence, complete sequence
Seq. No. Seq. ID
                   137873
                  LIB22-013-Q1-E1-G4
Method
                  BLASTN
                   g4586024
NCBI GI
BLAST score
                   331
E value
                   0.0e + 00
```

Match length 335 % identity 53

NCBI Description Arabidopsis thaliana chromosome II BAC T13C7 genomic

137879



sequence, complete sequence

```
Seq. No.
                  137874
Seq. ID
                  LIB22-013-Q1-E1-G9
Method
                  BLASTN
NCBI GI
                  g4757403
BLAST score
                  140
                  9.0e-73
E value
Match length
                  432
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MJL12, complete sequence
Seq. No.
                  137875
Seq. ID
                  LIB22-013-Q1-E1-H6
Method
                  BLASTX
                  g3450842
NCBI GI
                  257
BLAST score
E value
                  8.0e-23
                  68
Match length
                  71
% identity
                  (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                  sativa]
                  137876
Seq. No.
Seq. ID
                  LIB22-014-Q1-E1-A1
Method
                  BLASTX
NCBI GI
                  g3377820
BLAST score
                  473
                  1.0e-47
E value
Match length
                  96
                  100
% identity
                  (AF076275) contains similarity to coatomer zeta chains
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  137877
Seq. ID
                  LIB22-014-Q1-E1-B12
Method
                  BLASTX
NCBI GI
                  q4263784
BLAST score
                  294
E value
                  1.0e-26
Match length
                  127
% identity
                  57
NCBI Description
                   (AC006068) putative glycogenin-2 protein [Arabidopsis
                  thaliana]
Seq. No.
                  137878
Seq. ID
                  LIB22-014-Q1-E1-B9
Method
                  BLASTX
NCBI GI
                  g2117612
BLAST score
                   449
                  7.0e-45
E value
Match length
                  90
                  97
% identity
NCBI Description catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
```



```
Seq. ID
                  LIB22-014-Q1-E1-D5
Method
                  BLASTN
NCBI GI
                  q4699904
BLAST score
                  244
                  1.0e-135
E value
                  274
Match length
                  96
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F1E22,
                  complete sequence
                  137880
Seq. No.
                  LIB22-014-Q1-E1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1586551
BLAST score
                  284
                  2.0e-25
E value
                  104
Match length
                  69
% identity
NCBI Description CCAAT-binding factor:SUBUNIT=B [Brassica napus]
Seq. No.
                  137881
                  LIB22-014-Q1-E1-E6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2335089
BLAST score
                  130
E value
                  6.0e-67
                  308
Match length
                  96
% identity
                  Arabidopsis thaliana chromosome II BAC T11A7 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  137882
Seq. No.
                  LIB22-014-Q1-E1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4558592
BLAST score
                  615
E value
                  3.0e-64
Match length
                  127
% identity
                  100
                  (AC006555) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  137883
Seq. No.
Seq. ID
                  LIB22-014-Q1-E1-H10
Method
                  BLASTX
NCBI GI
                  g2191159
BLAST score
                  325
E value
                  2.0e-30
Match length
                  91
% identity
                  79
NCBI Description
                  (AF007270) Similar to serine hydroxymethyltransferase;
```

Seq. No. 137884

Seq. ID LIB22-014-Q1-E1-H7

BLASTN Method NCBI GI g4589430

16555

thaliana cDNA W43384 [Arabidopsis thaliana]

coded for by A. thaliana cDNA T42313; coded for by A.



```
BLAST score 244
E value 1.0e-135
Match length 410
% identity 98
NCBI Description Arabidops
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence

Seq. No. 137885

Seq. ID LIB22-015-Q1-E1-F12

Method BLASTN
NCBI GI g4519193
BLAST score 169
E value 4.0e-90
Match length 328
% identity 63

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC11, complete sequence

Seq. No. 137886

Seq. ID LIB22-016-Q1-E1-A12

Method BLASTN
NCBI GI g2245031
BLAST score 197
E value 1.0e-107
Match length 269
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 137887

Seq. ID LIB22-016-Q1-E1-B4

Method BLASTN
NCBI GI g3451055
BLAST score 311
E value 1.0e-175
Match length 360
% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20

(ESSAII project)

Seq. No. 137888

Seq. ID LIB22-016-Q1-E1-F1

Method BLASTX
NCBI GI g417073
BLAST score 183
E value 4.0e-14
Match length 62
% identity 60

NCBI Description GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)

>gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC
1.4.1.14) - alfalfa >gi 166412 (L01660) NADH-glutamate

synthase [Medicago sativa]

Seq. No. 137889

Seq. ID LIB22-016-Q1-E1-G1

Method BLASTX NCBI GI g4263711



```
BLAST score
E value
                  1.0e-37
Match length
                  85
                  88
% identity
                  (AC006223) putative CCR4-associated transcription factor
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  137890
                  LIB22-016-Q1-E1-G10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4572664
BLAST score
                  415
E value
                  0.0e+00
Match length
                  415
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC F25P17 genomic
NCBI Description
                  sequence, complete sequence
                  137891
Seq. No.
                  LIB22-016-Q1-E1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4337188
BLAST score
                  161
E value
                  2.0e-11
Match length
                  40
                  82
% identity
                  (AC006403) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  137892
Seq. No.
                  LIB22-016-Q1-E1-H7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4263753
BLAST score
                  260
E value
                  1.0e-144
                  409
Match length
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome V map near 60.5 cM,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  137893
                  LIB22-017-Q1-E1-A2
Seq. ID
Method
                  BLASTX
                  g4581150
NCBI GI
                  171
BLAST score
E value
                  2.0e-12
Match length
                  41
% identity
                  83
NCBI Description
                  (AC006919) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  137894
Seq. ID
                  LIB22-017-Q1-E1-A4
Method
                  BLASTN
```

Method BLASTN
NCBI GI g4558586
BLAST score 218
E value 1.0e-119
Match length 303
% identity 100

```
Arabidopsis thaliana chromosome 1 BAC T518 seguence,
NCBI Description
                  complete sequence
                  137895
Seq. No.
                  LIB22-017-Q1-E1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4585991
BLAST score
                  285
E value
                  1.0e-25
Match length
                  91
                  54
% identity
                  (AC005287) very similar to mouse Dhm1 and Dhm2 [Arabidopsis
NCBI Description
                  thaliana]
                  137896
Seq. No.
                  LIB22-017-Q1-E1-B8
Seq. ID
Method
                  BLASTX
                  g2781394
NCBI GI
BLAST score
                  418
                  3.0e-41
E value
                  87
Match length
                  100
% identity
NCBI Description (U70424) O-methyltransferase 1 [Arabidopsis thaliana]
```

 Seq. No.
 137897

 Seq. ID
 LIB22-017-Q1-E1-C11

 Method
 BLASTX

 NCBI GI
 g4581146

 BLAST score
 421

 E value
 1.0e-41

 Match length
 91

Seq. No. 137898

Seq. ID LIB22-017-Q1-E1-C8

Method BLASTX
NCBI GI g4115377
BLAST score 141
E value 3.0e-09
Match length 44
% identity 55

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 137899

Seq. ID LIB22-017-Q1-E1-D3

Method BLASTX
NCBI GI g2911057
BLAST score 431
E value 9.0e-43
Match length 83
% identity 100

NCBI Description (AL021961) caffeoyl-CoA O-methyltransferase - like protein

[Arabidopsis thaliana]

Seq. No. 137900

Method

NCBI GI

BLAST score

BLASTN

383

g3241924



```
LIB22-017-Q1-E1-E3
Seq. ID
Method
                  BLASTN
                  g2244950
NCBI GI
BLAST score
                  88
                  2.0e-42
E value
Match length
                  88
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  137901
Seq. No.
                  LIB22-017-Q1-E1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3335375
BLAST score
                  284
                  5.0e-26
E value
                  69
Match length
% identity
                  80
                  (AC003028) putative amidase [Arabidopsis thaliana]
NCBI Description
                  137902
Seq. No.
                  LIB22-017-Q1-E1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3763915
BLAST score
                  207
E value
                  1.0e-113
Match length
                  366
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC F14B2 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  137903
Seq. No.
                  LIB22-017-Q1-E1-F1
Seq. ID
Method
                  BLASTN
                  g2828182
NCBI GI
BLAST score
                  211
E value
                  1.0e-115
Match length
                  246
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOJ9, complete sequence [Arabidopsis thaliana]
                  137904
Seq. No.
Seq. ID
                  LIB22-017-Q1-E1-F11
Method
                  BLASTX
NCBI GI
                  g1402904
BLAST score
                  473
E value
                  8.0e-48
Match length
                  90
                  100
% identity
NCBI Description
                  (X98313) peroxidase [Arabidopsis thaliana]
Seq. No.
                  137905
                  LIB22-017-Q1-E1-F12
Seq. ID
```



E value 0.0e+00 Match length 387 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNC6, complete sequence [Arabidopsis thaliana]

Seq. No. 137906

Seq. ID LIB22-017-Q1-E1-F7

Method BLASTX
NCBI GI g2129759
BLAST score 334
E value 3.0e-31
Match length 68
% identity 99

NCBI Description UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana

>gi 1143392 emb CAA90941 (Z54214) uridine diphosphate

glucose epimerase [Arabidopsis thaliana]

Seq. No. 137907

Seq. ID LIB22-017-Q1-E1-G1

Method BLASTX
NCBI GI g4572681
BLAST score 635
E value 1.0e-66
Match length 127
% identity 98

NCBI Description (AC006954) putative ubiquitin carboxyl terminal hydrolase

[Arabidopsis thaliana]

Seq. No. 137908

Seq. ID LIB22-017-Q1-E1-G11

Method BLASTX
NCBI GI g2894574
BLAST score 427
E value 2.0e-42
Match length 81
% identity 100

NCBI Description (AL021890) peroxidase prxr1 [Arabidopsis thaliana]

>gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1

[Arabidopsis thaliana]

Seq. No. 137909

Seq. ID LIB22-018-Q1-E1-A2

Method BLASTX
NCBI GI g2104949
BLAST score 380
E value 5.0e-37
Match length 84
% identity 83

NCBI Description (U96716) MAP kinase-like protein [Selaginella lepidophylla]

Seq. No. 137910

Seq. ID LIB22-018-Q1-E1-A5

Method BLASTN
NCBI GI g4006885
BLAST score 146
E value 1.0e-76



Match length 182 % identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 137911

Seq. ID LIB22-018-Q1-E1-E11

Method BLASTN
NCBI GI g3702734
BLAST score 327
E value 0.0e+00
Match length 327
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNB8, complete sequence [Arabidopsis thaliana]

Seq. No. 137912

Seq. ID LIB22-018-Q1-E1-F3

Method BLASTN
NCBI GI g4581084
BLAST score 207
E value 1.0e-113
Match length 304
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC T30F21 genomic

sequence, complete sequence

Seq. No. 137913

Seq. ID LIB22-018-Q1-E1-G12

Method BLASTN
NCBI GI g2760169
BLAST score 223
E value 1.0e-122
Match length 283
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MFB13, complete sequence [Arabidopsis thaliana]

Seq. No. 137914

Seq. ID LIB22-018-Q1-E1-H12

Method BLASTX
NCBI GI g4567235
BLAST score 353
E value 9.0e-34
Match length 92
% identity 70

NCBI Description (AC007119) putative phosphatidylinositol/phophatidylcholine

transfer protein [Arabidopsis thaliana]

Seq. No. 137915

Seq. ID LIB22-019-Q1-E1-A4

Method BLASTN
NCBI GI g3869070
BLAST score 46
E value 5.0e-17
Match length 195
% identity 72



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGO3, complete sequence [Arabidopsis thaliana]

Seq. No. 137916

Seq. ID LIB22-019-Q1-E1-E10

Method BLASTX
NCBI GI g4835226
BLAST score 262
E value 1.0e-22
Match length 85
% identity 58

NCBI Description (AL049862) putative protein [Arabidopsis thaliana]

Seq. No. 137917

Seq. ID LIB22-019-Q1-E1-F2

Method BLASTX
NCBI GI g3582329
BLAST score 241
E value 2.0e-20
Match length 103
% identity 47

NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 137918

Seq. ID LIB22-020-Q1-E1-A10

Method BLASTX
NCBI GI g3319344
BLAST score 576
E value 1.0e-59
Match length 130
% identity 87

NCBI Description (AF077407) contains similarity to UDP-glucoronosyl and

UDP-glucosyl transferases (Pfam: UDPGT.hmm, score: 85.94)

[Arabidopsis thaliana]

Seq. No. 137919

Seq. ID LIB22-020-Q1-E1-B12

Method BLASTN
NCBI GI g4539290
BLAST score 110
E value 4.0e-55
Match length 194
% identity 90

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19

(ESSA project)

Seq. No. 137920

Seq. ID LIB22-020-Q1-E1-B5

Method BLASTX
NCBI GI g4263777
BLAST score 207
E value 2.0e-16
Match length 58
% identity 62

NCBI Description (AC006068) putative serine carboxypeptidase II [Arabidopsis

thaliana] >gi 4510391_gb_AAD21479.1_ (AC007017) putative

serine carboxypeptidase II [Arabidopsis thaliana]



```
Seq. No.
                  137921
Seq. ID
                  LIB22-020-Q1-E1-D9
Method
                  BLASTX
NCBI GI
                  q4768986
BLAST score
                  148
E value
                  1.0e-09
                   99
Match length
% identity
                  34
                  (AF140493) hypothetical protein [Oryza sativa]
NCBI Description
Seq. No.
                  137922
Seq. ID
                  LIB22-020-Q1-E1-E4
Method
                  BLASTN
NCBI GI
                  q4454022
BLAST score
                  47
                  1.0e-17
E value
Match length
                  132
% identity
                   74
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16
NCBI Description
                   (ESSAII project)
Seq. No.
                  137923
Seq. ID
                  LIB22-020-Q1-E1-G7
Method
                  BLASTN
NCBI GI
                  q2924768
BLAST score
                   62
E value
                   9.0e-27
Match length
                  126
% identity
                   87
                  Arabidopsis thaliana chromosome II BAC F25I18 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   137924
Seq. ID
                  LIB22-021-Q1-E1-B12
Method
                  BLASTX
NCBI GI
                   q3152589
BLAST score
                   587
E value
                   5.0e-61
Match length
                   125
% identity
                   81
NCBI Description
                   (AC002986) Strong similarity to lupeol synthase gb U49919
                   from A. thaliana (second gene in a series of three with
                   similar homologies). [Arabidopsis thaliana]
                   137925
Seq. No.
Seq. ID
                   LIB22-021-Q1-E1-B2
Method
                  BLASTN
NCBI GI
                   g3449317
BLAST score
                   124
                   9.0e-64
E value
                   124
Match length
```

% identity 100

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MKM21, complete sequence [Arabidopsis thaliana]

Seq. No. 137926



Seq. ID LIB22-021-Q1-E1-B9

Method BLASTN
NCBI GI g4586349
BLAST score 65
E value 5.0e-28

Match length 89 % identity 93

NCBI Description Arabidopsis thaliana DNA for glucose-1-phosphate

adenylyltransferase, complete cds

Seq. No. 137927

Seq. ID LIB22-021-Q1-E1-C10

Method BLASTN
NCBI GI g3046848
BLAST score 115
E value 6.0e-58
Match length 353
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18C1, complete sequence [Arabidopsis thaliana]

Seq. No. 137928

Seq. ID LIB22-021-Q1-E1-F6

Method BLASTX
NCBI GI g4587541
BLAST score 611
E value 9.0e-64
Match length 118
% identity 100

NCBI Description (AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase

with GDSL-motif family. ESTs gb_T44453, gb_T04815,

gb_T45993, gb_R30138, gb_AI099570 and gb_T22281 come from

this gene. [Arabidopsis thaliana]

Seq. No. 137929

Seq. ID LIB22-021-Q1-E1-G10

Method BLASTX
NCBI GI g4388828
BLAST score 169
E value 2.0e-12
Match length 56
% identity 70

NCBI Description (AC006528) putative zinc-finger protein [Arabidopsis

thaliana]

Seq. No. 137930

Seq. ID LIB22-021-Q1-E1-H10

Method BLASTX
NCBI GI g4335737
BLAST score 172
E value 3.0e-12
Match length 79
% identity 46

NCBI Description (AC006248) putative serine/threonine kinase [Arabidopsis

thaliana]

Seq. No. 137931



LIB22-022-Q1-E1-A12 Seq. ID Method BLASTN NCBI GI a3080430 82 BLAST score 1.0e-38 E value Match length 122 % identity Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19 NCBI Description (ESSAII project) 137932 Seq. No. Seq. ID LIB22-022-Q1-E1-E9 Method BLASTX NCBI GI q3757529 BLAST score 366 3.0e-35 E value Match length 73 100 % identity NCBI Description (AC005167) tetracycline transporter-like protein [Arabidopsis thaliana] Seq. No. 137933 LIB22-022-Q1-E1-G1 Seq. ID Method BLASTN NCBI GI g3132469 BLAST score 178 1.0e-95 E value Match length 320 98 % identity Arabidopsis thaliana chromosome II BAC T29F13 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 137934 Seq. ID LIB22-022-Q1-E1-G2 Method BLAŚTX NCBI GI q4758356 BLAST score 375 4.0e-36 E value Match length 115 % identity 66 flap structure-specific endonuclease 1; MATURATION FACTOR 1 NCBI Description (MF1); DNase IV; RAD2_HUMAN >gi_729475_sp_P39748_FEN1_HUMAN FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) >gi_1362788_pir__A56531 DNA structure-specific endonuclease
FEN1 - human >gi_704377_bbs_157592 DNase IV=nuclear 42 kda
5' -> 3' exonuclease [human, HeLa cells, Peptide, 380 aa] >gi_642090 (L37374) endonuclease [Homo sapiens] >gi_3169155 (ACO04770) FEN1 HUMAN; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN [Homo sapiens] >gi_3980293_emb_CAA54166_ (X76771) flap endonuclease-1 [Homo sapiens]

Seq. No. 137935

LIB22-022-Q1-E1-G8 Seq. ID

Method BLASTN NCBI GI g3548797 BLAST score 40 3.0e-13 E value

```
Match length
% identity
                 Arabidopsis thaliana chromosome II BAC T18E12 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  137936
Seq. No.
                  LIB22-023-Q1-E1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213597
                  431
BLAST score
                  1.0e-42
E value
Match length
                  88
                  98
% identity
NCBI Description (AC000348) T7N9.17 [Arabidopsis thaliana]
                  137937
Seq. No.
                  LIB22-023-Q1-E1-D11
Seq. ID
                  BLASTX
Method
NCBI GI
                 61170711
BLAST score
                  326
                  3.0e-30
E value
                  88
Match length
                  75
% identity
NCBI Description
                  SHAGGY RELATED PROTEIN KINASE ASK-ALPHA
                  >gi_541901_pir__S41596 protein kinase ASK-alpha (EC
                  2.7.1.-) - Arabidopsis thaliana >gi_460832_emb_CAA53181_
                  (X75432) shaggy related kinase [Arabidopsis thaliana]
                  >gi 1769889 emb CAA48538 (X68525) serine /threonine
                  protein kinase [Arabidopsis thaliana]
Seq. No.
                  137938
```

 Seq. No.
 137938

 Seq. ID
 LIB22-023-Q1-E1-E11

 Method
 BLASTX

 NCBI GI
 g3510250

NCBI GI g3510250
BLAST score 590
E value 3.0e-61
Match length 114
% identity 100

NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 137939

Seq. ID LIB22-023-Q1-E1-E9

Method BLASTX
NCBI GI g1495269
BLAST score 465
E value 1.0e-46
Match length 126
% identity 74

NCBI Description (X97829) product similar to ccr protein, Citrus paradisi;

PIR: S52663 [Arabidopsis thaliana]

>gi 1550735 emb CAA66824 (X98130) unknown [Arabidopsis

thaliana]

Seq. No. 137940

Seq. ID LIB22-023-Q1-E1-F11

Method BLASTX NCBI GI g1495804

Match length

% identity

133

99



```
BLAST score
E value
                  1.0e-10
Match length
                  118
% identity
                   40
                  (X96406) 13-lipoxygenase [Solanum tuberosum]
NCBI Description
Seq. No.
                  137941
                  LIB22-023-Q1-E1-F9
Seq. ID
Method
                  BLASTN
                  g2264321
NCBI GI
BLAST score
                  252
E value
                  1.0e-139
Match length
                  443
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXM12, complete sequence [Arabidopsis thaliana]
                  137942
Seq. No.
                  LIB22-023-Q1-E1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3142290
BLAST score
                  567
E value
                  1.0e-58
Match length
                  122
% identity
                  99
                   (AC002411) Contains similarity to gb_Z69902 from C.
NCBI Description
                  elegans. [Arabidopsis thaliana]
Seq. No.
                  137943
Seq. ID
                  LIB22-023-Q1-E1-G9
Method
                  BLASTX
NCBI GI
                  g1652892
BLAST score
                   280
E value
                  7.0e-25
Match length
                   142
% identity
                   26
NCBI Description
                  (D90909) ABC transporter [Synechocystis sp.]
Seq. No.
                  137944
Seq. ID
                  LIB22-023-Q1-E1-H10
Method
                  BLASTN
NCBI GI
                  g3386593
BLAST score
                   327
E value
                   0.0e+00
Match length
                   384
% identity
                   98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F4I18 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  137945
Seq. ID
                  LIB22-024-Q1-E1-A1
                  BLASTX
Method
NCBI GI
                  g4633131
BLAST score
                   703
                  1.0e-74
E value
```



(AF110407) ATP sulfurylase precursor [Arabidopsis thaliana]

>qi 4803653 emb CAB42640.1 (AJ012586) sulfate

adenylyltransferase [Arabidopsis thaliana]

137946 Seq. No.

NCBI Description

LIB22-024-Q1-E1-A2 Seq. ID

Method BLASTN q2477521 NCBI GI BLAST score 28 5.0e-06 E value Match length 348

% identity NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic

sequence, complete sequence [Arabidopsis thaliana]

137947 Seq. No.

LIB22-024-Q1-E1-A3 Seq. ID

16

Method BLASTX NCBI GI g2129559 BLAST score 371 1.0e-35 E value 128 Match length % identity

NCBI Description cellulase homolog OR16pep - Arabidopsis thaliana

>gi_1022807 (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi 3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN

[Arabidopsis thaliana]

Seq. No. 137948

LIB22-024-Q1-E1-A4 Seq. ID

Method BLASTX NCBI GI q4567286 BLAST score 101 E value 4.0e-04 Match length 78 % identity

(AC006841) putative coatomer alpha subunit [Arabidopsis NCBI Description

thalianal

137949 Seq. No.

LIB22-024-Q1-E1-C3 Seq. ID

Method BLASTX NCBI GI q4572671 BLAST score 357 E value 4.0e-34 Match length 116 % identity 54

NCBI Description (AC006954) putative cyclic nucleotide regulated ion channel

[Arabidopsis thaliana]

Seq. No. 137950

Seq. ID LIB22-024-Q1-E1-C8

Method BLASTX NCBI GI g4539438 BLAST score 256

Match length

% identity

64

66



```
3.0e-22
E value
Match length
                  101
% identity
                  58
                  (AL049523) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  137951
Seq. No.
                  LIB22-024-Q1-E1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4335744
BLAST score
                  301
E value
                  1.0e-169
                  301
Match length
% identity
                  91
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T4M8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  137952
Seq. No.
                  LIB22-024-Q1-E1-E10
Seq. ID
Method
                  BLASŤX
                  g2062169°
NCBI GI
BLAST score
                  441
                  6.0e-44
E value
                  113
Match length
                  71
% identity
NCBI Description
                  (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis
                  thaliana]
                  137953
Seq. No.
Seq. ID
                  LIB22-024-Q1-E1-E6
Method
                  BLASTN
                  g17681
NCBI GI
BLAST score
                  226
                  1.0e-124
E value
Match length
                  226
% identity
                  100
NCBI Description A.thaliana mRNA for Wilm's tumor suppressor homologue
                  137954
Seq. No.
                  LIB22-024-Q1-E1-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2462930
BLAST score
                  137
E value
                  2.0e-71
Match length
                  141
% identity
                  99
NCBI Description dArabidopsis thaliana mRNA for UDP-glucose:sterol
                  glucosyltransferase
Seq. No.
                  137955
Seq. ID
                  LIB22-024-Q1-E1-H10
Method
                  BLASTX
NCBI GI
                  g728905
BLAST score
                  207
                  6.0e-17
E value
```

16569

NCBI Description PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC



RETICULUM CA2+-ATPASE) >gi_1078206_pir__S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) >gi 171114 (L01795) ATPase [Saccharomyces cerevisiae] >gi 595560 (U12980) Drs2p: Membrane spanning

Ca-ATPase(P-type), member of the cation transport(E1-E2)

ATPase [Saccharomyces cerevisiae]

Seq. No. 137956

Seq. ID LIB22-025-Q1-E1-A1

Method BLASTN NCBI GI g4006885 BLAST score 231 E value 1.0e-127 Match length 235 100 % identity

Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig NCBI Description

fragment No

Seq. No.

137957 Seq. ID LIB22-025-Q1-E1-A10

Method BLASTX NCBI GI g2134982 BLAST score 280 E value 5.0e-25 Match length 102

55 % identity de-ubiquitinase - human >gi_1122278_emb_CAA62690_ (X91349) NCBI Description

de-ubiquitinase [Homo sapiens]

Seq. No. 137958

Seq. ID LIB22-025-Q1-E1-A6

Method BLASTX NCBI GI g2281113 BLAST score 587 6.0e-61 E value Match length 123 % identity

(AC002333) endochitinase isolog [Arabidopsis thaliana] NCBI Description

>gi 2288989 (AC002335) endochitinase isolog [Arabidopsis

thaliana]

Seq. No. 137959

Seq. ID LIB22-025-Q1-E1-B1

Method BLASTN NCBI GI q4587641 BLAST score 142 E value 3.0e-74Match length 176 % identity

NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic

sequence, complete sequence

137960 Seq. No.

Seq. ID LIB22-025-Q1-E1-B6

Method BLASTX NCBI GI g3894168 BLAST score 245



E value 7.0e-21 Match length 105 % identity 43

NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis

thaliana]

Seq. No. 137961

Seq. ID LIB22-025-Q1-E1-B8

Method BLASTX
NCBI GI g135497
BLAST score 639
E value 5.0e-67
Match length 121
% identity 96

NCBI Description TUBULIN BETA CHAIN (BETA-1 AND BETA-2)

>gi_84375_pir__S00683 tubulin beta-1 chain - Stylonychia lemnae (SGC5) >gi_10159_emb_CAA29853_ (X06653) beta-1

tubulin (AA 1 - 442) [Stylonychia lemnae]

>gi 578493 emb CAA29995 (X06874) beta-2 tubulin (AA·1 -

442) [Stylonychia lemnae]

Seq. No. 137962

Seq. ID LIB22-025-Q1-E1-B9

Method BLASTN
NCBI GI g3241925
BLAST score 276
E value 1.0e-154
Match length 318
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOK9, complete sequence [Arabidopsis thaliana]

Seq. No. 137963

Seq. ID LIB22-025-Q1-E1-D9

Method BLASTX
NCBI GI 94588001
BLAST score 295
E value 9.0e-27
Match length 119
% identity 61

NCBI Description (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 137964

Seq. ID LIB22-025-Q1-E1-E1

Method BLASTX
NCBI GI 94585978
BLAST score 306
E value 9.0e-64
Match length 120
% identity 98

NCBI Description (AC005287) NADP specific isocitrate dehydrogenase

[Arabidopsis thaliana]

Seq. No. 137965

Seq. ID LIB22-025-Q1-E1-E4

Method BLASTN



```
NCBI GI
                  q3873174
BLAST score
                  319
E value
                  1.0e-179
Match length
                  323
% identity
                  61
                  Genomic sequence for Arabidopsis thaliana BAC F14N23,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  137966
Seq. ID
                  LIB22-025-Q1-E1-F5
Method
                  BLASTN
NCBI GI
                  g2494106
BLAST score
                  126
E value
                  2.0e-64
                  416
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  137967
Seq. No.
                  LIB22-025-Q1-E1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827143
BLAST score
                  225
                  3.0e-33
E value
Match length
                  81
% identity
                  88
                   (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  137968
Seq. ID
                  LIB22-026-Q1-E1-A6
Method
                  BLASTX
NCBI GI
                  g2558657
BLAST score
                  495
E value
                  2.0e-50
Match length
                  93
% identity
                  98
NCBI Description
                  (AC002354) No definition line found [Arabidopsis thaliana]
                  137969
Seq. No.
                  LIB22-026-Q1-E1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3894179
BLAST score
                  42
E value
                  2.0e-14
Match length
                  62
% identity
                  92
                  Arabidopsis thaliana chromosome II BAC F13H10 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  137970
Seq. No.
```

Seq. ID LIB22-026-Q1-E1-B10

Method BLASTX
NCBI GI g450880
BLAST score 636
E value 1.0e-66



Match length 124 % identity 99 NCBI Description (X77199) heat shock cognate 70-1 [Arabidopsis thaliana] Seq. No. 137971

Seq. ID LIB22-026-Q1-E1-B6
Method BLASTX
NCBI GI g3738340
BLAST score 412
E value 2.0e-40
Match length 111
% identity 68

NCBI Description (AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No. 137972

Seq. ID LIB22-026-Q1-E1-B9

Method BLASTX
NCBI GI g4567273
BLAST score 702
E value 2.0e-74
Match length 132
% identity 100

NCBI Description (AC006841) putative vacuolar proton ATPase subunit

[Arabidopsis thaliana]

Seq. No. 137973

Seq. ID LIB22-026-Q1-E1-C5

Method BLASTX
NCBI GI g3289002
BLAST score 118
E value 6.0e-06
Match length 139
% identity 3

NCBI Description (AF073522) CRP1 [Zea mays]

Seq. No. 137974

Seq. ID LIB22-026-Q1-E1-D4

Method BLASTX
NCBI GI g458969
BLAST score 229
E value 5.0e-19
Match length 99
% identity 46

NCBI Description (U00033) similar to ACV synthetase and other enzymes which

act via an atp-dependent covalent binding of AMP to their

substrate [Caenorhabditis elegans]

Seq. No. 137975

Seq. ID LIB22-026-Q1-E1-E10

Method BLASTX
NCBI GI g3757524
BLAST score 287
E value 9.0e-26
Match length 58
% identity 100

NCBI Description (AC005167) tetracycline transporter-like protein

[Arabidopsis thaliana]

% identity

NCBI Description

99



```
137976
Seq. No.
                   LIB22-026-Q1-E1-E6
Seq. ID
Method
                   BLASTN
                   q3449321
NCBI GI
                   63
BLAST score
                   4.0e-27
E value
Match length
                   176
                   90
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MTG10, complete sequence [Arabidopsis thaliana]
                   137977
Seq. No.
Seq. ID
                   LIB22-026-Q1-E1-F8
Method
                   BLASTX
                   g4371286
NCBI GI
                   102
BLAST score
                   6.0e-21
E value
Match length
                   54
                   96
% identity
                   (AC006260) putative C-terminal RING-finger protein
NCBI Description
                   [Arabidopsis thaliana]
                   137978
Seq. No.
Seq. ID
                   LIB22-027-Q1-E1-A8
                   BLASTN
Method
NCBI GI
                   g2262135
                   196
BLAST score
                   1.0e-106
E value
Match length
                   401
                   99
% identity
                   Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
NCBI Description
                   cM, complete sequence
                   137979
Seq. No.
Seq. ID
                   LIB22-027-Q1-E1-C12
Method
                   BLASTX
NCBI GI
                   q1169228
BLAST score
                   215
E value
                   3.0e-17
Match length
                   73
% identity
                   56
                   RNA HELICASE-LIKE PROTEIN DB10 >gi 1084413 pir S42639
NCBI Description
                   helicase-like protein - Wood tobacco
>gi_563986_dbj_BAA03763_ (D16247) RNA helicase like protein
                   DB10 [Nicotiana sylvestris]
                   137980
Seq. No.
Seq. ID
                   LIB22-027-Q1-E1-C4
Method
                   BLASTX
NCBI GI
                   g3176687
BLAST score
                   666
E value
                   3.0e-70
                   123
Match length
```

(AC003671) Strong similarity to trehalose-6-phosphate

synthase homolog from A. thaliana chromosome 4 contig

```
An Property to
```

gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb R64855 come from this gene. [Arabidopsis thaliana]

Seq. No. 137981

Seq. ID LIB22-027-Q1-E1-C7

Method BLASTN
NCBI GI g3868722
BLAST score 47
E value 2.0e-17
Match length 83

% identity 89
NCBI Description Arabidopsis thaliana BAC T19G15, from chromosome V near

60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No. 137982

Seq. ID LIB22-027-Q1-E1-E1

Method BLASTX
NCBI GI g2618687
BLAST score 260
E value 9.0e-23
Match length 102
% identity 54

NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 137983

Seq. ID LIB22-027-Q1-E1-F12

Method BLASTN
NCBI GI g1699056
BLAST score 365
E value 0.0e+00
Match length 369
% identity 100

NCBI Description Arabidopsis thaliana 27 kDa unknown protein mRNA, complete

cds

Seq. No. 137984

Seq. ID LIB22-027-Q1-E1-G2

Method BLASTN
NCBI GI g2244870
BLAST score 347
E value 0.0e+00
Match length 375
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 137985

Seq. ID LIB22-028-Q1-E1-A3

Method BLASTX
NCBI GI g2809246
BLAST score 178
E value 4.0e-13
Match length 66
% identity 48

NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]

Seq. No. 137986

BLAST score

E value

86

3.0e-41



```
LIB22-028-Q1-E1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3449330
                  381
BLAST score
                  0.0e+00
E value
                  400
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDJ14, complete sequence [Arabidopsis thaliana]
                  137987
Seq. No.
Seq. ID
                  LIB22-028-Q1-E1-B6
Method
                  BLASTN
                  g285954
NCBI GI
BLAST score
                  41
                  9.0e-14
E value
Match length
                  173
                  92
% identity
NCBI Description Human mRNA for KIAA0021 gene, complete cds
                  137988
Seq. No.
                  LIB22-028-Q1-E1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244762
                  304
BLAST score
                  9.0e-28
E value
                  66
Match length
                  79
% identity
NCBI Description (Z97335) major latex protein [Arabidopsis thaliana]
                  137989
Seq. No.
                  LIB22-028-Q1-E1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q452470
BLAST score
                   490
E value
                   1.0e-49
Match length
                   99
                   99
% identity
NCBI Description (U05218) ATP sulfurylase [Arabidopsis thaliana]
                  137990
Seq. No.
                  LIB22-028-Q1-E1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2459445
                   228
BLAST score
                   7.0e-19
E value
Match length
                   103
% identity
                   24
                   (AC002332) putative ribonucleoprotein [Arabidopsis
NCBI Description
                   thaliana]
                   137991
Seq. No.
Seq. ID
                   LIB22-028-Q1-E1-D7
Method
                  BLASTN
                   g4235150
NCBI GI
```



Match length 90
% identity 99
NCBI Description Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence

Seq. No. 137992
Seq. ID LIB22-028-Q1-E1-F11

Method BLASTX
NCBI GI g1076334
BLAST score 557
E value 2.0e-57
Match length 108
% identity 100

NCBI Description hypothetical protein HYP1 - Arabidopsis thaliana >gi_499168_emb_CAA56145_ (X79707) HYP1 [Arabidopsis

thaliana]

Seq. No. 137993

Seq. ID LIB22-028-Q1-E1-F5

Method BLASTX
NCBI GI g1399277
BLAST score 339
E value 5.0e-32
Match length 62
% identity 100

NCBI Description (U31836) calmodulin-domain protein kinase CDPK isoform 7

[Arabidopsis thaliana]

Seq. No. 137994

Seq. ID LIB22-028-Q1-E1-F8

Method BLASTX
NCBI GI g4490750
BLAST score 163
E value 2.0e-11
Match length 33
% identity 97

NCBI Description (AL035708) GTP-binding protein GB3 [Arabidopsis thaliana]

Seq. No. 137995

Seq. ID LIB22-028-Q1-E1-G11

Method BLASTX
NCBI GI g4587550
BLAST score 187
E value 4.0e-14
Match length 75
% identity 52

NCBI Description (AC006577) EST gb R64848 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 137996

Seq. ID LIB22-028-Q1-E1-G8

Method BLASTX
NCBI GI g4581146
BLAST score 426
E value 4.0e-42
Match length 93
% identity 92



NCBI Description (AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No. 137997

Seq. ID LIB22-028-Q1-E1-H12

Method BLASTX
NCBI GI g4220514
BLAST score 423
E value 1.0e-41
Match length 102
% identity 77

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 137998

Seq. ID LIB22-028-Q1-E1-H7

Method BLASTX
NCBI GI g4165154
BLAST score 509
E value 7.0e-52
Match length 119
% identity 81

NCBI Description (AF115482) topoisomerase I [Nicotiana tabacum]

Seq. No. 137999

Seq. ID LIB22-028-Q1-E1-H8

Method BLASTN
NCBI GI g4646215
BLAST score 276
E value 1.0e-154
Match length 296
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T22013 genomic

sequence, complete sequence

Seq. No. 138000

Seq. ID LIB22-028-Q1-E1-H9

Method BLASTN
NCBI GI g3702724
BLAST score 312
E value 1.0e-175
Match length 384
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K17N15, complete sequence [Arabidopsis thaliana]

Seq. No. 138001

Seq. ID LIB22-029-Q1-E1-D6

Method BLASTN
NCBI GI 94581138
BLAST score 76
E value 6.0e-35
Match length 189
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC F1011 genomic

sequence, complete sequence

Seq. No. 138002

Method NCBI GI

BLAST score



```
LIB22-029-Q1-E1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3241922
                  143
BLAST score
                  6.0e-75
E value
                  167
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MLM24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138003
Seq. ID
                  LIB22-029-Q1-E1-F2
Method
                  BLASTX
NCBI GI
                  q4588002
                  471
BLAST score
                  1.0e-47
E value
Match length
                  92
                  100
% identity
                  (AF085279) hypothetical ankyrin-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  138004
Seq. No.
Seq. ID
                  LIB22-029-Q1-E1-F4
Method
                  BLASTN
NCBI GI
                  q4415905
BLAST score
                  261
                  1.0e-145
E value
Match length
                   261
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC F13K3 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   138005
Seq. ID
                  LIB22-029-Q1-E1-G12
Method
                   BLASTX
NCBI GI
                   q3859595
BLAST score
                   361
E value
                   2.0e-34
Match length
                   79
% identity
                   94
                  (AF104919) No definition line found [Arabidopsis thaliana]
NCBI Description
                   138006
Seq. No.
Seq. ID
                   LIB22-029-Q1-E1-G4
                   BLASTX
Method
                   g1514643
NCBI GI
BLAST score
                   428
                   2.0e-42
E value
                   102
Match length
% identity
                   42
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
NCBI Description
                   138007
Seq. No.
Seq. ID
                   LIB22-029-Q1-E1-G5
                   BLASTX
```

16579

g1363489



E value Match length 91 99 % identity thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis NCBI Description thaliana >gi 984052 emb CAA61592 (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana] Seq. No. 138008 Seq. ID LIB22-029-Q1-E1-G9 Method BLASTX NCBI GI q4510401 BLAST score 525 7.0e-54 E value Match length 104 % identity (AC006587) putative general negative regulator of NCBI Description transcription [Arabidopsis thaliana] 138009 Seq. No. LIB22-029-Q1-E1-H9 Seq. ID BLASTX Method q4508069 NCBI GI BLAST score 309 E value 6.0e-29 62 Match length 97 % identity (AC005882) 12246 [Arabidopsis thaliana] NCBI Description Seq. No. 138010 LIB22-030-Q1-E1-B5 Seq. ID Method BLASTX NCBI GI g2894306 BLAST score 396 E value 1.0e-38 Match length 106 % identity 79 (AJ223329) ubiquitin extension protein [Nicotiana tabacum] NCBI Description Seq. No. 138011 LIB22-030-Q1-E1-B9 Seq. ID BLASTX Method g3912953 NCBI GI BLAST score 163 2.0e-11 E value 58 Match length 57 % identity PUTATIVE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE DEAMINASE (ACC NCBI Description DEAMINASE) >gi 3256439_dbj_BAA29122.1_ (AP000001) 328aa long hypothetical 1-aminocyclopropane-1-carboxylate deaminase [Pyrococcus horikoshii]

138012 Seq. No.

Seq. ID LIB22-030-Q1-E1-C8

Method BLASTN g2564051 NCBI GI BLAST score 318 1.0e-179 E value



Match length % identity 100 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana] Seq. No. 138013 Seq. ID LIB22-030-Q1-E1-D2 Method BLASTX NCBI GI g2388580 321 BLAST score E value 8.0e-30 Match length 82 % identity 67 (AC000098) Similar to Sequence 10 from patent 5477002 NCBI Description (gb 1253956). [Arabidopsis thaliana] Seq. No. 138014 Seq. ID LIB22-030-Q1-E1-D3 Method BLASTN NCBI GI g2618602 BLAST score 116 E value 9.0e-59 Match length 220 % identity 89 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana] Seq. No. 138015 LIB22-030-Q1-E1-E1 Seq. ID Method BLASTX NCBI GI g2702281 BLAST score 502 E value 4.0e-51 Match length 112 % identity 50 NCBI Description (AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana] Seq. No. 138016 Seq. ID LIB22-030-Q1-E1-F1 Method BLASTX NCBI GI g3522939 BLAST score 674 E value 4.0e-71 Match length 127 % identity 99 NCBI Description (AC004411) putative squamosa-promoter binding protein [Arabidopsis thaliana]

Seq. No. 138017

Seq. ID LIB22-030-Q1-E1-F2

Method BLASTN NCBI GI g4587641 BLAST score 287 1.0e-160 E value Match length 287 100 % identity





```
Arabidopsis thaliana chromosome I BAC F20D21 genomic
NCBI Description
                  sequence, complete sequence
                  138018
Seq. No.
                  LIB22-030-Q1-E1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3482977
BLAST score
                   603
E value
                   6.0e-63
Match length
                  116
% identity
                   99
NCBI Description
                  (AL031369) putative protein [Arabidopsis thaliana]
                  138019
Seq. No.
                  LIB22-030-Q1-E1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3080433
BLAST score
                   324
                   4.0e-30
E value
                   112
Match length
% identity
                   52
                   (AL022605) putative gamma-glutamyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                   138020
Seq. No.
Seq. ID
                   LIB22-031-Q1-E1-A2
Method
                  BLASTN
NCBI GI
                   q3688169
BLAST score
                   178
E value
                   1.0e-95
Match length
                   253
                   95
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21
                   (ESSAII project)
Seq. No.
                   138021
                   LIB22-031-Q1-E1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3913379
BLAST score
                   414
                   1.0e-40
E value
Match length
                   77
                   100
% identity
                  CRYPTOCHROME 2 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR)
NCBI Description
                   >gi 1857038 (U43397) cryptochrome 2 apoprotein [Arabidopsis
                   thaliana]
```

138022 Seq. No.

LIB22-031-Q1-E1-C8 Seq. ID

Method BLASTN g3132469 NCBI GI BLAST score 195 1.0e-105 E value Match length 381 100 % identity

Arabidopsis thaliana chromosome II BAC T29F13 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                  LIB22-031-Q1-E1-D5
Method
                  BLASTX
NCBI GI
                  g4008006
                  223
BLAST score
                  3.0e-18
E value
Match length
                  76
                  57
% identity
                  (AF084034) receptor-like protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  138024
Seq. No.
Seq. ID
                  LIB22-031-Q1-E1-E3
Method
                  BLASTN
NCBI GI
                  g2914688
BLAST score
                  84
                  1.0e-39
E value
Match length
                  241
                  95
% identity
                  Arabidopsis thaliana chromosome II BAC F24L7 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  138025
Seq. No.
Seq. ID
                  LIB22-031-Q1-E1-F11
Method
                  BLASTX
NCBI GI
                  q3924613
BLAST score
                  484
E value
                  7.0e-49
Match length
                   92
                   100
% identity
                   (AF069442) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4263512 gb AAD15338 (AC004044) hypothetical protein
                   [Arabidopsis thaliana]
Seq. No.
                   138026
Seq. ID
                  LIB22-031-Q1-E1-F5
Method
                  BLASTN
                   q4757401
NCBI GI
BLAST score
                   214
E value
                   1.0e-117
Match length
                   287
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGH6, complete sequence
Seq. No.
                   138027
Seq. ID
                   LIB22-031-Q1-E1-F8
Method
                   BLASTN
NCBI GI
                   q3985957
BLAST score
                   345
E value
                   0.0e+00
Match length
                   373
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MYN8, complete sequence [Arabidopsis thaliana]
```



Seq. No. 138028

Seq. ID LIB22-031-Q1-E1-G3

Method BLASTN
NCBI GI g3859658
BLAST score 130
E value 6.0e-67
Match length 311
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1

(ESSAII project)

Seq. No. 138029

Seq. ID LIB22-031-Q1-E1-H9

Method BLASTX
NCBI GI g2827139
BLAST score 274
E value 8.0e-25
Match length 55
% identity 87

NCBI Description (AF027172) cellulose synthase catalytic subunit

[Arabidopsis thaliana] >gi_4049343 emb_CAA22568 (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis

thaliana]

Seq. No. 138030

Seq. ID LIB22-032-Q1-E1-C10

Method BLASTX
NCBI GI g3249084
BLAST score 429
E value 1.0e-42
Match length 83
% identity 35

NCBI Description (AC004473) Similar to red-1 (related to thioredoxin) gene

gb_X92750 from Mus musculus. ESTs gb_AA712687 and gb_Z37223 come from this gene [Arabidopsis thaliana]

Seq. No. 138031

Seq. ID LIB22-032-Q1-E1-C12

Method BLASTX
NCBI GI g2829921
BLAST score 384
E value 2.0e-37
Match length 102
% identity 81

NCBI Description (AC002291) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 138032

Seq. ID LIB22-032-Q1-E1-C2

Method BLASTX
NCBI GI g4160532
BLAST score 297
E value 5.0e-27
Match length 108
% identity 53

NCBI Description (AJ011304) sphingosine-1-phosphate lyase [Homo sapiens]

Seq. No. 138033

Seq. ID

Method



```
LIB22-032-Q1-E1-D6
Seq. ID
Method
                  BLASTN
                  q3510336
NCBI GI
                  47
BLAST score
                  2.0e-17
E value
                  59
Match length
                  95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K18J17, complete sequence [Arabidopsis thaliana]
                  138034
Seq. No.
Seq. ID
                  LIB22-032-Q1-E1-F10
Method
                  BLASTX
NCBI GI
                  g4455787
BLAST score
                   206
E value
                  2.0e-16
Match length
                  73
                  47
% identity
NCBI Description
                   (AL035536) putative DNA polymerase accessory protein
                   [Schizosaccharomyces pombe]
                  138035
Seq. No.
                  LIB22-032-Q1-E1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1161926
BLAST score
                   84
                   3.0e-11
E value
Match length
                   53
                   72
% identity
                   (U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine
NCBI Description
                  max]
Seq. No.
                   138036
Seq. ID
                  LIB22-032-Q1-E1-H11
Method
                   BLASTN
NCBI GI
                   g4262221
BLAST score
                   143
                   1.0e-74
E value
                   297
Match length
% identity
                   99
                  Arabidopsis thaliana chromosome II BAC F10A8 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   138037
Seq. ID
                   LIB22-033-Q1-E1-C4
Method
                   BLASTN
NCBI GI
                   g4544405
BLAST score
                   363
                   0.0e+00
E value
Match length
                   363
% identity
                   100
                  Arabidopsis thaliana chromosome II BAC F2818 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   138038
```

16585

LIB22-033-Q1-E2-A9

BLASTN



```
NCBI GI
BLAST score
                   320
                   1.0e-180
E value
                   320
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F17K2 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138039
                  LIB22-033-Q1-E2-B12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3702731
BLAST score
                  233
                  1.0e-128
E value
                  377
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFC19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138040
                  LIB22-033-Q1-E2-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3142302
BLAST score
                   486
E value
                   3.0e-49
                  101
Match length
% identity
                   66
                   (AC002411) Strong similarity to myosin heavy chain
NCBI Description
                   gb Z34293 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                   138041
                  LIB22-033-Q1-E2-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2262167
BLAST score
                   546
E value
                   3.0e-56
Match length
                   104
                   100
% identity
NCBI Description
                   (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
                   thaliana]
Seq. No.
                   138042
Seq. ID
                   LIB22-033-Q1-E2-G9
Method
                   BLASTN
NCBI GI
                   q3789706
BLAST score
                   263
E value
                   1.0e-146
Match length
                   360
% identity
                   100
                  Arabidopsis thaliana chromosome 1 BAC F15K9 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
```

138043 Seq. No. Seq. ID LIB22-034-Q1-E2-A1

Method BLASTX NCBI GI g3880145

BLAST score 207

BLAST score

Match length

E value

191

251

1.0e-103



```
1.0e-16
E value
Match length
                  85
                  46
% identity
                  (Z68319) similar to tyrosine specific protein phosphatase;
NCBI Description
                  cDNA EST yk460c9.5 comes from this gene [Caenorhabditis
                  elegans]
Seq. No.
                  138044
                  LIB22-034-Q1-E2-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4558665
BLAST score
                  203
E value
                  4.0e-16
Match length
                  98
                  48
% identity
                  (AC007063) putative white protein [Arabidopsis thaliana]
NCBI Description
                  138045
Seq. No.
                  LIB22-034-Q1-E2-B8
Seq. ID
Method
                  BLASTN
                  g4455321
NCBI GI
BLAST score
                  49
                  6.0e-19
E value
                  145
Match length
                  84
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10
NCBI Description
                   (ESSAII project)
                  138046
Seq. No.
Seq. ID
                  LIB22-034-Q1-E2-D6
Method
                  BLASTN
                  g3201608
NCBI GI
BLAST score
                  45
E value
                  1.0e-16
Match length
                  109
                  85
% identity
                  Arabidopsis thaliana chromosome II BAC F7F1 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138047
                  LIB22-034-Q1-E2-E12
Seq. ID
Method
                  BLASTN
                  g4469002
NCBI GI
                  256
BLAST score
E value
                  1.0e-142
                  256
Match length
% identity
                   48
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
NCBI Description
                   (ESSA project)
Seq. No.
                   138048
Seq. ID
                  LIB22-034-Q1-E2-E7
Method
                  BLASTN
NCBI GI
                   g4586098
```

吹

Match length

363



```
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13
                  (ESSA project)
                  138049
Seq. No.
                  LIB22-034-Q1-E2-E8
Seq. ID
Method
                  BLASTN
                  g4589445
NCBI GI
                  214
BLAST score
E value
                  1.0e-117
Match length
                  334
% identity
                  91
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWL2, complete sequence
                  138050
Seq. No.
                  LIB22-034-Q1-E2-F10
Seq. ID
Method
                  BLASTN
                  g4049332
NCBI GI
BLAST score
                  144
                  2.0e-75
E value
Match length
                  230
                  94
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4
                  (ESSAII project)
Seq. No.
                  138051
                  LIB22-034-Q1-E2-F11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2244829
BLAST score
                  319
E value
                  1.0e-179
Match length
                  343
% identity
                  98
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  138052
                  LIB22-034-Q1-E2-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3413696
BLAST score
                  227
E value
                  1.0e-124
Match length
                  413
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC T19L18 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No. Seq. ID
                  138053
                  LIB22-034-Q1-E2-H1
Method
                  BLASTN
NCBI GI
                  q4092471
BLAST score
                  194
E value
                  1.0e-105
```

% identity 100
NCBI Description Arabidopsis thaliana BAC F9M13 from chromosome IV near 21.5

Seq. No.

138059



cM, complete sequence

```
吨:
Seq. No.
                  138054
                  LIB22-034-Q1-E2-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244884
BLAST score
                  131
E value
                  9.0e-29
Match length
                  79
                  91
% identity
NCBI Description
                  (Z97338) glucosyltransferase [Arabidopsis thaliana]
Seq. No.
                  138055
Seq. ID
                  LIB22-035-Q1-E1-B11
Method
                  BLASTX
NCBI GI
                  q3046694
BLAST score
                  191
E value
                  7.0e-15
Match length
                  54
                  74
% identity
                   (AL022224) vacuolar sorting receptor-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  138056
                  LIB22-035-Q1-E1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3292829
BLAST score
                  180
E value
                   3.0e-13
Match length
                  82
                  50
% identity
NCBI Description
                  (AL031018) putative protein [Arabidopsis thaliana]
                  138057
Seq. No.
Seq. ID
                  LIB22-035-Q1-E1-C12
Method
                  BLASTX
NCBI GI
                  g1402916
BLAST score
                   470
E value
                   3.0e-47
                   90
Match length
                   100
% identity
                   (X98319) peroxidase [Arabidopsis thaliana]
NCBI Description
                  >gi_1429217_emb_CAA67311_ (X98775) peroxidase ATP12a
                   [Arabidopsis thaliana]
Seq. No.
                   138058
Seq. ID
                  LIB22-035-Q1-E1-C3
Method
                  BLASTN
NCBI GI
                  g4432847
BLAST score
                  130
E value
                   7.0e-67
                   359
Match length
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC F13B15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
```



LIB22-035-Q1-E1-E1 Seq. ID Method BLASTX g2997755 NCBI GI 211 BLAST score 6.0e-17 E value 118 Match length % identity 39 (AF054823) TFIIH transcription/DNA repair factor p52 NCBI Description subunit [Mus musculus] 138060 Seq. No. LIB22-035-Q1-E1-F9 Seq. ID BLASTX Method NCBI GI g4580531 BLAST score 550 1.0e-56 E value 125 Match length 86 % identity (AF036309) scarecrow-like 14 [Arabidopsis thaliana] NCBI Description Seq. No. 138061 LIB22-035-Q1-E1-H10 Seq. ID BLASTX Method g3559805 NCBI GI BLAST score 213 1.0e-45 E value 105 Match length 88 % identity (AJ006787) putative phytochelatin synthetase [Arabidopsis NCBI Description thaliana] 138062 Seq. No. LIB22-035-Q1-E1-H12 Seq. ID Method BLASTX NCBI GI g4753653 BLAST score 320 E value 1.0e-29 Match length 118 86 % identity NCBI Description (AL049751) putative protein [Arabidopsis thaliana] Seq. No. 138063 LIB22-035-Q1-E1-H7 Seq. ID Method BLASTX NCBI GI g2245110 262 BLAST score 6.0e-23 E value 49 Match length % identity 98 (Z97343) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 138064

LIB22-036-Q1-E1-A11 Seq. ID

Method BLASTN NCBI GI g3241926 BLAST score 200 1.0e-108 E value



Match length 204 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSG15, complete sequence [Arabidopsis thaliana]

Seq. No. 138065

Seq. ID LIB22-036-Q1-E1-C12

Method BLASTN
NCBI GI g4589415
BLAST score 70
E value 3.0e-31
Match length 175
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K14A3, complete sequence

Seq. No. 138066

Seq. ID LIB22-036-Q1-E1-G1

Method BLASTX
NCBI GI g4583544
BLAST score 203
E value 6.0e-16
Match length 46
% identity 85

NCBI Description (Z95637) acyl-CoA:1-acylglycerol-3-phosphate

acyltransferase [Brassica napus]

Seq. No. 138067

Seq. ID LIB22-036-Q1-E1-G11

Method BLASTN
NCBI GI g4732167
BLAST score 89
E value 1.0e-42
Match length 212
% identity 100

NCBI Description Arabidopsis thaliana BAC F28D6

Seq. No. 138068

Seq. ID LIB22-037-Q1-E1-B8

Method BLASTX
NCBI GI g1791309
BLAST score 178
E value 1.0e-13
Match length 37
% identity 95

NCBI Description (U83500) cystathionine gamma-synthase [Arabidopsis

thaliana] >gi_2852454_dbj_BAA24699_ (AB010888)

cystathionine gamma-synthase [Arabidopsis thaliana]

Seq. No. 138069

Seq. ID LIB22-037-Q1-E1-C8

Method BLASTX
NCBI GI g1168470
BLAST score 410
E value 4.0e-40
Match length 82
% identity 100



NCBI Description PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522)

Arabidopsis thaliana >gi_21/829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis

thaliana]

Seq. No. 138070

Seq. ID LIB22-037-Q1-E1-D2

Method BLASTX
NCBI GI g4468807
BLAST score 437
E value 3.0e-43
Match length 131
% identity 68

NCBI Description (AL035601) cytochrome P450 monooxygenase-like protein

[Arabidopsis thaliana]

Seq. No. 138071

Seq. ID LIB22-037-Q1-E1-F4

Method BLASTX
NCBI GI g2632103
BLAST score 449
E value 4.0e-45
Match length 86
% identity 99

NCBI Description (Z98759) arginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 138072

Seq. ID LIB22-037-Q1-E1-H8

Method BLASTX
NCBI GI g1906000
BLAST score 530
E value 3.0e-54
Match length 112
% identity 88

NCBI Description (U90428) blue copper-binding protein II [Arabidopsis

thaliana]

Seq. No. 138073

Seq. ID LIB22-038-Q1-E1-B6

Method BLASTN
NCBI GI g4519193
BLAST score 127
E value 5.0e-65
Match length 422
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC11, complete sequence

Seq. No. 138074

Seq. ID LIB22-038-Q1-E1-D8

Method BLASTN
NCBI GI g3859658
BLAST score 155
E value 5.0e-82
Match length 199
% identity 94



```
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1
                   (ESSAII project)
Seq. No.
                   138075
Seq. ID
                  LIB22-038-Q1-E1-F4
Method
                  BLASTN
NCBI GI
                   g4757407
BLAST score
                   32
E value
                   1.0e-08
                   75
Match length
% identity
                   95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQD19, complete sequence
                   138076
Seq. No.
Seq. ID
                  LIB22-038-Q1-E1-G10
Method
                  BLASTN
                   g4757388
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
Match length
                   161
                   80
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   F15L12, complete sequence
                   138077
Seq. No.
                   LIB22-038-Q1-E1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4415908
BLAST score
                   278
E value
                   9.0e-25
Match length
                   95
                   54
% identity
NCBI Description
                   (AC006282) unknown protein [Arabidopsis thaliana]
Seq. No.
                   138078
Seq. ID
                   LIB22-038-Q1-E1-G7
Method
                   BLASTX
NCBI GI
                   g1702987
BLAST score
                   553
                   6.0e-57
E value
Match length
                   122
% identity
                   93
NCBI Description
                  14-3-3-LIKE PROTEIN GF14 PHI >gi 1493805 (L09111) GF14
                   protein phi chain [Arabidopsis thaliana] >gi 2232146
                   (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis
                   thaliana]
                   138079
Seq. No.
```

Seq. ID LIB22-038-Q1-E1-H11

BLASTN Method g2506048 NCBI GI BLAST score 391 0.0e+00 E value 391 Match length 100 % identity

NCBI Description Arabidopsis thaliana DNA for alternative oxidase (AOX1c



gene), complete cds

```
138080
Seq. No.
                  LIB22-039-Q1-E1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2088654
BLAST score
                  216
                  2.0e-17
E value
                  64
Match length
                  72
% identity
                  (AF002109) 60S acidic ribosomal protein PO isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  138081
                  LIB22-039-Q1-E1-B2
Seq. ID
Method
                  BLASTN
                  q4185128
NCBI GI
BLAST score
                  146
E value
                  9.0e-77
Match length
                  170
                  96
% identity
                  Arabidopsis thaliana chromosome II P1 MSF3 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  138082
Seq. No.
                  LIB22-039-Q1-E1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1518540
BLAST score
                   353
                   2.0e-33
E value
Match length
                  71
                   87
% identity
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
Seq. No.
                   138083
Seq. ID
                  LIB22-039-Q1-E1-C7
Method
                   BLASTN
NCBI GI
                   q3402745
BLAST score
                   295
E value
                   1.0e-165
Match length
                   315
                   85
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5
NCBI Description
                   (ESSAII project)
Seq. No.
                   138084
Seq. ID
                   LIB22-039-Q1-E1-E7
Method
                   BLASTN
                   g2618602
NCBI GI
BLAST score
                   246
                   1.0e-136
E value
Match length
                   369
% identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSJ1, complete sequence [Arabidopsis thaliana]
```

Seq. No. 138085



```
LIB22-039-Q1-E1-E9
Seq. ID
Method
                  BLASTN
                  q4519187
NCBI GI
BLAST score
                  198
                  1.0e-107
E value
Match length
                  389
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                  K1G2, complete sequence
Seq. No.
                  138086
Seq. ID
                  LIB22-039-Q1-E1-F1
Method
                  BLASTX
NCBI GI
                   q730526
BLAST score
                   205
E value
                   1.0e-16
Match length
                   35
% identity
                   100
                  60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
NCBI Description
                   >gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis
                   thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein
                   [Arabidopsis thaliana]
Seq. No.
                   138087
                   LIB22-039-Q1-E1-F11
Seq. ID
Method
                   BLASTN
                   q4558521
NCBI GI
BLAST score
                   63
                   2.0e-27
E value
Match length
                   101
                   93
% identity
                   Genomic sequence for Arabidopsis thaliana BAC T10024,
NCBI Description
                   complete sequence
Seq. No.
                   138088
                   LIB22-039-Q1-E1-F7
Seq. ID
Method
                   BLASTN
                   q2351062
NCBI GI
BLAST score
                   295
                   1.0e-165
E value
                   328
Match length
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MAH20, complete sequence [Arabidopsis thaliana]
                   138089
Seq. No.
Seq. ID
                   LIB22-039-Q1-E1-F9
Method
                   BLASTN
NCBI GI
                   g2642152
                   157
BLAST score
                   4.0e-83
E value
                   235
Match length
                   97
```

% identity

Arabidopsis thaliana chromosome II BAC T5I7 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

138090 Seq. No.



```
LIB22-039-Q1-E1-G12
Seq. ID
Method
                  BLASTN
                  q4006885
NCBI GI
                  137
BLAST score
                  5.0e-71
E value
Match length
                  386
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                  fragment No
                  138091
Seq. No.
                  LIB22-039-Q1-E1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2895510
BLAST score
                  395
                  1.0e-38
E value
                  73
Match length
                  100
% identity
                  (AF033204) putative pectin methylesterase [Arabidopsis
NCBI Description
                  thaliana]
                  138092
Seq. No.
                  LIB22-039-Q1-E1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4049399
BLAST score
                  516
                  1.0e-52
E value
                  96
Match length
                  100
% identity
NCBI Description (Y09581) FRO2 [Arabidopsis thaliana]
                  138093
Seq. No.
                  LIB22-039-Q1-E1-H6
Seq. ID
Method
                  BLASTX
                   q2384673
NCBI GI
BLAST score
                   426
E value
                   5.0e-42
Match length
                   81
                   100
% identity
                   (AF012658) putative potassium transporter AtKT3p
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   138094
Seq. ID
                   LIB22-040-Q1-E1-A5
Method
                   BLASTX
                   g2897946
NCBI GI
BLAST score
                   150
                   1.0e-09
E value
                   115
Match length
% identity
                   37
                   (AF007544) prostate-specific membrane antigen [Homo
NCBI Description
                   sapiens]
```

Seq. No. 138095

Seq. ID LIB22-040-Q1-E1-B6

Method BLASTX NCBI GI g2642448



BLAST score 250 E value 5.0e-22 Match length 57 % identity 40

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]

>gi_3169187 (AC004401) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 138096

Seq. ID LIB22-040-Q1-E1-C7

Method BLASTN
NCBI GI 94559375
BLAST score 261
E value 1.0e-145
Match length 321
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC F11C10 genomic

sequence, complete sequence

Seq. No. 138097

Seq. ID LIB22-040-Q1-E1-E11

Method BLASTN
NCBI GI g3212846
BLAST score 243
E value 1.0e-134
Match length 418
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138098

Seq. ID LIB22-040-Q1-E1-E12

Method BLASTN
NCBI GI g1402907
BLAST score 160
E value 7.0e-85
Match length 160
% identity 100

NCBI Description A.thaliana mRNA for peroxidase, prxr3

Seq. No. 138099

Seq. ID LIB22-040-Q1-E1-G1

Method BLASTN
NCBI GI g4519193
BLAST score 201
E value 1.0e-109
Match length 245
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC11, complete sequence

Seq. No. 138100

Seq. ID LIB22-040-Q1-E1-G8

Method BLASTN
NCBI GI g3193282
BLAST score 44
E value 1.0e-15



```
Match length
% identity
                   84
```

NCBI Description Arabidopsis thaliana BAC T14P8

138101 Seq. No.

LIB22-041-Q1-E1-A12 Seq. ID

Method BLASTX g3063472 NCBI GI 623 BLAST score 4.0e-65 E value Match length 116 % identity 99

NCBI Description (AC003981) F22013.34 [Arabidopsis thaliana]

138102 Seq. No.

Seq. ID LIB22-041-Q1-E1-A9

Method BLASTN NCBI GI g4757417 BLAST score 130 3.0e-67 E value Match length 166 95 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

T30G6, complete sequence

Seq. No. 138103

LIB22-041-Q1-E1-B5 Seq. ID

Method BLASTX NCBI GI q2499608 BLAST score 475 E value 9.0e-48 Match length 118 81 % identity

MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 4 (MAP KINASE 4) NCBI Description

(ATMPK4) >gi_2129645_pir__S40470 mitogen-activated protein kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana

>gi 457400 dbj BAA04867 (D21840) MAP kinase [Arabidopsis

thaliana]

Seq. No. 138104

Seq. ID LIB22-041-Q1-E1-B6

Method BLASTX NCBI GI g3193309 BLAST score 148 4.0e-24 E value Match length 83 % identity 77

(AF069300) No definition line found [Arabidopsis thaliana] NCBI Description

Seq. No. 138105

Seq. ID LIB22-041-Q1-E1-B9

BLASTX Method g4469023 NCBI GI BLAST score 528 5.0e-54E value 118 Match length % identity 85



```
NCBI Description
                  (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                  138106
                  LIB22-041-Q1-E1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4519190
BLAST score
                  186
E value
                  1.0e-100
Match length
                  395
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K6A12, complete sequence
Seq. No.
                  138107
                  LIB22-041-Q1-E1-C9
Seq. ID
Method
                  BLASTN
                  g2980787
NCBI GI
BLAST score
                  203
E value
                  1.0e-110
Match length
                  327
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2
NCBI Description
                  (ESSAII project)
Seq. No.
                  138108
                  LIB22-041-Q1-E1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3063691
BLAST score
                  222
E value
                  1.0e-18
Match length
                  45
                  84
% identity
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                  138109
Seq. ID
                  LIB22-041-Q1-E1-G2
Method
                  BLASTN
NCBI GI
                  g4567237
BLAST score
                  258
E value
                  1.0e-143
Match length
                  309
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC T22F11 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  138110
Seq. ID
                  LIB22-042-Q1-E1-B1
Method
                  BLASTX
NCBI GI
                  q134976
BLAST score
                  42
```

E value 6.0e-43Match length 90 % identity 100

GLUCOSE TRANSPORTER (SUGAR CARRIER) >gi 81619 pir \$12042 NCBI Description

glucose transport protein STP1 - Arabidopsis thaliana >gi_16520_emb_CAA39037_ (X55350) glucose transporter

[Arabidopsis thaliana]



```
138111
Seq. No.
                  LIB22-042-Q1-E1-C5
Seq. ID
Method
                  BLASTN
                  g633027
NCBI GI
                  244
BLAST score
                  1.0e-135
E value
                  244
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana mRNA for protein phosphatase 2C
                  138112
Seq. No.
                  LIB22-042-Q1-E1-F3
Seq. ID
Method
                  BLASTX
                  g2576361
NCBI GI
BLAST score
                   600
                  2.0e-62
E value
                  112
Match length
% identity
                   100
                  (U39782) lysine and histidine specific transporter
NCBI Description
                   [Arabidopsis thaliana]
                  138113
Seq. No.
Seq. ID
                  LIB22-042-Q1-E1-H11
Method
                  BLASTX
NCBI GI
                   g99697
                   713
BLAST score
                   1.0e-75
E value
                   135
Match length
% identity
                   99
                  glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone
NCBI Description
                   lambdaAtgsr2) - Arabidopsis thaliana
Seq. No.
                   138114
                   LIB22-043-Q1-E1-B5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4454049
                   225
BLAST score
                   1.0e-18
E value
Match length
                   60
% identity
                   (AL035394) 98b like protein [Arabidopsis thaliana]
NCBI Description
                   138115
Seq. No.
Seq. ID
                   LIB22-043-Q1-E1-B6
Method
                   BLASTX
                   g2144191
NCBI GI
BLAST score
                   151
E value
                   8.0e-10
Match length
                   82
% identity
                   46
                   glucan 1,4-beta-glucosidase (EC 3.2.1.74) - Microbispora
NCBI Description
                   bispora >gi 149826 (L06134) glucan-glucohydrolase
```

[Microbispora bispora]

Seq. No.

Seq. ID LIB22-043-Q1-E1-C1

138116



```
Method
                  BLASTX
NCBI GI
                  q128405
BLAST score
                  284
E value
                  1.0e-25
Match length
                  75
% identity
                  71
NCBI Description
                  NODULIN 21 (N-21) >gi_99942_pir__S08632 nodulin-21 -
                  soybean >gi_18694_emb_CAA34506_ (X16488) nodulin-21 (AA
                  1-201) [Glycine max]
Seq. No.
                  138117
Seq. ID
                  LIB22-043-Q1-E1-C10
Method
                  BLASTN
NCBI GI
                  q4469002
BLAST score
                  91
E value
                  5.0e-44
Match length
                  134
% identity
                  96
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
                  (ESSA project)
Seq. No.
                  138118
Seq. ID
                  LIB22-043-Q1-E1-C12
Method
                  BLASTX
NCBI GI
                  g1170373
BLAST score
                  686
E value
                  1.0e-72
Match length
                  133
% identity
                  100
                  HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi 1072473 pir $46302
NCBI Description
                  heat shock cognate protein 70-1 - Arabidopsis Thaliana
                  >gi 397482 emb CAA52684 (X74604) heat shock protein 70
                  cognate [Arabidopsis thaliana]
Seq. No.
                  138119
Seq. ID
                  LIB22-043-Q1-E1-C5
Method
                  BLASTN
NCBI GI
                  g2760168
BLAST score
                  259
E value
                  1.0e-144
Match length
                  384
% identity
                  97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MEE6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138120
Seq. ID
                  LIB22-043-Q1-E1-C9
Method
                  BLASTX
NCBI GI
                  q4522003
```

BLAST score 466 E value 9.0e-47 Match length 90 % identity

NCBI Description (AC007069) putative protein kinase [Arabidopsis thaliana]

Seq. No. 138121

Seg. ID LIB22-043-Q1-E1-D11



```
Method
                  BLASTX
NCBI GI
                  q1490554
BLAST score
                  401
                  4.0e-39
E value
Match length
                  81
% identity
                  100
NCBI Description
                  (U63633) S-adenosylmethionine decarboxylase [Arabidopsis
Seq. No.
                  138122
Seq. ID
                  LIB22-043-Q1-E1-E10
Method
                  BLASTX
NCBI GI
                  q1063415
BLAST score
                  624
E value
                  3.0e-65
Match length
                  118
% identity
                  100
NCBI Description (L40948) K+ channel protein [Arabidopsis thaliana]
Seq. No.
                  138123
Seq. ID
                  LIB22-043-Q1-E1-E6
Method
                  BLASTX
NCBI GI
                  q1708461
BLAST score
                  474
E value
                  1.0e-47
Match length
                  113
% identity
                  85
NCBI Description IAA-AMINO ACID HYDROLASE HOMOLOG 1 PRECURSOR >qi 902789
                  (U23795) ILL1 [Arabidopsis thaliana]
                  >gi 2921829 gb AAC04865.1 (AF047031) IAA-amino acid
                  hydrolase [Arabidopsis thaliana]
Seq. No.
                  138124
Seq. ID
                  LIB22-043-Q1-E1-F12
Method
                  BLASTN
NCBI GI
                  q4678219
BLAST score
                  193
E value
                  1.0e-104
Match length
                  323
                  82
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F9C22 genomic
                  sequence, complete sequence
Seq. No.
                  138125
Seq. ID
                  LIB22-043-Q1-E1-H11
Method
                  BLASTX
NCBI GI
                  g99741
BLAST score
                  328
E value
                  1.0e-30
                  130
Match length
% identity
                  25
NCBI Description P-glycoprotein pgpl - Arabidopsis thaliana
```

Seq. No. 138126

Seq. ID LIB22-044-Q1-E1-F12

Method BLASTN NCBI GI g2244829



BLAST score 401 E value 0.0e+00 Match length 401 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 138127

Seq. ID LIB22-044-Q1-E1-G8

Method BLASTX
NCBI GI g2160156
BLAST score 660
E value 1.0e-69
Match length 122
% identity 100

NCBI Description (AC000132) Strong similarity to S. pombe leucyl-tRNA

synthetase (gb_Z73100). [Arabidopsis thaliana]

Seq. No. 138128

Seq. ID LIB22-044-Q1-E1-H1

Method BLASTN
NCBI GI g2760829
BLAST score 245
E value 1.0e-135
Match length 349
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F18A8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138129

Seq. ID LIB22-044-Q1-E1-H10

Method BLASTN
NCBI GI g3241917
BLAST score 96
E value 1.0e-46
Match length 275
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19B1, complete sequence [Arabidopsis thaliana]

Seq. No. 138130

Seq. ID LIB22-045-Q1-E1-A8

Method BLASTX
NCBI GI 94587547
BLAST score 243
E value 1.0e-20
Match length 86
% identity 53

NCBI Description (AC006577) Contains similarity to DNA-binding protein Gt-2

gb_X68261 from Oryza sativa. [Arabidopsis thaliana]

Seq. No. 138131

Seq. ID LIB22-045-Q1-E1-B2

Method BLASTX NCBI GI g116923 BLAST score 143 E value 5.0e-09



Match length 48 % identity 54

NCBI Description COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)

>gi_111414_pir__S13520 beta-COP protein - rat
>gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus

norvegicus]

Seq. No. 138132

Seq. ID LIB22-045-Q1-E1-B7

Method BLASTX
NCBI GI g1654140
BLAST score 200
E value 1.0e-15
Match length 85
% identity 54

NCBI Description (U37840) lipoxygenase [Lycopersicon esculentum]

Seq. No. 138133

Seq. ID LIB22-045-Q1-E1-B8

Method BLASTN
NCBI GI g3643588
BLAST score 230
E value 1.0e-126
Match length 365
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138134

Seq. ID LIB22-045-Q1-E1-D1

Method BLASTX
NCBI GI g2529229
BLAST score 549
E value 2.0e-56
Match length 117
% identity 90

NCBI Description (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No. 138135

Seq. ID LIB22-045-Q1-E1-F5

Method BLASTX
NCBI GI g3360289
BLAST score 343
E value 3.0e-32
Match length 139
% identity 43

NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase

1 [Zea mays]

Seq. No. 138136

Seq. ID LIB22-045-Q1-E1-F7

Method BLASTN
NCBI GI g2072987
BLAST score 51
E value 1.0e-20
Match length 51
% identity 100



NCBI Description Arabidopsis thaliana putative G-protein-coupled receptor (GCR1) mRNA, complete cds

Seq. No. 138137

Seq. ID LIB22-045-Q1-E1-G6

Method BLASTX
NCBI GI g3935177
BLAST score 666
E value 4.0e-70
Match length 137
% identity 94

NCBI Description (AC004557) F17L21.20 [Arabidopsis thaliana]

Seq. No. 138138

Seq. ID LIB22-045-Q1-E1-H3

Method BLASTN
NCBI GI g3766106
BLAST score 338
E value 0.0e+00
Match length 338
% identity 100

NCBI Description Arabidopsis thaliana chromosome 1 BAC F9K20 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 138139

Seq. ID LIB22-046-Q1-E1-A1

Method BLASTX
NCBI GI g1076331
BLAST score 180
E value 2.0e-13
Match length 74
% identity 49

NCBI Description histidine transport protein - Arabidopsis thaliana

>gi_510238_emb_CAA54634_ (X77503) oligopeptide transporter
1-1 [Arabidopsis thaliana] >gi 744157_prf 2014244A His

transporter [Arabidopsis thaliana]

Seq. No. 138140

Seq. ID LIB22-046-Q1-E1-D3

Method BLASTX
NCBI GI g2674107
BLAST score 140
E value 1.0e-08
Match length 60
% identity 48

NCBI Description (AF023451) guanine nucleotide-exchange protein [Bos taurus]

Seq. No. 138141

Seq. ID LIB22-046-Q1-E1-D8

Method BLASTX
NCBI GI g1669387
BLAST score 537
E value 5.0e-55
Match length 99
% identity 100

NCBI Description (U41998) actin 2 [Arabidopsis thaliana]



```
Seq. No.
                   138142
                   LIB22-046-Q1-E1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4678337
BLAST score
                   612
E value
                   6.0e-64
Match length
                   120
% identity
                   100
NCBI Description (AL049658) putative protein [Arabidopsis thaliana]
Seq. No.
                   138143
Seq. ID
                  LIB22-046-Q1-E1-E11
Method
                  BLASTX
NCBI GI
                   q3136336
BLAST score
                   344
E value
                  1.0e-32
Match length
                  81
% identity
                   44
NCBI Description (AF064552) calmodulin; Cam [Apium graveolens]
                  138144
Seq. No.
Seq. ID
                  LIB22-046-Q1-E1-F5
Method
                  BLASTX
NCBI GI
                  g1170373
BLAST score
                  147
E value
                  3.0e-20
Match length
                  71
% identity
                  77
NCBI Description
                  HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302
                  heat shock cognate protein 70-1 - Arabidopsis thaliana
                  >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70
                  cognate [Arabidopsis thaliana]
Seq. No.
                  138145
Seq. ID
                  LIB22-046-Q1-E1-G12
Method
                  BLASTN
NCBI GI
                  q2088638
BLAST score
                  344
E value
                  0.0e+00
Match length
                  356
% identity
                  99
NCBI Description Arabidopsis thaliana chromosome II BAC T28M21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138146
Seq. ID
                  LIB22-047-Q1-E1-A10
Method
                  BLASTN
NCBI GI
                  g1931636
BLAST score
                  119
E value
                  2.0e-60
Match length
                  191
% identity
                  98
```

NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No. 138147

Seq. ID LIB22-047-Q1-E1-B11

Method BLASTX



```
NCBI GI g3258572
BLAST score 215
E value 7.0e-22
Match length 71
% identity 79
```

NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 138148

Seq. ID LIB22-047-Q1-E1-C4

Method BLASTX
NCBI GI g267073
BLAST score 536
E value 5.0e-55
Match length 99
% identity 99

NCBI Description TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin

beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)

beta-3 tubulin [Arabidopsis thaliana]

Seq. No. 138149

Seq. ID LIB22-047-Q1-E1-D5

Method BLASTX
NCBI GI g1890352
BLAST score 435
E value 3.0e-43
Match length 81
% identity 55

NCBI Description (X91398) transcription factor L2 [Arabidopsis thaliana]

Seq. No. 138150

Seq. ID LIB22-047-Q1-E1-G2

Method BLASTN
NCBI GI g3449315
BLAST score 193
E value 1.0e-104
Match length 368
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K23L20, complete sequence [Arabidopsis thaliana]

Seq. No. 138151

Seq. ID LIB22-048-Q1-E1-B3

Method BLASTN
NCBI GI g4455321
BLAST score 233
E value 1.0e-128
Match length 266
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10

(ESSAII project)

Seq. No. 138152

Seq. ID LIB22-048-Q1-E1-C11

Method BLASTX NCBI GI g166765 BLAST score 584



E value 1.0e-60 Match length 111 % identity 100

NCBI Description (M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]

Seq. No. 138153

Seq. ID LIB22-048-Q1-E1-D11

Method BLASTX
NCBI GI g231536
BLAST score 620
E value 8.0e-65
Match length 124
% identity 100

NCBI Description CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)

(LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase

(EC 3.4.11.1) - Arabidopsis thaliana

>gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase
[Arabidopsis thaliana] >gi 4115380 (AC005967) putative

leucine aminopeptidase [Arabidopsis thaliana]

Seq. No. 138154

Seq. ID LIB22-048-Q1-E1-D9

Method BLASTX
NCBI GI g4512615
BLAST score 686
E value 2.0e-72
Match length 133
% identity 100

NCBI Description (AC004793) Strong similarity to gb_X59970 3-isopropylmalate

dehydrogenase (IMDH) from Brassica napus. EST gb F14478

comes from this gene. [Arabidopsis thaliana]

Seq. No. 138155

Seq. ID LIB22-048-Q1-E1-E11

Method BLASTX
NCBI GI g4567286
BLAST score 322
E value 7.0e-30
Match length 59
% identity 60

NCBI Description (AC006841) putative coatomer alpha subunit [Arabidopsis

thaliana]

Seq. No. 138156

Seq. ID LIB22-048-Q1-E1-G10

Method BLASTX
NCBI GI g2961390
BLAST score 600
E value 2.0e-62
Match length 111
% identity 100

NCBI Description (AL022141) beta-galactosidase like protein [Arabidopsis

thaliana]

Seq. No. 138157

Seq. ID LIB22-048-Q1-E1-G3



```
Method
                   BLASTX
NCBI GI
                   q2995943
BLAST score
                   169
E value
                   6.0e-12
Match length
                   96
% identity
                   43
NCBI Description
                   (AF053560) cytochrome c oxidase subunit Vb precursor
                   [Mesembryanthemum crystallinum]
Seq. No.
                   138158
Seq. ID
                   LIB22-049-Q1-E1-A7
Method
                   BLASTN
NCBI GI
                   g4519193
BLAST score
                   121
E value
                   2.0e-61
Match length
                   418
% identity
                   98
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDC11, complete sequence
Seq. No.
                   138159
Seq. ID
                  LIB22-049-Q1-E1-B3
Method
                  BLASTN
NCBI GI
                   g3449316
BLAST score
                   277
E value
                   1.0e-154
Match length
                   417
% identity
                   92
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9D7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138160
Seq. ID
                  LIB22-049-Q1-E1-B5
Method
                  BLASTX
NCBI GI
                  g4191782
BLAST score
                  673
E value
                  5.0e-71
Match length
                  140
% identity
                  91
NCBI Description
                  (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
Seq. No.
                  138161
Seq. ID
                  LIB22-049-Q1-E1-F3
Method
                  BLASTX
NCBI GI
                  g4586053
BLAST score
                  205
E value
                  2.0e-16
Match length
                  56
% identity
                  59
NCBI Description
                  (AC007020) putative lacasse [Arabidopsis thaliana]
Seq. No.
                  138162
Seq. ID
                  LIB22-050-Q1-E1-B4
```

Method BLASTN NCBI GI g3668073 BLAST score 200 E value 1.0e-108



```
Match length
                   388
                   100
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T4C15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   138163
Seq. ID
                   LIB22-050-Q1-E1-H2
Method
                   BLASTX
NCBI GI
                   g629669
BLAST score
                   142
E value
                   3.0e-09
Match length
                   74
% identity
                   41
NCBI Description hypothetical protein - tomato
Seq. No.
                   138164
Seq. ID
                   LIB22-051-Q1-E1-B7
Method
                   BLASTX
NCBI GI
                   g1403134
BLAST score
                   413
                                                          ٠ سه -
E value
                   1.0e-40
Match length
                   83
% identity
                   98
NCBI Description (X98453) peroxidase [Arabidopsis thaliana]
Seq. No.
                   138165
Seq. ID
                   LIB22-051-Q1-E1-C6
Method
                   BLASTN
NCBI GI
                   q4490324
BLAST score
                   93
E value
                   1.0e-44
Match length
                   219
% identity
                   88
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14
                   (ESSA project)
Seq. No.
                  138166
Seq. ID
                  LIB22-051-Q1-E1-E3
Method
                  BLASTN
NCBI GI
                  g4249393
BLAST score
                  211
E value
                  1.0e-115
Match length
                  419
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T9J23 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138167
Seq. ID
                  LIB22-051-Q1-E1-F11
Method
                  BLASTN
NCBI GI
                  q3241927
BLAST score
                  35
```

NCBI GI g3241927
BLAST score 35
E value 4.0e-10
Match length 88
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTE17, complete sequence [Arabidopsis thaliana]



Seq. No. 138168 Seq. ID LIB22-051-Q1-E1-F3 Method BLASTN NCBI GI g3449325 BLAST score 246 E value 1.0e-136 Match length 285 % identity 98 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16H17, complete sequence [Arabidopsis thaliana] Seq. No. 138169 Seq. ID LIB22-051-Q1-E1-G9

Method BLASTN
NCBI GI g2584827
BLAST score 123
E value 3.0e-63
Match length 123
% identity 100

NCBI Description Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,

complete sequence [Arabidopsis thaliana]

 Seq. No.
 138170

 Seq. ID
 LIB22-052-Q1-E1-A7

 Method
 BLASTN

 NODI GI
 DESCRIPTION

NCBI GI g2564044
BLAST score 279
E value 1.0e-155
Match length 407
% identity 100
NCBI Description Arabidons

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19P17, complete sequence [Arabidopsis thaliana]

Seq. No. 138171

Seq. ID LIB22-052-Q1-E1-A8

Method BLASTN
NCBI GI g4490291
BLAST score 135
E value 3.0e-70
Match length 156
% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5

(ESSA project)

Seq. No. 138172

Seq. ID LIB22-052-Q1-E1-B11

Method BLASTX
NCBI GI g1702986
BLAST score 464
E value 2.0e-46
Match length 95
% identity 99

NCBI Description 14-3-3-LIKE PROTEIN GF14 CHI >gi 1255987 (U09377) GF14chi

isoform [Arabidopsis thaliana] > gi_1256534 (L09112) GF14

chi chain [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                   LIB22-052-Q1-E1-B4
Method
                   BLASTX
NCBI GI
                   g1550740
BLAST score
                   450
E value
                   6.0e-45
Match length
                   118
% identity
                   77
NCBI Description (Y07961) GDP-associated inhibitor [Arabidopsis thaliana]
Seq. No.
                   138174
Seq. ID
                   LIB22-052-Q1-E1-C1
Method
                   BLASTN
NCBI GI
                   a3510343
BLAST score
                   350
E value
                   0.0e + 00
Match length
                   380
% identity
                   98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MJC20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   138175
Seq. ID
                   LIB22-052-Q1-E1-C4
Method
                   BLASTX
NCBI GI
                   q120675
BLAST score
                   486
E value
                   4.0e-49
Match length
                   110
% identity
                   85
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                   >gi_21143_emb_CAA27844 (X04301) GAPDH (aa 1-338) [Sinapis
                   alba]
Seq. No.
                   138176
Seq. ID
                  LIB22-052-Q1-E1-C8
Method
                  BLASTX
NCBI GI
                  q3738309
BLAST score
                   493
E value
                   6.0e - 50
Match length
                  120
% identity
                  79
NCBI Description
                  (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                  138177
Seq. ID
                  LIB22-052-Q1-E1-C9
Method
                  BLASTX
NCBI GI
                  g3328101
BLAST score
                  299
                  2.0e-27
E value
Match length
                  85
% identity
                  61
```

NCBI Description (AF073995) beta-galactosidase [synthetic construct]

Seq. No. 138178

Seq. ID LIB22-052-Q1-E1-D6



```
Method
                   BLASTX
NCBI GI
                   g4539386
BLAST score
                   173
E value
                   2.0e-12
Match length
                   91
% identity
                   45
NCBI Description
                  (AL035526) extensin-like protein [Arabidopsis thaliana]
Seq. No.
                   138179
Seq. ID
                   LIB22-052-Q1-E1-E11
Method
                   BLASTX
NCBI GI
                   g2498943
BLAST score
                   215
E value
                   3.0e-17
Match length
                   91
% identity
                   42
NCBI Description
                  PUTATIVE SPERMIDINE SYNTHASE (PUTRESCINE
                   AMINOPROPYLTRANSFERASE) (SPDSY) >gi_2129288_pir__B64339
                   spermidine synthase (EC 2.5.1.16) - Methanococcus
                   jannaschii >gi_1591033 (U67486) spermidine synthase (speE)
                   [Methanococcus jannaschii]
Seq. No.
                   138180
Seq. ID
                  LIB22-052-Q1-E1-E6
Method
                  BLASTX
NCBI GI
                  g2827559
BLAST score
                   326
E value
                   3.0e-30
Match length
                  76
% identity
                  80
                   (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
                  >gi_3292808_emb_CAA19798 (AL031018) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                  138181
Seq. ID
                  LIB22-052-Q1-E1-G6
Method
                  BLASTN
NCBI GI
                  g2828182
BLAST score
                  298
                  1.0e-167
E value
Match length
                  376
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MOJ9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138182
Seq. ID
                  LIB22-053-Q1-E1-B4
Method
                  BLASTX
NCBI GI
                  g4586049
BLAST score
                  285
E value
                  1.0e-25
Match length
                  118
% identity
                  47
NCBI Description
                  (AC007020) hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 138183

Seq. ID LIB22-053-Q1-E1-F8



Method BLASTX
NCBI GI g3193302
BLAST score 139
E value 1.0e-08
Match length 60
% identity 48

NCBI Description (AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 166.20) and to legume lectins

beta domain (Pfam: lectin_legB.hmm, score: 139.32)

[Arabidopsis thaliana]

[Arabidopsis tharian

Seq. No. 138184

Seq. ID LIB22-053-Q1-E1-H12

Method BLASTN
NCBI GI g2959766
BLAST score 326
E value 0.0e+00
Match length 330
% identity 100

NCBI Description Arabidopsis thaliana DNA for the glutathione-conjugate

transporter AtMRP4

Seq. No. 138185

Seq. ID LIB22-053-Q1-E1-H6

Method BLASTX
NCBI GI g3785972
BLAST score 385
E value 1.0e-37
Match length 85
% identity 89

NCBI Description (AC005560) putative auxin transport protein [Arabidopsis

thaliana] >gi_4262249 gb AAD14542 (AC006200) putative

auxin transport protein [Arabidopsis thaliana]

Seq. No. 138186

Seq. ID LIB22-054-Q1-E1-G6

Method BLASTX
NCBI GI g2262113
BLAST score 144
E value 2.0e-09
Match length 46
% identity 59

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 138187

Seq. ID LIB22-054-Q1-E2-A6

Method BLASTN
NCBI GI g3046850
BLAST score 99
E value 5.0e-49
Match length 99
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K24G6, complete sequence [Arabidopsis thaliana]

Seq. No. 138188

Seq. ID LIB22-054-Q1-E2-C12



```
Method
                   BLASTX
NCBI GI
                   g3757522
BLAST score
                   421
E value
                   1.0e-41
Match length
                   96
% identity
                   91
                  (AC005167) putative splicing factor [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   138189
Seq. ID
                   LIB22-054-Q1-E2-C7
Method
                   BLASTX
NCBI GI
                   g4559339
BLAST score
                   200
E value
                   1.0e-15
Match length
                   56
% identity
                   79
NCBI Description
                   (AC007087) putative ATP-dependent RNA helicase [Arabidopsis
                   thaliana]
Seq. No.
                   138190
Seq. ID
                  LIB22-054-Q1-E2-D12
Method
                  BLASTN
NCBI GI
                   q4415928
BLAST score
                   307
E value
                  1.0e-172
Match length
                   311
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13A10 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138191
Seq. ID
                  LIB22-054-Q1-E2-D7
Method
                  BLASTN
NCBI GI
                  q4589411
BLAST score
                  78
E value
                  2.0e-36
Match length
                  106
% identity
                  93
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  F5H8, complete sequence
Seq. No.
                  138192
Seq. ID
                  LIB22-054-Q1-E2-E3
Method
                  BLASTN
NCBI GI
                  g4755185
BLAST score
                  260
E value
                  1.0e-144
Match length
                  272
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F5G3 genomic
                  sequence, complete sequence
```

Seq. No. 138193

Seq. ID LIB22-054-Q1-E2-F1

Method BLASTN NCBI GI g2980787

BLAST score 84



```
E value 1.0e-39
Match length 196
% identity 95
NCBI Description Arabidon (ESSAII
```

NCBI Description Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No. 138194

Seq. ID LIB22-055-Q1-E1-A2

Method BLASTN
NCBI GI g3785992
BLAST score 331
E value 0.0e+00
Match length 331
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138195

Seq. ID LIB22-055-Q1-E1-B12

Method BLASTN
NCBI GI g3241939
BLAST score 156
E value 9.0e-83
Match length 164
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T26J13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138196

Seq. ID LIB22-055-Q1-E1-B9

Method BLASTX
NCBI GI g4206155
BLAST score 228
E value 6.0e-19
Match length 78
% identity 56

NCBI Description (AF109219) Mcd4p homolog [Homo sapiens]

Seq. No. 138197

Seq. ID LIB22-055-Q1-E1-C8

Method BLASTX
NCBI GI g1773042
BLAST score 688
E value 9.0e-73
Match length 135
% identity 99

NCBI Description (U82203) IDH-I [Arabidopsis thaliana]

Seq. No. 138198

Seq. ID LIB22-055-Q1-E1-H1

Method BLASTN
NCBI GI g4756963
BLAST score 324
E value 0.0e+00
Match length 324
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23



(ESSA project)

```
Seq. No.
                   138199
Seq. ID
                   LIB22-056-Q1-E1-A6
Method
                   BLASTX
NCBI GI
                   g135433
BLAST score
                   730
E value
                   1.0e-77
Match length
                   138
% identity
                   99
                   TUBULIN ALPHA CHAIN >gi_578450_emb_CAA77810_ (Z11763)
NCBI Description
                   alpha-Tubulin [Oxytricha granulifera]
Seq. No.
                   138200
Seq. ID
                   LIB22-056-Q1-E1-D4
Method
                   BLASTN
NCBI GI
                   g4582444
BLAST score
                   308
E value
                   1.0e-173
Match length
                   364
% identity
                   96
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T9H9 genomic
                   sequence, complete sequence
Seq. No.
                   138201
Seq. ID
                   LIB22-056-Q1-E1-D6
Method
                   BLASTX
NCBI GI
                   q2117612
BLAST score
                   650
E value
                   3.0e-68
Match length
                   127
% identity
                   98
NCBI Description catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
Seq. No.
                   138202
Seq. ID
                   LIB22-056-Q1-E1-D7
Method
                  BLASTX
NCBI GI
                  g3702336
BLAST score
                  280
E value
                  3.0e-25
Match length
                  91
% identity
                   60
NCBI Description
                   (AC005397) putative 3-methyl-2-oxobutanoate
                  hydroxy-methyl-transferase [Arabidopsis thaliana]
Seq. No.
                  138203
Seq. ID
                  LIB22-056-Q1-E1-E12
Method
                  BLASTX
NCBI GI
                  g3834306
BLAST score
                  423
E value
                  9.0e-42
Match length
                  111
% identity
NCBI Description
                  (AC005679) EST gb_R65024 comes from this gene. [Arabidopsis
                  thaliana]
```

Seq. No. 138204



```
Seq. ID
                   LIB22-056-Q1-E1-E9
Method
                   BLASTX
NCBI GI
                   q2146731
BLAST score
                   374
E value
                   5.0e-36
Match length
                   111
% identity
                   33
                   FK506-binding protein - Arabidopsis thaliana >gi 1354207
NCBI Description
                   (U49453) rof1 [Arabidopsis thaliana]
Seq. No.
                   138205
Seq. ID
                   LIB22-056-Q1-E1-F2
Method
                   BLASTN
                   g3859658
NCBI GI
BLAST score
                   352
E value
                   0.0e + 00
Match length
                   425
% identity
                   100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1
                   (ESSAII project)
Seq. No.
                   138206
Seq. ID
                  LIB22-056-Q1-E1-F7
Method
                  BLASTN
NCBI GI
                   q4415928
BLAST score
                  174
E value
                   4.0e-93
Match length
                   384
% identity
                   98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13A10 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138207
Seq. ID
                  LIB22-056-Q1-E1-F9
Method
                  BLASTN
NCBI GI
                  q4662628
BLAST score
                  362
E value
                  0.0e + 00
Match length
                  362
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC F27010 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  138208
Seq. ID
                  LIB22-056-Q1-E1-G4
Method
                  BLASTN
NCBI GI
                  g2351062
BLAST score
                  153
E value
                  6.0e-81
```

Match length 180 % identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAH20, complete sequence [Arabidopsis thaliana]

Seq. No. 138209

Seq. ID LIB22-056-Q1-E1-H2

Method BLASTN



```
NCBI GI
                  q2191157
BLAST score
                  129
E value
                  2.0e-66
Match length
                  203
                  94
% identity
NCBI Description Arabidopsis thaliana BAC IG002P16
Seq. No.
                  138210
Seq. ID
                  LIB22-057-Q1-E1-H6
Method
                  BLASTX
NCBI GI
                  g4206209
BLAST score
                  322
E value
                  4.0e-42
                  97
Match length
% identity
                  82
NCBI Description (AF071527) putative glucan synthase component [Arabidopsis
                  thaliana] >gi_4263042_gb AAD15311 (AC005142) putative
                  glucan synthase component [Arabidopsis thaliana]
Seq. No.
                  138211
Seq. ID
                  LIB22-058-Q1-E1-A9
Method
                  BLASTN
NCBI GI
                  q3449333
BLAST score
                  384
E value
                  0.0e+00
Match length
                  405
% identity
                  58
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MXF12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138212
Seq. ID
                  LIB22-058-Q1-E1-B9
Method
                  BLASTN
NCBI GI
                  q3702315
BLAST score
                  174
                  4.0e-93
E value
                  295
Match length
                  98
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T3F17 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138213
Seq. ID
                  LIB22-058-Q1-E1-C4
Method
                  BLASTN
NCBI GI
                  q3293582
BLAST score
                  384
E value
                  0.0e + 00
```

Match length 411

100

NCBI Description Arabidopsis thaliana BAC T15F16

Seq. No. 138214 LIB22-058-Q1-E1-D2 Seq. ID Method BLASTN NCBI GI q4159709 BLAST score 150 E value 6.0e-79

% identity



Match length 98 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MLN21, complete sequence

Seq. No. 138215

Seq. ID LIB22-058-Q1-E1-H5

Method BLASTX NCBI GI g129809 BLAST score 603 E value 9.0e-63 Match length 125 % identity 94

NCBI Description PEROXIDASE C2 PRECURSOR >gi_81665_pir__JH0149 peroxidase

(EC 1.11.1.7) C2 precursor - horseradish

>gi_217932_dbj_BAA14143_ (D90115) peroxidase isozyme

[Armoracia rusticana]

Seq. No. 138216

Seq. ID LIB22-059-Q1-E1-A5

Method BLASTX NCBI GI q3193284 BLAST score 367 E value 5.0e-35 Match length 133 % identity 53

(AF069298) No definition line found [Arabidopsis thaliana] NCBI Description

Seq. No. 138217

Seq. ID LIB22-059-Q1-E1-C4

Method BLASTN NCBI GI g4159705 BLAST score 137 E value 5.0e-71 Match length 372 % identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGD8, complete sequence

Seq. No. 138218

Seq. ID LIB22-059-Q1-E1-D11

Method BLASTX NCBI GI g1170089 BLAST score 535 E value 9.0e-55 Match length 106 % identity 100

NCBI Description GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)

>gi_481822_pir__S39542 probable glutathione transferase (EC

2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione

S-transferase [Arabidopsis thaliana]

138219 Seq. No.

LIB22-059-Q1-E1-D2 Seq. ID

Method BLASTX

```
NCBI GI
                   g4191791
BLAST score
                   173
E value
                   6.0e-16
Match length
                   65
% identity
                   72
NCBI Description
                   (AC005917) putative sf21 {Helianthus annuus} protein
                   [Arabidopsis thaliana]
Seq. No.
                   138220
Seq. ID
                   LIB22-059-Q1-E1-D5
Method
                  BLASTX
NCBI GI
                   g2129549
BLAST score
                   473
E value
                  2.0e-47
Match length
                  88
% identity
                  99
NCBI Description
                  calcium-dependent protein kinase (EC 2.7.1.-) CDPK19 -
                  Arabidopsis thaliana >gi_2129551_pir__S71778
                  calcium-dependent protein kinase 19 - Arabidopsis thaliana
                  >gi_836942 (U20624) calcium-dependent protein kinase
                   [Arabidopsis thaliana] >gi_836948 (U20627)
                  calcium-dependent protein kinase [Arabidopsis thaliana]
Seq. No.
                  138221
Seq. ID
                  LIB22-059-Q1-E1-F11
Method
                  BLASTX
NCBI GI
                  q2842469
BLAST score
                  146
E value
                  4.0e-09
Match length
                  68
% identity
                  43
NCBI Description
                  (AL021747) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                  138222
Seq. ID
                  LIB22-059-Q1-E1-F6
Method
                  BLASTN
NCBI GI
                  q4756963
BLAST score
                  368
E value
                  0.0e+00
Match length
                  403
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                  (ESSA project)
Seq. No.
                  138223
Seq. ID
                  LIB22-059-Q1-E1-G3
Method
                  BLASTN
NCBI GI
                  g3241924
BLAST score
                  134
```

E value 3.0e-69 Match length 393 % identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNC6, complete sequence [Arabidopsis thaliana]

Seq. No. 138224

Seq. ID LIB22-059-Q1-E1-G8



Method BLASTX
NCBI GI g2435522
BLAST score 276
E value 7.0e-30
Match length 136
% identity 51

NCBI Description (AF024504) contains similarity to other AMP-binding enzymes

[Arabidopsis thaliana]

Seq. No. 138225

Seq. ID LIB22-059-Q1-E1-H4

Method BLASTN
NCBI GI g3128136
BLAST score 237
E value 1.0e-130
Match length 361
% identity 67

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K1F13, complete sequence [Arabidopsis thaliana]

Seq. No. 138226

Seq. ID LIB22-060-Q1-E1-A11

Method BLASTN
NCBI GI g2618605
BLAST score 167
E value 3.0e-89
Match length 183
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUK11, complete sequence [Arabidopsis thaliana]

Seq. No. 138227

Seq. ID LIB22-060-Q1-E1-A12

Method BLASTX
NCBI GI g2492504
BLAST score 605
E value 4.0e-63
Match length 120
% identity 50

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG

>gi_1669660 emb CAA70565 (Y09396) protein of AAA family

[Capsicum annuum]

Seq. No. 138228

Seq. ID LIB22-060-Q1-E1-B1

Method BLASTX
NCBI GI g2914700
BLAST score 347
E value 4.0e-33
Match length 88
% identity 83

NCBI Description (AC003974) tRNA-processing protein SEN3-like [Arabidopsis

thaliana]

Seq. No. 138229

Seq. ID LIB22-060-Q1-E1-C11

Method BLASTX



NCBI GI g3080389 BLAST score 457 E value 8.0e-46 Match length 88 % identity 100

NCBI Description (AL022603) putative membrane associated protein

[Arabidopsis thaliana]

Seq. No. 138230

Seq. ID LIB22-060-Q1-E1-D1

Method BLASTN NCBI GI g3688169

BLAST score 81 E value 5.0e-38 Match length 169 % identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21

(ESSAII project)

Seq. No. 138231

Seq. ID LIB22-060-Q1-E1-H2

Method BLASTN
NCBI GI g2288979
BLAST score 346
E value 0.0e+00
Match length 346
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T01024 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138232

Seq. ID LIB22-060-Q1-E1-H4

Method BLASTN
NCBI GI g3193311
BLAST score 143
E value 1.0e-74
Match length 278
% identity 98

NCBI Description Arabidopsis thaliana BAC F6N15

Seq. No. 138233

Seq. ID LIB22-060-Q1-E1-H6

Method BLASTN
NCBI GI g4199934
BLAST score 34
E value 1.0e-09
Match length 221
% identity 72

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 138234

Seq. ID LIB22-061-Q1-E2-A7

Method BLASTN
NCBI GI g4519185
BLAST score 129
E value 2.0e-66



Match length 181 % identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K15015, complete sequence

Seq. No. 138235

Seq. ID LIB22-061-Q1-E2-D10

Method BLASTX
NCBI GI g2506788
BLAST score 244
E value 1.0e-20
Match length 99
% identity 42

NCBI Description GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (RAB

GERANYLGERANYLTRANSFERASE BETA SUBUNIT) (RAB GERANYL-GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) >gi_1332508_emb_CAA66638_(X98001) geranylgeranyl transferase II [Homo sapiens]

Seq. No. 138236

Seq. ID LIB22-061-Q1-E2-F6

Method BLASTX
NCBI GI g3868857
BLAST score 328
E value 1.0e-30
Match length 80
% identity 84

NCBI Description (AB013886) RAV1 [Arabidopsis thaliana]

Seq. No. 138237

Seq. ID LIB22-061-Q1-E2-G11

Method BLASTN
NCBI GI g3367567
BLAST score 290
E value 1.0e-162
Match length 294
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20

(ESSAII project)

Seq. No. 138238

Seq. ID LIB22-062-Q1-E1-A10

Method BLASTX
NCBI GI g3789911
BLAST score 253
E value 8.0e-22
Match length 95
% identity 52

NCBI Description (AF081802) developmental protein DG1118 [Dictyostelium

discoideum]

Seq. No. 138239

Seq. ID LIB22-062-Q1-E1-A12

Method BLASTN
NCBI GI g469113
BLAST score 89
E value 9.0e-43



Match length % identity 100

NCBI Description A.thaliana (Columbia) Dr4 mRNA

Seq. No.

138240

Seq. ID

LIB22-062-Q1-E1-A7

Method NCBI GI BLAST score E value

BLASTN g2618600 212

1.0e-116 304

Match length 97 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.

138241

Seq. ID

LIB22-062-Q1-E1-A8

Method BLASTN NCBI GI q450242 BLAST score 39 E value 1.0e-12 Match length 59 % identity 92

NCBI Description Actinidia deliciosa var. deliciosa (pKIWI505) mRNA,

complete cds

Seq. No.

138242

LIB22-062-Q1-E1-D6 Seq. ID

Method BLASTX g3264805 NCBI GI BLAST score 711 E value 2.0e-75 Match length 141 % identity 100

NCBI Description (AF071788) phosphoenolpyruvate carboxylase [Arabidopsis

thaliana] >gi_4079630_emb_CAA10486_ (AJ131710) phospho

enole pyruvate carboxylase [Arabidopsis thaliana]

Seq. No. 138243

Seq. ID LIB22-062-Q1-E1-E11

Method BLASTN g2564044 NCBI GI BLAST score 130 3.0e-67 E value Match length 146 97 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19P17, complete sequence [Arabidopsis thaliana]

Seq. No. 138244

Seq. ID LIB22-062-Q1-E1-E7

Method BLASTN NCBI GI g4314374 BLAST score 410 E value 0.0e + 00Match length 410 % identity 100





NCBI Description Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138245

Method BLASTX
NCBI GI g1370166
BLAST score 539
E value 3.0e-55
Match length 105

Seq. ID

% identity

NCBI Description (Z73932) RAB1C [Lotus japonicus]

LIB22-062-Q1-E1-G6

Seq. No. 138246

Seq. ID LIB22-062-Q1-E1-H10

98

Method BLASTN
NCBI GI g2109292
BLAST score 279
E value 1.0e-156
Match length 279
% identity 100

NCBI Description Arabidopsis thaliana serine/threonine protein kinase mRNA,

complete cds

Seq. No. 138247

Seq. ID LIB22-062-Q1-E1-H7

Method BLASTX
NCBI GI g4263517
BLAST score 453
E value 3.0e-45
Match length 137
% identity 79

NCBI Description (AC004044) similar to PHZF, catalyzing the hydroxylation of

phenazine-1-carboxylic acid to

2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis

thaliana]

Seq. No. 138248

Seq. ID LIB22-063-Q1-E1-A12

Method BLASTN
NCBI GI g1402874
BLAST score 347
E value 0.0e+00
Match length 355
% identity 100

NCBI Description A.thaliana 81kb genomic sequence

Seq. No. 138249

Seq. ID LIB22-063-Q1-E1-A2

Method BLASTX
NCBI GI g3915458
BLAST score 276
E value 2.0e-24
Match length 83
% identity 65

NCBI Description PUTATIVE ABC TRANSPORTER C8C9.18 IN CHROMOSOME I

Seq. ID

138255

LIB22-063-Q1-E1-C6



```
Seq. No.
                   138250
                   LIB22-063-Q1-E1-A5
Seq. ID
Method
                   BLASTN "
NCBI GI
                   q2244788
BLAST score
                   93
E value
                   5.0e-45
Match length
                   183
                   99
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
Seq. No.
                   138251
Seq. ID
                   LIB22-063-Q1-E1-B1
Method
                   BLASTX
                   g4455276
NCBI GI
BLAST score
                   554
E value
                   4.0e-57
Match length
                   107
% identity
                   100
NCBI Description
                   (AL035527) peptide transporter-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   138252
Seq. ID
                   LIB22-063-Q1-E1-B7
Method
                   BLASTN
NCBI GI
                   q3985957
BLAST score
                   329
E value
                   0.0e+00
Match length
                   329
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MYN8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   138253
Seq. ID
                   LIB22-063-Q1-E1-B8
Method
                  BLASTN
NCBI GI
                   g4220641
BLAST score
                   79
E value
                   7.0e-37
Match length
                   104
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUL3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138254
Seq. ID
                  LIB22-063-Q1-E1-C11
Method
                  BLASTN
NCBI GI
                  g2459406
BLAST score
                  231
E value
                  1.0e-127
Match length
                  355
% identity
                  74
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F4P9 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```



Method BLASTX
NCBI GI g1655932
BLAST score 284
E value 2.0e-25
Match length 133
% identity 48

NCBI Description (U66565) RUSH-1beta [Oryctolagus cuniculus]

Seq. No. 138256

Seq. ID LIB22-063-Q1-E1-C9

Method BLASTN
NCBI GI g2494106
BLAST score 166
E value 2.0e-88
Match length 340
% identity 99

NCBI Description Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 138257

Seq. ID LIB22-063-Q1-E1-E2

Method BLASTN
NCBI GI g2252823
BLAST score 294
E value 1.0e-165
Match length 346
% identity 99

NCBI Description Arabidopsis thaliana BAC IG005I10

Seq. No. 138258

Seq. ID LIB22-063-Q1-E1-E3

Method BLASTN
NCBI GI g3264774
BLAST score 251
E value 1.0e-139
Match length 312
% identity 100

NCBI Description Arabidopsis thaliana BAC T8A17 chromosome IV, complete

sequence [Arabidopsis thaliana]

Seq. No. 138259

Seq. ID LIB22-063-Q1-E1-E6

Method BLASTX
NCBI GI 94587987
BLAST score 614
E value 4.0e-64
Match length 137
% identity 80

NCBI Description (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 138260

Seq. ID LIB22-063-Q1-E1-E9

Method BLASTN
NCBI GI 94733952
BLAST score 27
E value 1.0e-05



Match length 225 % identity 92

NCBI Description Arabidopsis thaliana chromosome I BAC F23H11 genomic

sequence, complete sequence

Seq. No. 138261

Seq. ID LIB22-063-Q1-E1-F2

Method BLASTX
NCBI GI g3582329
BLAST score 488
E value 2.0e-49
Match length 95
% identity 100

NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.

% identity

138262 LIB22-063-Q1-E1-G8

77

Seq. ID LIB22-0
Method BLASTX
NCBI GI g231587
BLAST score 530
E value 3.0e-54
Match length 133

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR

>gi_283001_pir__S25304 H+-transporting ATP synthase (EC
3.6.1.34) beta chain precursor, mitochondrial - rice
>gi_218147_dbj_BAA01372_ (D10491) mitochondrial F1-ATPase

[Oryza sativa]

Seq. No. 138263

Seq. ID LIB22-064-Q1-E1-A5

Method BLASTN
NCBI GI g3869068
BLAST score 106
E value 1.0e-52
Match length 206
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC16, complete sequence [Arabidopsis thaliana]

Seq. No. 138264

Seq. ID LIB22-064-Q1-E1-B1

Method BLASTN
NCBI GI g4539290
BLAST score 276
E value 1.0e-154
Match length 348
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19

(ESSA project)

Seq. No. 138265

Seq. ID LIB22-064-Q1-E1-B2

Method BLASTN
NCBI GI g4220634
BLAST score 226
E value 1.0e-124



Match length 318 % identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9H21, complete sequence [Arabidopsis thaliana]

Seq. No. 138266

Seq. ID LIB22-064-Q1-E1-B5

Method BLASTN
NCBI GI g2828278
BLAST score 336
E value 0.0e+00
Match length 398
% identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16

(ESSAII project)

Seq. No. 138267

Seq. ID LIB22-064-Q1-E1-B8

Method BLASTN
NCBI GI g469113
BLAST score 384
E value 0.0e+00
Match length 384
% identity 100

NCBI Description A.thaliana (Columbia) Dr4 mRNA

Seq. No. 138268

Seq. ID LIB22-064-Q1-E1-C12

Method BLASTN
NCBI GI g2618599
BLAST score 57
E value 2.0e-23
Match length 272
% identity 82

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBD2, complete sequence [Arabidopsis thaliana]

Seq. No. 138269

Seq. ID LIB22-064-Q1-E1-C2

Method BLASTN
NCBI GI g4220638
BLAST score 127
E value 5.0e-65
Match length 379
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MIF21, complete sequence [Arabidopsis thaliana]

Seq. No. 138270

Seq. ID LIB22-064-Q1-E1-C5

Method BLASTX
NCBI GI g3075399
BLAST score 161
E value 5.0e-11
Match length 73
% identity 51

NCBI Description (AC004484) SF16-like protein [Arabidopsis thaliana]



```
Seq. No.
                  138271
Seq. ID
                  LIB22-064-Q1-E1-C9
Method
                  BLASTX
                  g2980806
NCBI GI
BLAST score
                  583
E value
                  2.0e-60
Match length
                  123
                  85
% identity
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]
Seq. No.
                  138272
                  LIB22-064-Q1-E1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4680181
BLAST score
                  204
E value
                  4.0e-16
Match length
                  105
% identity
                  47
NCBI Description (AF111709) unknown [Oryza sativa subsp. indica]
Seq. No.
                  138273
                  LIB22-064-Q1-E1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023216
BLAST score
                  166
E value
                  2.0e-53
Match length
                  127
% identity
                  76
NCBI Description 14-3-3-LIKE PROTEIN GF14 MU >gi 1531629 (U60444) GF14 mu
                  [Arabidopsis thaliana]
Seq. No.
                  138274
Seq. ID
                  LIB22-064-Q1-E1-F12
Method
                  BLASTN
NCBI GI
                  g682727
BLAST score
                  57
E value
                  9.0e-24
                  77
Match length
                  95
% identity
NCBI Description Arabidopsis thaliana
                  S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A
                  3-O-methyltransferase homologue mRNA, complete cds
Seq. No.
                  138275
Seq. ID
                  LIB22-064-Q1-E1-G2
Method
                  BLASTN
NCBI GI
                  g2264306
BLAST score
                  42
E value
                  1.0e-14
Match length
                  208
                  95
% identity
```

Seq. ID LIB22-064-Q1-E1-G9

MBK5, complete sequence [Arabidopsis thaliana]

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



Method BLASTN
NCBI GI 94220643
BLAST score 290
E value 1.0e-162
Match length 375
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 138277

Seq. ID LIB22-065-Q1-E1-A5

Method BLASTX
NCBI GI g2618723
BLAST score 595
E value 7.0e-62
Match length 132
% identity 89

NCBI Description (U49073) IAA17 [Arabidopsis thaliana] >gi 2921756

(AF040631) IAA17/AXR3 protein [Arabidopsis thaliana] >gi 4389514 gb AAB70451_ (AC000104) Identical to

Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs gb_H36782 and gb_F14074 come from this gene. [Arabidopsis

thaliana]

Seq. No. 138278

Seq. ID LIB22-065-Q1-E1-B10

Method BLASTX
NCBI GI g3450842
BLAST score 191
E value 1.0e-14
Match length 55
% identity 64

NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza

sativa]

Seq. No. 138279

Seq. ID LIB22-065-Q1-E1-B4

Method BLASTN
NCBI GI g2645198
BLAST score 132
E value 5.0e-68
Match length 416
% identity 99

NCBI Description Arabidopsis thaliana chromosome I BAC T26J12 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138280

Seq. ID LIB22-065-Q1-E1-B5

Method BLASTN
NCBI GI g2245031
BLAST score 70
E value 5.0e-31
Match length 419
% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No



Seq. ID LIB22-065-Q1-E1-B7

Method BLASTN
NCBI GI g4185128
BLAST score 143
E value 1.0e-74
Match length 421
% identity 99

NCBI Description Arabidopsis thaliana chromosome II P1 MSF3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138282

Seq. ID LIB22-065-Q1-E1-C1

Method BLASTX
NCBI GI g2393724
BLAST score 144
E value 6.0e-09
Match length 70
% identity 41

NCBI Description (U80819) glutathione-S-transferase homolog [Mus musculus]

Seq. No. 138283

Seq. ID LIB22-065-Q1-E1-C10

Method BLASTN
NCBI GI g4589444
BLAST score 168
E value 6.0e-90
Match length 168
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWF20, complete sequence

Seq. No. 138284

Seq. ID LIB22-065-Q1-E1-C3

Method BLASTX
NCBI GI 9465702
BLAST score 218
E value 1.0e-17
Match length 134
% identity 33

NCBI Description PROBABLE RIBOSOMAL PROTEIN B0303.15 IN CHROMOSOME III

>gi_283555_pir__S27795 ribosomal protein L11 homolog -Caenorhabditis elegans >gi_156201 (M77697) ribosomal

protein L11 [Caenorhabditis elegans]

Seq. No. 138285

Seq. ID LIB22-065-Q1-E1-C5

Method BLASTN
NCBI GI g4589438
BLAST score 410
E value 0.0e+00
Match length 413
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQJ2, complete sequence

Seq. No. 138286

```
LIB22-065-Q1-E1-C9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3510343
                  393
BLAST score
                  0.0e+00
E value
Match length
                  393
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MJC20, complete sequence [Arabidopsis thaliana]
                  138287
Seq. No.
                  LIB22-065-Q1-E1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2358139
                  239
BLAST score
                  1.0e-132
E value
Match length
                  264
                  97
% identity
NCBI Description Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete
                  sequence [Arabidopsis thaliana]
                  138288
Seq. No.
                  LIB22-065-Q1-E1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3176874
BLAST score
                  204
                  5.0e-16
E value
Match length
                  93
                   42
% identity
NCBI Description
                  (AF065639) cucumisin-like serine protease [Arabidopsis
                  thaliana]
                  138289
Seq. No.
                  LIB22-065-Q1-E1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3785992
BLAST score
                   361
                   0.0e+00
E value
Match length
                   361
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC T6A23 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   138290
Seq. No.
Seq. ID
                   LIB22-065-Q1-E1-E3
Method
                  BLASTX
NCBI GI
                   q4220482
BLAST score
                   202
```

Method BLASTX
NCBI GI g4220482
BLAST score 202
E value 9.0e-16
Match length 107
% identity 27

NCBI Description (AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 138291

Seq. ID LIB22-065-Q1-E1-E4

Method BLASTN NCBI GI g2351066



BLAST score 168
E value 2.0e-89
Match length 409
% identity 64

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOP9, complete sequence [Arabidopsis thaliana]

Seq. No. 138292

Seq. ID LIB22-065-Q1-E1-E5

Method BLASTN
NCBI GI g2924653
BLAST score 219
E value 1.0e-120
Match length 399
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDA7, complete sequence [Arabidopsis thaliana]

Seq. No. 138293

Seq. ID LIB22-065-Q1-E1-F5

Method BLASTX
NCBI GI g3947448
BLAST score 301
E value 2.0e-27
Match length 135
% identity 46

NCBI Description (AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3

comes from this gene; cDNA EST yk475f6.5 comes from this

gene; cDNA EST yk499g5.5 comes from this gene

[Caenorhabdi... >gi_3947543 emb_CAA88952 (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5

comes from this gene [Caenorhabditi

Seq. No. 138294

Seq. ID LIB22-065-Q1-E1-F7

Method BLASTX
NCBI GI g3688799
BLAST score 555
E value 4.0e-57
Match length 111
% identity 99

NCBI Description (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis

thaliana]

Seq. No. 138295

Seq. ID LIB22-065-Q1-E1-G10

Method BLASTX
NCBI GI g1170840
BLAST score 323
E value 4.0e-30
Match length 115
% identity 89

NCBI Description LOW-TEMPERATURE-INDUCED 78 KD PROTEIN

(DESSICATION-RESPONSIVE PROTEIN 29B) >gi_419759_pir__\$30154



low-temperature-induced protein 78 - Arabidopsis thaliana >gi_16390_emb_CAA47903_ (X67671) lti78 [Arabidopsis thaliana] >gi_348692 (L22567) cor78 [Arabidopsis thaliana]

Seq. No. 138296

Seq. ID LIB22-065-Q1-E1-G5

Method BLASTX
NCBI GI g2108252
BLAST score 396
E value 2.0e-38
Match length 108

% identity 38

NCBI Description (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]

>gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
[Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_

(AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No. 138297

Seq. ID LIB22-065-Q1-E1-G7

Method BLASTN
NCBI GI g4713947
BLAST score 30
E value 3.0e-07
Match length 311
% identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC T16B23 genomic

sequence, complete sequence

Seq. No. 138298

Seq. ID LIB22-066-Q1-E1-B12

Method BLASTN
NCBI GI 94589419
BLAST score 306
E value 1.0e-172
Match length 328
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K2I5, complete sequence

Seq. No. 138299

Seq. ID LIB22-066-Q1-E1-B2

Method BLASTX
NCBI GI g2924509
BLAST score 229
E value 6.0e-19
Match length 100
% identity 46

NCBI Description (AL022023) subtilisin proteinase-like [Arabidopsis

thaliana]

Seq. No. 138300

Seq. ID LIB22-066-Q1-E1-C4

Method BLASTX
NCBI GI g2244910
BLAST score 262
E value 8.0e-23
Match length 135

% identity NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana] 138301 Seq. No. Seq. ID LIB22-066-Q1-E1-D11 Method BLASTN NCBI GI g4468801 BLAST score 183 2.0e-98 E value 357 Match length % identity 98 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project) Seq. No. 138302

Seq. ID LIB22-066-Q1-E1-D12
Method BLASTN
NCBI GI g2335089
BLAST score 310
E value 1.0e-174
Match length 355
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

 Seq. No.
 138303

 Seq. ID
 LIB22-066-Q1-E1-E12

 Method
 BLASTX

 NCBI GI
 g2435519

 BLAST score
 228

 E value
 6.0e-19

BLAST score 228
E value 6.0e-19
Match length 102
% identity 54
NCRI Description

NCBI Description (AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW:P34110)

[Arabidopsis thaliana]

Seq. No. 138304

Seq. ID LIB22-066-Q1-E1-F12

Method BLASTX
NCBI GI g2642429
BLAST score 252
E value 9.0e-22
Match length 117
% identity 12

NCBI Description (AC002391) putative poly(A)-binding protein [Arabidopsis

thaliana]

Seq. No. 138305

Seq. ID LIB22-066-Q1-E1-F9

Method BLASTN
NCBI GI g4544381
BLAST score 356
E value 0.0e+00
Match length 359
% identity 73

NCBI Description Arabidopsis thaliana chromosome II BAC F16F14 genomic

Method

BLASTN



sequence, complete sequence

```
Seq. No.
                   138306
Seq. ID
                   LIB22-066-Q1-E1-G12
Method
                   BLASTX
NCBI GI
                   g3599968
BLAST score
                   628
E value
                   9.0e-66
Match length
                   125
% identity
                   100
NCBI Description (AF032123) clp protease [Arabidopsis thaliana]
Seq. No.
                   138307
Seq. ID
                   LIB22-066-Q1-E1-G3
Method
                   BLASTN
NCBI GI
                   g3869070
BLAST score
                   403
E value
                   0.0e+00
Match length
                   411
% identity
                   100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MGO3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   138308
Seq. ID
                   LIB22-066-Q1-E1-G6
Method
                   BLASTN
NCBI GI
                   g4757400
BLAST score
                   173
E value
                   1.0e-92
Match length
                   262
% identity
                   92
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MFJ20, complete sequence
Seq. No.
                   138309
Seq. ID
                   LIB22-066-Q1-E1-G9
Method
                   BLASTN
NCBI GI
                   g2191157
BLAST score
                   195
                   1.0e-105
E value
Match length
                   195
                   100
% identity
NCBI Description Arabidopsis thaliana BAC IG002P16
Seq. No.
                   138310
Seq. ID
                  LIB22-066-Q1-E1-H2
Method
                  {\tt BLASTX}
NCBI GI
                  g3327060
BLAST score
                   291
E value
                  2.0e-26
Match length
                  116
% identity
                   48
NCBI Description (AB014523) KIAA0623 protein [Homo sapiens]
Seq. No.
                  138311
Seq. ID
                  LIB22-067-Q1-E1-A2
```



NCBI GI g4581103 BLAST score 153 E value 1.0e-80 Match length 349 % identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC T24I21 genomic

sequence, complete sequence

Seq. No. 138312

Seq. ID LIB22-067-Q1-E1-B1

Method BLASTX
NCBI GI g3702121
BLAST score 296
E value 3.0e-27
Match length 83
% identity 69

NCBI Description (AJ011681) retinoblastoma-related protein [Chenopodium

rubrum]

Seq. No. 138313

Seq. ID LIB22-067-Q1-E1-B2

Method BLASTX
NCBI GI g1449179
BLAST score 239
E value 1.0e-20
Match length 49
% identity 96

NCBI Description (D86506) N-ethylmaleimide sensitive fusion protein

[Nicotiana tabacum]

Seq. No. 138314

Seq. ID LIB22-067-Q1-E1-C11

Method BLASTX
NCBI GI g1171993
BLAST score 409
E value 4.0e-40
Match length 92
% identity 89

NCBI Description PHENYLALANINE AMMONIA-LYASE 2 >gi_1076370_pir__S52991

phenylalanine ammonia-lyase (EC 4.3.1.5) - Arabidopsis thaliana >gi_497421 (L33678) phenylalanine ammonia lyase

[Arabidopsis thaliana]

Seq. No. 138315

Seq. ID LIB22-067-Q1-E1-C9

Method BLASTN
NCBI GI 94490324
BLAST score 254
E value 1.0e-141
Match length 291
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14

(ESSA project)

Seq. No. 138316

Seq. ID LIB22-067-Q1-E1-E1

Method BLASTX

```
NCBI GI
                     193290
BLAST score
                   144
E value
                   4.0e-09
Match length
                   66
                   47
% identity
NCBI Description
                   (AF069298) contains similarity to a protein kinase domain
                   (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta
                   domain (Pfam: lectin_legB.hmm, score: 125.64) and legume
                   lectins alpha domain (Pfam: lectin legA.hmm, score: 16.72)
                   [Arabido
                  138317
Seq. No.
Seq. ID
                  LIB22-067-Q1-E1-E10
Method
                  BLASTN
NCBI GI
                  g2104523
BLAST score
                   212
E value
                   1.0e-116
Match length
                   364
% identity
                   98
                  Arabidopsis thaliana BAC T10M13 from chromosome IV, from
NCBI Description
                   10.8 cM to 11.6 cM, complete sequence
Seq. No.
                   138318
Seq. ID
                  LIB22-067-Q1-E1-E6
Method
                  BLASTX
NCBI GI
                  q1083160
BLAST score
                  211
E value
                  3.0e-17
Match length
                  70
% identity
                  56
NCBI Description
                  mannosyl-oligosaccharide 1,2-alpha-mannosidase (EC
                  3.2.1.113) - rabbit (fragment)
Seq. No.
                  138319
Seq. ID
                  LIB22-067-Q1-E1-F6
Method
                  BLASTX
NCBI GI
                  q2738248
BLAST score
                  527
                  7.0e-54
E value
Match length
                  103
% identity
                  98
NCBI Description
                  (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
Seq. No.
                  138320
Seq. ID
                  LIB22-067-Q1-E1-H12
                  BLASTX
Method
NCBI GI
                  g1402904
BLAST score
                  469
                  3.0e-47
E value
Match length
                  90
% identity
                  99
NCBI Description (X98313) peroxidase [Arabidopsis thaliana]
```

Seq. ID LIB22-068-Q1-E1-A10

Method BLASTX



```
NCBI GI g2738248
BLAST score 672
E value 7.0e-71
Match length 126
% identity 100
```

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No. 138322

Seq. ID LIB22-068-Q1-E1-B12

Method BLASTX
NCBI GI g4587584
BLAST score 366
E value 5.0e-35
Match length 130
% identity 52

NCBI Description (AC007232) unknown protein [Arabidopsis thaliana]

Seq. No. 138323

Seq. ID LIB22-068-Q1-E1-C12

Method BLASTX
NCBI GI g3641837
BLAST score 430
E value 5.0e-51
Match length 132
% identity 86

NCBI Description (AL023094) Nonclathrin coat protein gamma - like protein

[Arabidopsis thaliana]

Seq. No. 138324

Seq. ID LIB22-068-Q1-E1-C6

Method BLASTX
NCBI GI g2252850
BLAST score 230
E value 4.0e-19
Match length 110
% identity 46

NCBI Description (AF013294) contains region of similarity to DNA binding

protein [Arabidopsis thaliana]

Seq. No. 138325

Seq. ID LIB22-068-Q1-E1-C9

Method BLASTX
NCBI GI g3617741
BLAST score 709
E value 3.0e-75
Match length 138
% identity 99

NCBI Description (AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis

thaliana]

Seq. No. 138326

Seq. ID LIB22-068-Q1-E1-D1

Method BLASTN
NCBI GI g2618605
BLAST score 357
E value 0.0e+00



Match length 357 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
MUK11, complete sequence [Arabidopsis thaliana]

Seq. No. 138327

Seq. ID LIB22-068-Q1-E1-D11

Method BLASTX
NCBI GI g3482975
BLAST score 168
E value 8.0e-12
Match length 107
% identity 35

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 138328

Seq. ID LIB22-068-Q1-E1-D4

Method BLASTX
NCBI GI g2493318
BLAST score 221
E value 5.0e-18
Match length 110
% identity 44

NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_

(Z25471) blue copper protein [Pisum sativum]

>gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]

Seq. No. 138329

Seq. ID LIB22-068-Q1-E1-E4

Method BLASTX
NCBI GI g3522929
BLAST score 411
E value 3.0e-40
Match length 84
% identity 95

NCBI Description (AC002535) putative dTDP-glucose 4-6-dehydratase

[Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 138330

Seq. ID LIB22-068-Q1-E1-E9

Method BLASTX
NCBI GI g3386546
BLAST score 500
E value 1.0e-50
Match length 129
% identity 77

NCBI Description (AF079503) H-protein promoter binding factor-2a

[Arabidopsis thaliana]

Seq. No. 138331

Seq. ID LIB22-068-Q1-E1-F8

Method BLASTX
NCBI GI g2129652
BLAST score 574
E value 2.0e-59
Match length 117



```
% identity
NCBI Description myosin heavy chain homolog - Arabidopsis thaliana
                  (fragment) >gi 699495 (U19616) myosin heavy chain homolog
                  [Arabidopsis thaliana]
Seq. No.
                  138332
Seq. ID
                  LIB22-068-Q1-E1-G11
Method
                 BLASTN
NCBI GI
                 q2833627
BLAST score
                 85
E value
                  1.0e-40
Match length
                  85
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome 1 BAC F1707 complete
                  sequence [Arabidopsis thaliana]
Seq. No.
                  138333
                 LIB22-068-Q1-E1-G9
Seq. ID
Method
                 BLASTX
NCBI GI
                 g2462836
BLAST score
                 527
                 5.0e-54
E value
Match length
                 116
                  88
% identity
NCBI Description (AF000657) beta-glucanase [Arabidopsis thaliana]
Seq. No.
                  138334
Seq. ID
                 LIB22-068-Q1-E1-H11
Method
                 BLASTX
NCBI GI
                  q1172873
BLAST score
                  255
                  5.0e-22
E value
Match length
                  112
% identity
                  49
NCBI Description CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir_
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi 435619 dbj BAA02374
                  (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.
                  138335
Seq. ID
                  LIB22-068-Q1-E1-H2
Method
                  BLASTX
NCBI GI
                  q2580440
BLAST score
                  251
E value
                  2.0e-21
Match length
                 61
% identity
                  77
NCBI Description (D87261) PCF2 [Oryza sativa]
Seq. No.
                  138336
Seq. ID
              - LIB22-069-Q1-E1-E5
Method
                 BLASTX
```

Method BLASTX
NCBI GI g3860420
BLAST score 143
E value 7.0e-09
Match length 40
% identity 72





NCBI Description (AJ011047) exo galactanase [Lupinus angustifolius]

Seq. No. 138337

Seq. ID LIB22-069-Q1-E1-E8

Method BLASTX
NCBI GI g2352492
BLAST score 366
E value 5.0e-35
Match length 69
% identity 100

NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis

thaliana] >gi_2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]

Seq. No. 138338

Seq. ID LIB22-069-Q1-E1-F3

Method BLASTN
NCBI GI g3738275
BLAST score 69
E value 1.0e-30
Match length 177
% identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC F17A22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138339

Seq. ID LIB22-069-Q1-E1-F6

Method BLASTX
NCBI GI g1708420
BLAST score 100
E value 5.0e-40
Match length 123
% identity 75

NCBI Description ISOFLAVONE REDUCTASE HOMOLOG P3 >gi_1361992 pir S57613

isoflavonoid reductase homolog - Arabidopsis thaliana >gi 886432_emb CAA89859 (Z49777) isoflavonoid reductase

homologue [Arabidopsis thaliana]

Seq. No. 138340

Seq. ID LIB22-069-Q1-E1-H3

Method BLASTX
NCBI GI g1084338
BLAST score 619
E value 1.0e-64
Match length 117
% identity 100

NCBI Description drought-induced protein Dr4 - Arabidopsis thaliana

>gi_469114_emb_CAA55323_ (X78586) Dr4 [Arabidopsis

thaliana]

Seq. No. 138341

Seq. ID LIB22-070-Q1-E1-A1

Method BLASTN
NCBI GI g4584519
BLAST score 217
E value 1.0e-119
Match length 337



% identity 99 NCBI Description Arabidopsis thaliana DNA o

CBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18

(ESSA project)

Seq. No. 138342

Seq. ID LIB22-070-Q1-E1-A11

Method BLASTN
NCBI GI 94220631
BLAST score 393
E value 0.0e+00
Match length 397
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K5J14, complete sequence [Arabidopsis thaliana]

Seq. No. 138343

Seq. ID LIB22-070-Q1-E1-C6

Method BLASTN
NCBI GI g3702731
BLAST score 176
E value 2.0e-94
Match length 244
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MFC19, complete sequence [Arabidopsis thaliana]

Seq. No. 138344

Seq. ID LIB22-070-Q1-E1-C8

Method BLASTX
NCBI GI g4678943
BLAST score 362
E value 1.0e-34
Match length 126
% identity 64

NCBI Description (AL049711) putative protein [Arabidopsis thaliana]

Seq. No. 138345

Seq. ID LIB22-070-Q1-E1-D6

Method BLASTN
NCBI GI g2880038
BLAST score 353
E value 0.0e+00
Match length 360
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T11J7 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138346

Seq. ID LIB22-070-Q1-E1-E1

Method BLASTN
NCBI GI g4454004
BLAST score 327
E value 0.0e+00
Match length 335
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6

(ESSAII project)



```
Seq. No.
                  138347
Seq. ID
                  LIB22-070-Q1-E1-E5
Method
                  BLASTN
NCBI GI
                  q2815519
BLAST score
                  120
E value
                  6.0e-61
Match length
                  190
% identity
NCBI Description
                  Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  138348
Seq. ID
                  LIB22-070-Q1-E1-F11
Method
                  BLASTX
NCBI GI
                  q2335099
BLAST score
                  271
                  7.0e-24
E value
Match length
                  84
% identity
                  60
NCBI Description
                  (AC002339) unknown protein [Arabidopsis thaliana]
Seq. No.
                  138349
Seq. ID
                  LIB22-070-Q1-E1-F2
Method
                  BLASTN
NCBI GI
                  q2062153
BLAST score
                  104
E value
                  6.0e-52
Match length
                  108
                  99
% identity
NCBI Description Arabidopsis thaliana chromosome III BAC T02004 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138350
Seq. ID
                  LIB22-070-Q1-E1-F5
Method
                  BLASTN
NCBI GI
                  q2827513
BLAST score
                  58
E value
                  8.0e-25
Match length
                  58
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16
NCBI Description
                  (ESSAII project)
Seq. No.
                  138351
Seq. ID
                  LIB22-070-Q1-E1-G8
Method
                  BLASTX
                  g3056591
                  229
                  6.0e-19
```

NCBI GI BLAST score E value Match length 130 % identity 44

(AC004255) T1F9.12 [Arabidopsis thaliana] NCBI Description

Seq. No. 138352

Seq. ID LIB22-070-Q1-E1-H10

Method BLASTX

```
NCBI GI
                   q3876712
BLAST score
                   207
E value
                   2.0e-16
Match length
                   81
% identity
                   51
NCBI Description
                   (Z46242) similar to malonyl-COA decarboxylase
                   [Caenorhabditis elegans]
Seq. No.
                   138353
Seq. ID
                   LIB22-071-Q1-E1-A2
Method
                   BLASTN
NCBI GI
                   g3702315
BLAST score
                   251
E value
                   1.0e-139
Match length
                   263
% identity
                   99
NCBI Description Arabidopsis thaliana chromosome II BAC T3F17 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   138354
Seq. ID
                  LIB22-071-Q1-E1-F1
Method
                  BLASTX
NCBI GI
                   q4678924
BLAST score
                   155
E value
                   3.0e-10
Match length
                  108
% identity
                   35
NCBI Description
                  (AL049711) putative protein [Arabidopsis thaliana]
Seq. No.
                  138355
Seq. ID
                  LIB22-071-Q1-E1-G3
Method
                  BLASTX
NCBI GI
                  g166765
BLAST score
                  591
E value
                  2.0e-61
Match length
                  114
% identity
                  99
NCBI Description
                  (M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]
Seq. No.
                  138356
Seq. ID
                  LIB22-071-Q1-E1-H3
Method
                  BLASTN
NCBI GI
                  g4755185
BLAST score
                  338
E value
                  0.0e+00
Match length
                  338
% identity
                  50
                  Arabidopsis thaliana chromosome II BAC F5G3 genomic
NCBI Description
                  sequence, complete sequence
```

Seq. ID LIB22-073-Q1-E1-A1

Method BLASTX NCBI GI g1864017 BLAST score 439 E value 1.0e-43 Match length 85

```
% identity
NCBI Description
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                  138358
Seq. ID
                  LIB22-073-Q1-E1-B3
Method
                  BLASTX
NCBI GI
                  g2894574
BLAST score
                  427
E value
                  2.0e-42
Match length
                  81
% identity
                  100
NCBI Description
                  (AL021890) peroxidase prxr1 [Arabidopsis thaliana]
                  >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1
                  [Arabidopsis thaliana]
Seq. No.
                  138359
Seq. ID
                  LIB22-073-Q1-E1-C8
                  BLASTN
                  q2760169
                  222
```

Method NCBI GI BLAST score E value 1.0e-122 Match length 348 % identity 100

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MFB13, complete sequence [Arabidopsis thaliana]

Seq. ID LIB22-073-Q1-E1-F3 Method BLASTX NCBI GI g3953458 BLAST score 564 E value 2.0e-58 Match length 110

138360

% identity 98

Seq. No.

NCBI Description (AC002328) F20N2.3 [Arabidopsis thaliana]

Seq. No. 138361

Seq. ID LIB22-073-Q1-E1-F5

Method BLASTX NCBI GI g3212869 BLAST score 535 E value 6.0e-55 Match length 104 % identity 99

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

138362 Seq. No.

Seq. ID LIB22-073-Q1-E1-G2

Method BLASTN NCBI GI g4220633 BLAST score 106 E value 5.0e-53 Match length 106 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K7J8, complete sequence [Arabidopsis thaliana]

BLAST score

Match length

% identity

E value

493

113

84

5.0e~50



```
Seq. No.
                  138363
Seq. ID
                  LIB22-073-Q1-E1-H5
Method
                  BLASTX
NCBI GI
                  g1170089
BLAST score
                  557
E value
                  2.0e-57
Match length
                  109
% identity
                  100
NCBI Description GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)
                  >gi_481822_pir__S39542 probable glutathione transferase (EC
                  2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789 dbj_BAA04554 (D17673) glutathione S-transferase
                   [Arabidopsis thaliana] >gi 3201614 (AC004669) glutathione
                  S-transferase [Arabidopsis thaliana]
Seq. No.
                  138364
                  LIB22-074-Q1-E1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267073
BLAST score
                  577
E value
                  9.0e-60
Match length
                  107
% identity
                  98
NCBI Description TUBULIN BETA-2/BETA-3 CHAIN >gi 320184 pir JQ1587 tubulin
                  beta chain - Arabidopsis thaliana >gi 166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
                  138365
Seq. No.
Seq. ID
                  LIB22-074-Q1-E1-B10
Method
                  BLASTX
NCBI GI
                  g2827716
BLAST score
                   401
E value
                  3.0e-39
Match length
                  81
% identity
                  98
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.
                  138366
Seq. ID
                  LIB22-074-Q1-E1-B2
Method
                  BLASTX
NCBI GI
                  g4263718
BLAST score
                  673
                  4.0e-71
E value
Match length
                  120
                  100
% identity
NCBI Description (AC006223) putative DNA topoisomerase III beta [Arabidopsis
                  thaliana]
Seq. No.
                  138367
Seq. ID
                  LIB22-074-Q1-E1-B8
Method
                  BLASTX
NCBI GI
                  g3080415
```

```
NCBI Description
                  (AL022604) cysteine proteinase-like protein [Arabidopsis
                  thaliana]
                  138368
Seq. No.
                  LIB22-074-Q1-E1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2961284
BLAST score
                  229
E value
                  3.0e-37
Match length
                  88
% identity
                  91
NCBI Description
                  (Y16848) cinnamyl alcohol dehydrogenase-like protein,
                  subunit a [Arabidopsis thaliana] >gi 4467103 emb CAB37537
                   (AL035538) cinnamyl alcohol dehydrogenase-like protein,
                  LCADa [Arabidopsis thaliana]
Seq. No.
                  138369
Seq. ID
                  LIB22-074-Q1-E1-E11
Method
                  BLASTX
NCBI GI
                  g1076662
BLAST score
                  495
E value
                  3.0e-50
Match length
                  129
% identity
                  72
                  H+-transporting ATPase (EC 3.6.1.35) (clone PHA1) - potato
NCBI Description
                  >gi_435003_emb_CAA54046_ (X76536) H(+)-transporting ATPase
                  [Solanum tuberosum]
Seq. No.
                  138370
Seq. ID
                  LIB22-074-Q1-E1-E3
Method
                  BLASTX
NCBI GI
                  g2650102
BLAST score
                  161
                  5.0e-11
E value
Match length
                  126
% identity
                  36
NCBI Description
                  (AE001068) cell division control protein 21 (cdc21)
                  [Archaeoglobus fulgidus]
Seq. No.
                  138371
Seq. ID
                  LIB22-074-Q1-E1-E5
Method
                  BLASTN
NCBI GI
                  q4159707
BLAST score
                  113
E value
                  8.0e-57
Match length
                  314
% identity
                  96
```

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MJK13, complete sequence

Seq. No. 138372

Seq. ID LIB22-074-Q1-E1-G10

Method BLASTN NCBI GI g4263038 BLAST score 34 E value 4.0e-10 Match length 74



```
% identity
 NCBI Description
                    Arabidopsis thaliana BAC T5L23 from chromosome IV, near 19
                    cM, complete sequence [Arabidopsis thaliana]
                    138373
 Seq. No.
                    LIB22-074-Q1-E1-G12
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g4733953
. BLAST score
                    67
                    2.0e-29
 E value
 Match length
                    246
 % identity
                    90
 NCBI Description
                   Arabidopsis thaliana chromosome I BAC F13011 genomic
                    sequence, complete sequence
 Seq. No.
                    138374
                    LIB22-074-Q1-E1-H3
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    q4539448
                    155
 BLAST score
 E value
                    9.0e-82
 Match length
                    392
 % identity
                    100
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23
                    (ESSA project)
                    138375
 Seq. No.
                    LIB22-075-Q1-E1-A4
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q4522004
 BLAST score
                    512
 E value
                    3.0e-52
 Match length
                    110
 % identity
                    95
                    (AC007069) putative histidine kinase, sensory transduction
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    138376
 Seq. ID
                    LIB22-075-Q1-E1-A8
 Method
                    BLASTN
 NCBI GI
                    q3869073
 BLAST score
                    346
                    0.0e+00
 E value
 Match length
                    346
 % identity
                    100
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                    MKN22, complete sequence [Arabidopsis thaliana]
```

LIB22-075-Q1-E1-B4 Seq. ID

Method BLASTX NCBI GI q585453 BLAST score 267 E value 9.0e-24Match length 85 % identity 66

NCBI Description MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT

MALIC ENZYME) (NADP-ME) >gi_1084300_pir__S43718 malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - common ice plant >gi_432380_emb_CAA45772_ (X64434) malate dehydrogenase (oxaloacetate decarboxylating) (NADP+) [Mesembryanthemum crystallinum]

Seq. No. 138378

Seq. ID LIB22-075-Q1-E1-C7

Method BLASTN
NCBI GI g4210448
BLAST score 100
E value 3.0e-49
Match length 128
% identity 93

NCBI Description Arabidopsis thaliana gene for ARR1 protein, complete cds

Seq. No. 138379

Seq. ID LIB22-075-Q1-E1-D8

Method BLASTN
NCBI GI g3128142
BLAST score 206
E value 1.0e-112
Match length 403
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQN23, complete sequence [Arabidopsis thaliana]

Seq. No. 138380

Seq. ID LIB22-075-Q1-E1-F4

Method BLASTN
NCBI GI g3241917
BLAST score 150
E value 3.0e-79
Match length 162
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19B1, complete sequence [Arabidopsis thaliana]

Seq. No. 138381

Seq. ID LIB22-075-Q1-E1-H7

Method BLASTX
NCBI GI g2979554
BLAST score 491
E value 8.0e-50
Match length 108
% identity 86

NCBI Description (AC003680) CDC4 like protein [Arabidopsis thaliana]

Seq. No. 138382

Seq. ID LIB22-075-Q1-E1-H8

Method BLASTX
NCBI GI g3033379
BLAST score 189
E value 2.0e-14
Match length 55
% identity 65

NCBI Description (AC004238) putative DNA-binding protein [Arabidopsis



```
138383
Seq. No.
Seq. ID
                  LIB22-076-Q1-E1-B7
Method
                  BLASTN
NCBI GI
                  g2264316
BLAST score
                  167
E value
                  4.0e-89
Match length
                  192
% identity
                  96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRO11, complete sequence [Arabidopsis thaliana]
                  138384
Seq. No.
Seq. ID
                  LIB22-076-Q1-E1-D1
Method
                  BLASTN
NCBI GI
                  q2245031
BLAST score
                  148
E value
                  2.0e-77
Match length
                  434
% identity
                  96
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
                  138385
Seq. No.
Seq. ID
                  LIB22-076-Q1-E1-E10
Method
                  BLASTX
NCBI GI
                  g4539004
BLAST score
                  245
E value
                  6.0e-21
Match length
                  61
% identity
                  72
NCBI Description
                  (AL049481) putative protein kinase [Arabidopsis thaliana]
                  138386
Seq. No.
Seq. ID
                  LIB22-076-Q1-E1-E11
Method
                  BLASTN
NCBI GI
                  q1946354
BLAST score
                  78
E value
                  7.0e-36
Match length
                  198
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T06B20 genomic
                  sequence, complete sequence
Seq. No.
                  138387
Seq. ID
                  LIB22-076-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                  q1531762
BLAST score
                  195
E value
                  7.0e-15
Match length
                  51
% identity
                  75
```

thaliana]
Seq. No. 138388

NCBI Description

16653

(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis

Seq. ID LIB22-076-01-E1-G9

Method BLASTX NCBI GI q3080435 BLAST score 527 5.0e-54 E value Match length 100 % identity 100

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 138389

Seq. ID LIB22-077-Q1-E1-A11

Method BLASTX NCBI GI q2738248 BLAST score 377 2.0e-36 E value Match length 79 % identity 90

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No. 138390

Seq. ID LIB22-077-Q1-E1-D12

Method BLASTN NCBI GI g3892698 BLAST score 201 E value 1.0e-109 Match length 201 % identity 45

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2

(ESSAII project)

Seq. No. 138391

LIB22-078-Q1-E1-A7 Seq. ID

Method BLASTX NCBI GI g99742 BLAST score 202 E value 8.0e-16 Match length 121 % identity 40

NCBI Description 2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 1

- Arabidopsis thaliana

Seq. No. Seq. ID 138392

LIB22-078-Q1-E1-C8

Method BLASTX NCBI GI g3122753 BLAST score 504 E value 3.0e-51 Match length 92 % identity 100

NCBI Description 60S RIBOSOMAL PROTEIN L44 >gi 2244789 emb CAB10211.1

(Z97336) ribosomal protein [Arabidopsis thaliana]

Seq. No. 138393

Seq. ID LIB22-078-Q1-E1-E2

Method BLASTX NCBI GI g3434965



BLAST score 279
E value 7.0e-25
Match length 110
% identity 47

NCBI Description (AB002530) mus-23 [Neurospora crassa]

Seq. No. 138394

Seq. ID LIB22-078-Q1-E1-F5

Method BLASTX
NCBI GI 94588008
BLAST score 297
E value 2.0e-27
Match length 82
% identity 63

NCBI Description (AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No. 138395

Seq. ID LIB22-078-Q1-E1-G2

Method BLASTX
NCBI GI g3482978
BLAST score 598
E value 2.0e-62
Match length 114
% identity 100

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 138396

Seq. ID LIB22-078-Q1-E1-G3

Method BLASTN
NCBI GI g3869074
BLAST score 245
E value 1.0e-135
Match length 396
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MMI9, complete sequence [Arabidopsis thaliana]

Seq. No. 138397

Seq. ID LIB22-078-Q1-E1-H7

Method BLASTN
NCBI GI g2618602
BLAST score 133
E value 9.0e-69
Match length 284
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 138398

Seq. ID LIB22-078-Q1-E1-H9

Method BLASTX
NCBI GI g1652057
BLAST score 190
E value 1.0e-14
Match length 65
% identity 57

NCBI Description (D90902) hypothetical protein [Synechocystis sp.]



Seq. ID LIB22-079-Q1-E1-A3

Method BLASTN NCBI GI g4235150 BLAST score 58 E value 2.0e-24 Match length 101 99 % identity

NCBI Description Arabidopsis thaliana chromosome I BAC T25B24 genomic

sequence, complete sequence

Seq. No. 138400

Seq. ID LIB22-079-Q1-E1-A4

Method BLASTN NCBI GI a3582315 BLAST score 346 E value 0.0e+00Match length 346 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T27A16 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138401

Seq. ID LIB22-079-Q1-E1-B3

Method BLASTN NCBI GI g1890129 BLAST score 217 E value 1.0e-119 Match length 228 % identity

NCBI Description Arabidopsis thaliana valyl tRNA synthetase (valRS) mRNA,

complete cds

Seq. No. Seq. ID 138402

LIB22-079-Q1-E1-B8

Method BLASTN NCBI GI g3702728 BLAST score 340 0.0e+00E value Match length 361 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19M13, complete sequence [Arabidopsis thaliana]

Seq. No. 138403

Seq. ID LIB22-079-Q1-E1-B9

Method BLASTN NCBI GI g3687221 BLAST score 413 E value 0.0e + 00Match length 417 100 % identity

Arabidopsis thaliana chromosome II BAC F6F22 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138404



Seq. ID LIB22-079-Q1-E1-F1

Method BLASTN
NCBI GI g2618683
BLAST score 56
E value 8.0e-23
Match length 184

NCBI Description Arabidopsis thaliana chromosome II BAC T32G6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138405

% identity

Seq. ID LIB22-080-Q1-E2-D10

Method BLASTX
NCBI GI g2244750
BLAST score 542
E value 1.0e-55
Match length 118
% identity 88

NCBI Description (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]

>gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase

[Arabidopsis thaliana]

Seq. No. 138406

Seq. ID LIB22-080-Q1-E2-D5

Method BLASTX
NCBI GI g3335368
BLAST score 176
E value 7.0e-13
Match length 107
% identity 41

NCBI Description (AC003028) hypothetical protein [Arabidopsis thaliana]

Seq. No. 138407

Seq. ID LIB22-080-Q1-E2-D6

Method BLASTX
NCBI GI g4581205
BLAST score 128
E value 2.0e-07
Match length 82
% identity 93

NCBI Description (Y17913) cyclic nucleotide and calmodulin-regulated ion

channel [Arabidopsis thaliana]

Seq. No. 138408

Seq. ID LIB22-080-Q1-E2-F12

Method BLASTX
NCBI GI g4512653
BLAST score 603
E value 7.0e-63
Match length 122
% identity 100

NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]

Seq. No. 138409

Seq. ID LIB22-080-Q1-E2-G2

Method BLASTN NCBI GI g3184270



BLAST score E value 6.0e-86 Match length 365 99 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC T8K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138410

Seq. ID LIB22-081-Q1-E1-C8

Method BLASTX NCBI GI g4033469 BLAST score 199 2.0e-15 E value Match length 40 % identity 93

NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP41

>gi_1707370_emb_CAA67799_ (X99436) splicing factor

[Arabidopsis thaliana]

Seq. No. 138411

Seq. ID LIB22-081-Q1-E1-D1

Method BLASTX NCBI GI q1175011 BLAST score 406 E value 6.0e-40 Match length 76 % identity 100

NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN

A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665)

plasma membrane intrinsic protein 1B [Arabidopsis thaliana]

Seq. No. 138412

Seq. ID LIB22-081-Q1-E2-A2

Method BLASTN NCBI GI g4490734 BLAST score 105 E value 3.0e-52 Match length 194 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone

project)

Seq. No. 138413

Seq. ID LIB22-081-Q1-E2-A6

Method BLASTN NCBI GI g2337888 BLAST score 196 E value 1.0e-106 Match length 421 % identity 98

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14J16,

complete sequence [Arabidopsis thaliana]

Seq. No. 138414

LIB22-081-Q1-E2-D5 Seq. ID

Method BLASTN



```
NCBI GI
                   q2462780
BLAST score
                   325
E value
                  0.0e + 00
Match length
                   333
% identity
                  100
NCBI Description
                  Arabidopsis thaliana carbamoyl phosphate synthetase small
                  subunit mRNA (carA), complete cds
Seq. No.
                  138415
Seq. ID
                  LIB22-081-Q1-E2-D7
Method
                  BLASTX
NCBI GI
                  q4454048
BLAST score
                  585
E value
                  1.0e-60
Match length
                  119
                  90
% identity
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                  138416
                  LIB22-081-Q1-E2-E4
Seq. ID
Method
                - BLASTN
NCBI GI
                  g2244829
BLAST score
                  143
E value
                  4.0e-75
Match length
                  143
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  138417
Seq. ID
                  LIB22-081-Q1-E2-E6
Method
                  BLASTN
NCBI GI
                  g2244829
BLAST score
                  143
E value
                  5.0e-75
Match length
                  143
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  138418
Seq. ID
                  LIB22-081-Q1-E2-G12
Method
                  BLASTN
NCBI GI
                  g3212846
BLAST score
                  107
E value
                  1.0e-53
Match length
                  115
% identity
                  98
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
```

Seq. ID LIB22-082-Q1-E1-A8

Method BLASTX NCBI GI g4455342 BLAST score 678 E value 1.0e-71

% identity

NCBI Description

98

complete cds



```
Match length
% identity
                   99
                   (AL035522) O-methyltransferase-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  138420
Seq. ID
                  LIB22-082-Q1-E1-B6
Method
                  BLASTX
NCBI GI
                  q2623962
BLAST score
                  427
E value
                   4.0e-42
Match length
                  91
% identity
                  91
                  (Y12540) isocitrate dehydrogenase (NADP+) [Apium
NCBI Description
                  graveolens]
Seq. No.
                  138421
Seq. ID
                  LIB22-082-Q1-E1-G5
Method
                  BLASTX
NCBI GI
                  g3212877
BLAST score
                  509
                  8.0e-52
E value
Match length
                  116
% identity
                  89
                  (AC004005) Lea-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  138422
Seq. ID
                  LIB22-082-Q1-E1-G7
Method
                  BLASTX
NCBI GI
                  q2760330
BLAST score
                   340
E value
                   5.0e-32
Match length
                  85
% identity
                  74
NCBI Description (AC002130) F1N21.15 [Arabidopsis thaliana]
Seq. No.
                  138423
Seq. ID
                  LIB22-082-Q1-E2-C8
Method
                  BLASTX
NCBI GI
                  q4262225
BLAST score
                   339
E value
                   9.0e-32
Match length
                  116
% identity
                  54
NCBI Description
                   (AC006200) putative phosphatidic acid phosphatase
                   [Arabidopsis thaliana]
Seq. No.
                  138424
Seq. ID
                  LIB22-082-Q1-E2-E10
Method
                  BLASTN
NCBI GI
                  g2618720
BLAST score
                  46
                  8.0e-17
E value
Match length
                  85
```

16660

Arabidopsis thaliana early auxin-induced (IAA16) mRNA,



```
Seq. No.
                  138425
Seq. ID
                  LIB22-082-Q1-E2-E12
Method
                  BLASTX
NCBI GI
                  g3738339
BLAST score
                  331
E value
                  7.0e-31
Match length
                  136
% identity
                  51
NCBI Description (AC005170) putative kinase [Arabidopsis thaliana]
                  138426
Seq. No.
Seq. ID
                  LIB22-082-Q1-E2-H1
Method
                  BLASTN
                  g4589426
NCBI GI
BLAST score
                  250
E value
                  1.0e-138
Match length
                  339
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDE13, complete sequence
Seq. No.
                  138427
Seq. ID
                  LIB22-083-Q1-E2-C11
Method
                  BLASTX
                  q4033365
NCBI GI
BLAST score
                  763
E value
                  2.0e-81
Match length
                  148
% identity
                  96
NCBI Description (AJ223499) ATP sulfurylase [Brassica juncea]
                  138428
Seq. No.
Seq. ID
                  LIB22-083-Q1-E2-D9
                  BLASTN
Method
NCBI GI
                  g2245031
BLAST score
                  85
                  3.0e-40
E value
Match length
                  217
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  138429
Seq. ID
                  LIB22-083-Q1-E2-E12
Method
                  BLASTX
NCBI GI
                  g3785981
BLAST score
                  776
                  5.0e-83
E value
Match length
                  142
                  100
% identity
NCBI Description (AC005560) putative major latex protein [Arabidopsis
                  thaliana]
```

Seq. No. 138430 Seq. ID LIB22-083-Q1-E2-G11

Method BLASTN



```
NCBI GI
                   q3004543
BLAST score
                   115
E value
                   8.0e-58
Match length
                   457
% identity
                   100
                  Arabidopsis thaliana chromosome II BAC F19F24 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138431
Seq. ID
                  LIB22-083-Q1-E2-H1
Method
                  BLASTN
NCBI GI
                  q4589430
BLAST score
                  103
E value
                   6.0e-51
                  235
Match length
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MLD14, complete sequence
Seq. No.
                  138432
                  LIB22-084-Q1-E1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3776578
BLAST score
                  238
                  5.0e-20
E value
Match length
                  94
% identity
                  50
NCBI Description
                  (AC005388) ESTs gb F13915 and gb F13916 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  138433
Seq. ID
                  LIB22-084-Q1-E1-C11
Method
                  BLASTX
NCBI GI
                  q1709698
BLAST score
                  143
E value
                  7.0e-09
Match length
                  55
% identity
                   49
NCBI Description
                  POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (POLYNUCLEOTIDE
                  PHOSPHORYLASE) (PNPASE) (VEGETATIVE PROTEIN 15) (VEG15)
                  >gi_2127172_pir__S70691 polynucleotide phosphorylase -
                  Bacillus subtilis >gi 1184680 (U29668) polynucleotide
                  phosphorylase [Bacillus subtilis] >gi_2634041_emb_CAB13542_
                   (Z99112) polynucleotide phosphorylase (PNPase) [Bacillus
                  subtilis] >gi_1589234_prf__2210369A polynucleotide
                  phosphorylase [Bacillus subtilis]
Seq. No.
                  138434
Seq. ID
                  LIB22-084-Q1-E1-D7
Method
                  BLASTN
NCBI GI
                  q2564050
BLAST score
                  141
```

E value 2.0e-73 Match length 312 % identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Method

NCBI GI

BLASTX

g1943751



```
138435
Seq. No.
Seq. ID
                  LIB22-084-Q1-E1-E10
                  BLASTX
Method
NCBI GI
                  g4454051
BLAST score
                  237
                  2.0e-20
E value
                  74
Match length
% identity
                  58
NCBI Description
                  (AL035394) putative polygalacturonase [Arabidopsis
                  thaliana]
Seq. No.
                  138436
Seq. ID
                  LIB22-084-Q1-E1-F10
Method
                  BLASTN
NCBI GI
                  q1871502
BLAST score
                  297
E value
                  1.0e-166
Match length
                  305
                  99
% identity
NCBI Description A.thaliana bfruct4 gene
Seq. No.
                  138437
Seq. ID
                  LIB22-084-Q1-E1-F12
Method
                  BLASTX
NCBI GI
                  q1483177
BLAST score
                  328
E value
                  1.0e-30
Match length
                  114
% identity
                  53
NCBI Description
                  (D86598) antifreeze-like protein (af70) [Picea abies]
Seq. No.
                  138438
Seq. ID
                  LIB22-085-Q1-E1-C11
Method
                  BLASTX
NCBI GI
                  g2895510
BLAST score
                  495
                  4.0e-50
E value
Match length
                  132
% identity
                  77
                  (AF033204) putative pectin methylesterase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  138439
Seq. ID
                  LIB22-085-Q1-E1-F11
Method
                  BLASTX
NCBI GI
                  g3329368
BLAST score
                  162
E value
                  2.0e-11
Match length
                  37
                  78
% identity
                  (AF031244) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  138440
Seq. ID
                  LIB22-085-Q1-E2-A6
```



BLAST score 246 E value 2.0e-21 Match length 62 % identity 76

NCBI Description (U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi_2078292 (U96455) ER-type

Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No. 138441

Seq. ID LIB22-085-Q1-E2-C4

Method BLASTX
NCBI GI g135535
BLAST score 455
E value 2.0e-45
Match length 94
% identity 98

NCBI Description T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)

(CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_(D11351) t-complex polypeptide 1 homologue [Arabidopsis

thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT

alpha/TCP-1 [Arabidopsis thaliana]

Seq. No. 138442

Seq. ID LIB22-085-Q1-E2-G12

Method BLASTX
NCBI GI g4587685
BLAST score 677
E value 2.0e-71
Match length 132
% identity 99

NCBI Description (AC007197) putative methylmalonate semi-aldehyde

dehydrogenase [Arabidopsis thaliana]

Seq. No. 138443

Seq. ID LIB22-086-Q1-E1-A10

Method BLASTX
NCBI GI g2462746
BLAST score 212
E value 4.0e-17
Match length 91
% identity 93

NCBI Description (AC002292) Similar to ATP-citrate-lyase [Arabidopsis

thaliana]

Seq. No. 138444

Seq. ID LIB22-086-Q1-E1-B2

Method BLASTN
NCBI GI g3985934
BLAST score 243
E value 1.0e-134
Match length 372
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJE7, complete sequence [Arabidopsis thaliana]



```
Seq. ID LIB22-086-Q1-E1-C9
```

Method BLASTN
NCBI GI g1490552
BLAST score 206
E value 1.0e-112
Match length 206
% identity 100

NCBI Description Arabidopsis thaliana S-adenosylmethionine decarboxylase

(SAMdc) mRNA, complete cds

Seq. No. 138446

Seq. ID LIB22-086-Q1-E1-D3

Method BLASTN
NCBI GI g2275194
BLAST score 231
E value 1.0e-127
Match length 312
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC T08I13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138447

Seq. ID LIB22-086-Q1-E1-E1

Method BLASTX
NCBI GI g1402908
BLAST score 444
E value 3.0e-44
Match length 101
% identity 85

NCBI Description (X98315) peroxidase [Arabidopsis thaliana]

>gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a

[Arabidopsis thaliana] >gi_4455802_emb_CAB37193 (AJ133036)

peroxidase [Arabidopsis thaliana]

Seq. No. 138448

Seq. ID LIB22-086-Q1-E1-E12

Method BLASTN
NCBI GI g2477521
BLAST score 122
E value 1.0e-62
Match length 122
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138449

Seq. ID LIB22-086-Q1-E1-E8

Method BLASTN
NCBI GI g2564050
BLAST score 223
E value 1.0e-122
Match length 307
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUA22, complete sequence [Arabidopsis thaliana]



```
Seq. ID
                   LIB22-086-Q1-E1-F6
Method
                  BLASTX
NCBI GI
                   q4713953
BLAST score
                   638
E value
                  7.0e-67
Match length
                   129
% identity
                   94
NCBI Description
                   (AC007293) subtilisin-like protease, 3' partial
                   [Arabidopsis thaliana]
Seq. No.
                  138451
Seq. ID
                  LIB22-086-Q1-E1-G5
Method
                  BLASTN
NCBI GI
                  q4753645
BLAST score
                  360
E value
                  0.0e + 00
Match length
                  360
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18
                   (ESSA project)
Seq. No.
                  138452
Seq. ID
                  LIB22-086-Q1-E1-G6
Method
                  BLASTN
NCBI GI
                  q2618602
BLAST score
                  420
E value
                  0.0e + 00
Match length
                  420
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138453
Seq. ID
                  LIB22-086-Q1-E1-H1
Method
                  BLASTX
NCBI GI
                  g4455342
BLAST score
                  354
                  9.0e-34
E value
Match length
                   64
% identity
                  100
                   (AL035522) O-methyltransferase-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  138454
Seq. ID
                  LIB22-086-Q1-E1-H10
Method
                  BLASTN
NCBI GI
                  g3063690
BLAST score
                  215
E value
                  1.0e-117
                  343
Match length
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11
NCBI Description
                   (ESSAII project)
```

(BOORII

Seq. ID LIB22-086-Q1-E1-H7

138455

Method BLASTX

E value

Match length

% identity

3.0e-58

106 100



```
NCBI GI
                  g3063445
BLAST score
                  182
E value
                  2.0e-13
Match length
                  118
% identity
NCBI Description
                 (AC003981) F22013.7 [Arabidopsis thaliana]
Seq. No.
                  138456
                  LIB22-087-Q1-E1-A1
Seq. ID
Method
                  BLASTN
                  g3242970
NCBI GI
BLAST score
                  164
E value
                  2.0e-87
Match length
                  164
% identity
                  100
                  Arabidopsis thaliana BAC T4I9, chromosome IV, near 17 cM,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  138457
                  LIB22-087-Q1-E1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3860243
BLAST score
                  61
                  4.0e-26
E value
Match length
                  145
                  86
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F15K20 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138458
Seq. ID
                  LIB22-087-Q1-E1-A6
Method
                  BLASTX
NCBI GI
                  g4680643
BLAST score
                  161
                  6.0e-11
E value
Match length
                  101
% identity
                  36
                 (AF132936) CGI-01 protein [Homo sapiens]
NCBI Description
Seq. No.
                  138459
Seq. ID
                  LIB22-087-Q1-E1-B6
Method
                  BLASTX
NCBI GI
                  g4454032
BLAST score
                  381
E value
                  9.0e-37
                  118
Match length
% identity
                  64
                 (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  138460
                  LIB22-087-Q1-E1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1707011
BLAST score
                  564
```



NCBI Description (U78721) auxin-repressed protein isolog [Arabidopsis thaliana]

Seq. No. 138461

Seq. ID LIB22-087-Q1-E1-C7

Method BLASTX
NCBI GI g2323410
BLAST score 292
E value 2.0e-26
Match length 138
% identity 46

NCBI Description (AF015913) Skb1Hs [Homo sapiens]

Seq. No. 138462

Seq. ID LIB22-087-Q1-E1-D2

Method BLASTX
NCBI GI g2462746
BLAST score 602
E value 1.0e-62
Match length 123
% identity 94

NCBI Description (AC002292) Similar to ATP-citrate-lyase [Arabidopsis

thaliana]

Seq. No. 138463

Seq. ID LIB22-087-Q1-E1-D6

Method BLASTN
NCBI GI g4185128
BLAST score 295
E value 1.0e-165
Match length 405
% identity 98

NCBI Description Arabidopsis thaliana chromosome II P1 MSF3 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138464

Seq. ID LIB22-087-Q1-E1-E2

Method BLASTX
NCBI GI g4585980
BLAST score 423
E value 1.0e-41
Match length 138
% identity 68

NCBI Description (AC005287) Very similar to TATA binding protein-associated

factor [Arabidopsis thaliana]

Seq. No. 138465

Seq. ID LIB22-087-Q1-E1-E6

Method BLASTX
NCBI GI g2130080
BLAST score 319
E value 2.0e-29
Match length 94
% identity 60

NCBI Description Nramp1 protein - rice >gi_1470320_bbs 177441 (S81897)

OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa,

indica, cv. IR 36, etiolated shoots, Peptide, 517 aa]





[Oryza sativa] >gi_2231132 (L41217) integral membrane protein [Oryza sativa]

Seq. No. 138466

Seq. ID LIB22-087-Q1-E1-F7

Method BLASTX
NCBI GI g2291190
BLAST score 164
E value 3.0e-11
Match length 97
% identity 25

NCBI Description (AF016422) contains similarity to TPR domains

[Caenorhabditis elegans]

Seq. No. 138467

Seq. ID LIB22-087-Q1-E1-G5

Method BLASTX
NCBI GI 94417280
BLAST score 523
E value 2.0e-53
Match length 118
% identity 90

NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No. 138468

Seq. ID LIB22-087-Q1-E1-H10

Method BLASTN
NCBI GI 94371278
BLAST score 219
E value 1.0e-120
Match length 243
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC T2N18 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138469

Seq. ID LIB22-087-Q1-E1-H2

Method BLASTN
NCBI GI g4581204
BLAST score 67
E value 7.0e-30
Match length 91
% identity 100

NCBI Description Arabidopsis thaliana mRNA for putative ion channel, cngc5

Seq. No. 138470

Seq. ID LIB22-087-Q1-E1-H8

Method BLASTN
NCBI GI g2264367
BLAST score 281
E value 1.0e-157
Match length 341
% identity 98

NCBI Description Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm,

complete sequence [Arabidopsis thaliana]



```
Seq. ID
                  LIB22-088-Q1-E1-A3
Method
                  BLASTN
NCBI GI
                  q3522932
BLAST score
                  286
E value
                  1.0e-160
Match length
                  290
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F14M4 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138472
Seq. ID
                  LIB22-088-Q1-E1-A8
Method
                  BLASTX
NCBI GI
                  q2352492
BLAST score
                  293
E value
                  1.0e-26
Match length
                  103
% identity
NCBI Description
                  (AF005047) transport inhibitor response 1 [Arabidopsis
                  thaliana] >gi 2352494 (AF005048) transport inhibitor
                  response 1 [Arabidopsis thaliana]
Seq. No.
                  138473
Seq. ID
                  LIB22-088-Q1-E1-B10
Method
                  BLASTN
NCBI GI
                  q4056429
BLAST score
                  373
E value
                  0.0e + 00
Match length
                  373
                  100
% identity
                  Arabidopsis thaliana chromosome 1 BAC F508 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  138474
Seq. ID
                  LIB22-088-Q1-E1-C3
                  BLASTN
Method
NCBI GI
                  q4455168
BLAST score
                  224
E value
                  1.0e-123
Match length
                  252
% identity
                  97
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10
                  (ESSAII project)
                  138475
Seq. No.
Seq. ID
                  LIB22-088-Q1-E1-F12
Method
                  BLASTX
```

NCBI GI q2118220 BLAST score 337 1.0e-31 E value Match length 98 71 % identity

H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain NCBI Description (clone AVA-P1) - Arabidopsis thaliana >gi 926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16

kDa proteolipid [Arabidopsis thaliana]





>gi_3096941_emb_CAA18851.1 (AL023094) vacuolar H+-transporting ATPase 16K chain [Arabidopsis thaliana]
>gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting ATPase 16K chain P2, vacuolar [Arabidopsis thaliana] >gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

```
Seq. No.
                  138476
Seq. ID
                  LIB22-088-Q1-E1-F3
Method
                  BLASTX
NCBI GI
                  g730544
BLAST score
                  162
E value
                  1.0e-11
Match length
                  64
% identity
                  66
NCBI Description 60S RIBOSOMAL PROTEIN L24
Seq. No.
                  138477
Seq. ID
                  LIB22-088-Q1-E1-G11
Method
                  BLASTX
NCBI GI
                  g2924777
BLAST score
                  123
E value
                  5.0e-29
Match length
                  91
% identity
                  77
```

NCBI Description (AC002334) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 138478 Seq. ID LIB22-088-Q1-E1-G2 Method BLASTN NCBI GI g4678266 BLAST score 205 E value 1.0e-111

Match length 366 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8

(ESSA project)

Seq. No. 138479

Seq. ID LIB22-088-Q1-E1-G9

Method BLASTX NCBI GI g1350680 BLAST score 589 E value 3.0e-61 Match length 121 % identity 94

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 138480

Seq. ID LIB22-088-Q1-E1-H12

Method BLASTN NCBI GI g4559375 BLAST score 237 1.0e-131 E value Match length 306 98 % identity



NCBI Description Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence

Seq. No. 138481

Seq. ID LIB22-089-Q1-E1-A8

Method BLASTN
NCBI GI g488786
BLAST score 65
E value 4.0e-28
Match length 169
% identity 85

NCBI Description B.oleracea putative imbibition protein mRNA

Seq. No. 138482

Seq. ID LIB22-089-Q1-E1-C12

Method BLASTX
NCBI GI g4006829
BLAST score 722
E value 9.0e-77
Match length 139
% identity 100

NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No. 138483

Seq. ID LIB22-089-Q1-E1-E8

Method BLASTN
NCBI GI g2618602
BLAST score 213
E value 1.0e-116
Match length 213
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 138484

Seq. ID LIB22-089-Q1-E1-F2

Method BLASTN
NCBI GI g3250673
BLAST score 125
E value 3.0e-64
Match length 133
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5

(ESSAII project)

Seq. No. 138485

Seq. ID LIB22-089-Q1-E1-F7

Method BLASTN
NCBI GI g3004543
BLAST score 227
E value 1.0e-125
Match length 355
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F19F24 genomic

sequence, complete sequence [Arabidopsis thaliana]



```
LIB22-089-Q1-E1-G10
Seq. ID
Method
                  BLASTX
                  g4096693
NCBI GI
BLAST score
                  221
E value
                  5.0e-18
Match length
                  65
                  100
% identity
NCBI Description
                  (U37235) cinnamate 4-hydroxylase [Arabidopsis thaliana]
                  138487
Seq. No.
                  LIB22-089-Q1-E1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3212102
BLAST score
                  174
                  5.0e-93
E value
                  419
Match length
                  100
% identity
                  Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  138488
Seq. No.
                  LIB22-089-Q1-E1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1480078
BLAST score
                  444
E value
                  3.0e-44
Match length
                  88
% identity
                  100
                  (X99696) shaggy-like protein kinase iota [Arabidopsis
NCBI Description
                  thaliana] >gi_2444277_gb_AAB71545.1_ (AF019927)
                  GSK3/shaggy-like protein kinase [Arabidopsis thaliana]
Seq. No.
                  138489
Seq. ID
                  LIB22-089-Q1-E1-H9
Method
                  BLASTX
                  g3386604
NCBI GI
BLAST score
                  202
                  7.0e-16
E value
Match length
                  107
% identity
                  36
NCBI Description
                  (AC004665) putative protein kinase [Arabidopsis thaliana]
                  138490
Seq. No.
Seq. ID
                  LIB23-001-Q1-E1-A5
Method
                  BLASTX
NCBI GI
                  q3445209
BLAST score
                  126
E value
                  3.0e-38
Match length
                  99
                  76
% identity
NCBI Description
                  (AC004786) putative serine carboxypeptidase I [Arabidopsis
                  thaliana]
```

138491 Seq. No.

Seq. ID LIB23-001-Q1-E1-C2

Method BLASTN NCBI GI g3176693



BLAST score 45 E value 2.0e-16 Match length 141 % identity 83

NCBI Description Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138492

Seq. ID LIB23-001-Q1-E1-C8

Method BLASTN
NCBI GI g3449320
BLAST score 396
E value 0.0e+00
Match length 400
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRB17, complete sequence [Arabidopsis thaliana]

Seq. No. 138493

Seq. ID LIB23-001-Q1-E1-C9

Method BLASTN
NCBI GI g516042
BLAST score 60
E value 1.0e-25
Match length 92
% identity 91

NCBI Description Arabidopsis thaliana Columbia Dwarfl (DWF1) mRNA, complete

cds

Seq. No. 138494

Seq. ID LIB23-001-Q1-E1-E4

Method BLASTN
NCBI GI g217842
BLAST score 33
E value 7.0e-09
Match length 61
% identity 89

NCBI Description A.thaliana mRNA for protein kinase

Seq. No. 138495

Seq. ID LIB23-001-Q1-E1-F4

Method BLASTX
NCBI GI g399013
BLAST score 476
E value 5.0e-48
Match length 96
% identity 98

NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)

>gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis

thaliana (fragment) >gi 16175 emb CAA46518 (X65549)

adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator

[Arabidopsis thaliana]

Seq. No. 138496

Seq. ID LIB23-001-Q1-E1-H3



Method NCBI GI q2244827 BLAST score 403 E value 2.0e-39 Match length 119 74 % identity

NCBI Description (297336) hypothetical protein [Arabidopsis thaliana]

138497 Seq. No.

LIB23-002-Q1-E1-B3 Seq. ID

Method BLASTX NCBI GI q4512660 BLAST score 343 2.0e-32 E value Match length 106 % identity 59

(AC006931) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi 4544467 gb AAD22374.1 AC006580 6 (AC006580)

hypothetical protein [Arabidopsis thaliana]

Seq. No. 138498

LIB23-002-Q1-E1-E1 Seq. ID

Method BLASTX NCBI GI q4538943 BLAST score 475 6.0e-48 E value Match length 102 % identity

NCBI Description (AL049483) putative beta-galactosidase [Arabidopsis

thaliana]

Seq. No. 138499

Seq. ID LIB23-002-Q1-E1-E4

Method BLASTN NCBI GI q4587986 BLAST score 43 E value 5.0e-15 Match length 131 % identity

Arabidopsis thaliana ABA-regulated gene cluster, complete NCBI Description

sequence

138500 Seq. No.

Seq. ID LIB23-002-Q1-E1-G11

Method BLASTN NCBI GI g3046856 BLAST score 74 6.0e-34 E value Match length 74 % identity 100

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MXI22, complete sequence [Arabidopsis thaliana]

Seq. No. 138501

Seq. ID LIB23-002-Q1-E1-G12

BLASTN Method NCBI GI g4580530



BLAST score 256 E value 1.0e-142 Match length 256 % identity 100

NCBI Description Arabidopsis thaliana scarecrow-like 14 (SCL14) mRNA,

partial cds

Seq. No. 138502

Seq. ID LIB23-003-Q1-E1-A11

Method BLASTX
NCBI GI g115783
BLAST score 101
E value 2.0e-22
Match length 68
% identity 81

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 138503

Seq. ID LIB23-003-Q1-E1-C10

Method BLASTX
NCBI GI g3941436
BLAST score 275
E value 6.0e-25
Match length 57
% identity 86

NCBI Description (AF062872) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 138504

Seq. ID LIB23-003-Q1-E1-D7

Method BLASTX
NCBI GI g3183454
BLAST score 172
E value 2.0e-12
Match length 98
% identity 38

NCBI Description HYPOTHETICAL 30.7 KD PROTEIN IN MCPC-KINA INTERGENIC REGION

>gi_2632217_emb_CAA10859_ (AJ222587) YkwC protein [Bacillus subtilis] >gi_2633767_emb_CAB13269_ (Z99111) similar to 3-hydroxyisobutyrate dehydrogenase [Bacillus subtilis]

Seq. No. 138505

Seq. ID LIB23-003-Q1-E1-H2

Method BLASTX
NCBI GI g2335096
BLAST score 589
E value 4.0e-61
Match length 116
% identity 100

NCBI Description (AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 138506

Seq. ID LIB23-004-Q1-E1-B6

Method BLASTN

BLAST score

E value Match length 372 1.0e-35

108



```
NCBI GI
                  q3212846
BLAST score
                  252
                  1.0e-139
E value
                  416
Match length
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138507
                  LIB23-004-Q1-E1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3096946
BLAST score
                  419
                  0.0e + 00
E value
Match length
                  434
                  99
% identity
                  Arabidopsis thaliana mRNA for putative cyclic
NCBI Description
                  nucleotide-regulated ion channel, cngc1
Seq. No.
                  138508
                  LIB23-004-Q1-E1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3461817
BLAST score
                  173
E value
                  1.0e-12
Match length
                  64
% identity
                  55
NCBI Description
                 (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                  138509
Seq. ID
                  LIB23-004-Q1-E1-E2
Method
                  BLASTN
NCBI GI
                  g4220643
BLAST score
                  435
                  0.0e + 00
E value
Match length
                  435
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MWD22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138510
Seq. ID
                  LIB23-004-Q1-E1-E9
Method
                  BLASTX
NCBI GI
                  g4633087
BLAST score
                  433
E value
                  3.0e-43
Match length
                  88
                  93
% identity
NCBI Description (AF102508) fizzy-related protein [Homo sapiens]
Seq. No.
                  138511
Seq. ID
                  LIB23-004-Q1-E1-G1
Method
                  BLASTX
NCBI GI
                  g2651314
```



% identity 69

NCBI Description (AC002336) putative ribosomal protein S26 [Arabidopsis

thaliana]

Seq. No. 138512

Seq. ID LIB23-005-Q1-E1-D6

Method BLASTN
NCBI GI g259446
BLAST score 89
E value 2.0e-42
Match length 244
% identity 71

NCBI Description glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana,

C24, mRNA, 680 nt]

Seq. No. 138513

Seq. ID LIB23-005-Q1-E1-E11

Method BLASTX
NCBI GI g445612
BLAST score 578
E value 7.0e-60
Match length 121
% identity 91

NCBI Description ribosomal protein S19 [Solanum tuberosum]

Seq. No. 138514

Seq. ID LIB23-005-Q1-E1-E2

Method BLASTN
NCBI GI g3047100
BLAST score 323
E value 0.0e+00
Match length 364
% identity 66

NCBI Description Arabidopsis thaliana BAC F6N23

Seq. No. 138515

Seq. ID LIB23-005-Q1-E1-E4

Method BLASTN
NCBI GI g4455168
BLAST score 348
E value 0.0e+00
Match length 348
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10

(ESSAII project)

Seq. No. 138516

Seq. ID LIB23-005-Q1-E1-F4

Method BLASTN
NCBI GI g2828185
BLAST score 322
E value 0.0e+00
Match length 322
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUD21, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                   138517
 Seq. ID
                   LIB23-005-Q1-E1-G5
Method
                   BLASTX
NCBI GI
                   g4204270
BLAST score
                   274
                   3.0e-24
E value
Match length
                   91
% identity
                   64
NCBI Description
                   (AC005223) branched-chain alpha-keto acid decarboxylase E1
                   beta subunit [Arabidopsis thaliana]
Seq. No.
                   138518
Seq. ID
                   LIB23-005-Q1-E1-H9
Method
                   BLASTX
NCBI GI
                   g4100433
BLAST score
                   321
E value
                   1.0e-29
Match length
                   107
% identity
                   62
NCBI Description
                   (AF000378) beta-glucosidase [Glycine max]
Seq. No.
                   138519
Seq. ID
                   LIB23-006-Q1-E1-B5
Method
                   BLASTX
NCBI GI
                   g115783
BLAST score
                   512
E value
                   4.0e-52
Match length
                   96
% identity
                   100
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
Seq. No.
                   138520
                   LIB23-006-Q1-E1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3287679
BLAST score
                   675
E value
                   3.0e-71
Match length
                   137
% identity
                   99
NCBI Description
                  (AC003979) T22J18.6 [Arabidopsis thaliana]
Seq. No.
                  138521
Seq. ID
                  LIB23-006-Q1-E1-D6
Method
                  BLASTX
NCBI GI
                  g4544402
BLAST score
                  190
E value
                  2.0e-14
Match length
                  137
% identity
                  31
NCBI Description
                  (AC007047) putative leucine rich repeat protein
                  [Arabidopsis thaliana]
```

Seq. No. 138522

Seq. ID LIB23-006-Q1-E1-E7



Method BLASTX
NCBI GI g4504909
BLAST score 250
E value 2.0e-21
Match length 119
% identity 45

NCBI Description karyopherin (importin) beta 3 >gi 2102696 (U72761)

karyopherin beta 3 [Homo sapiens]

Seq. No. 138523

Seq. ID LIB23-006-Q1-E1-F3

Method BLASTX
NCBI GI g2911067
BLAST score 516
E value 9.0e-53
Match length 111
% identity 94

NCBI Description (AL021960) UV-damaged DNA-binding protein-like [Arabidopsis

thaliana]

Seq. No. 138524

Seq. ID LIB23-006-Q1-E1-G10

Method BLASTN
NCBI GI g4006885
BLAST score 261
E value 1.0e-145
Match length 309
% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 138525

Seq. ID LIB23-006-Q1-E1-G3

Method BLASTX
NCBI GI g2738248
BLAST score 440
E value 9.0e-44
Match length 120
% identity 77

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No. 138526

Seq. ID LIB23-006-Q1-E1-H12

Method BLASTN
NCBI GI g3449317
BLAST score 185
E value 1.0e-100
Match length 185
% identity 91

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MKM21, complete sequence [Arabidopsis thaliana]

Seq. No. 138527

Seq. ID LIB23-007-Q1-E1-B10

Method BLASTN NCBI GI g4325323



BLAST score 218 E value 1.0e-119 Match length 248 % identity 96

NCBI Description Arabidopsis thaliana lysyl-tRNA synthetase mRNA, complete

cds

Seq. No. 138528

Seq. ID LIB23-007-Q1-E1-B11

Method BLASTN
NCBI GI g3075383
BLAST score 137
E value 5.0e-71
Match length 353
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T1D16 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138529

Seq. ID LIB23-007-Q1-E1-B3

Method BLASTN
NCBI GI g4589438
BLAST score 336
E value 0.0e+00
Match length 336
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQJ2, complete sequence

Seq. No. 138530

Seq. ID LIB23-007-Q1-E1-B4

Method BLASTX
NCBI GI g1853966
BLAST score 484
E value 6.0e-49
Match length 111
% identity 86

NCBI Description (D83511) ATMYC1 [Arabidopsis thaliana]

Seq. No. 138531

Seq. ID LIB23-007-Q1-E1-C1

Method BLASTN
NCBI GI g2244747
BLAST score 301
E value 1.0e-169
Match length 354
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 138532

Seq. ID LIB23-007-Q1-E1-C3

Method BLASTX
NCBI GI g4753658
BLAST score 163
E value 2.0e-11
Match length 80



% identity 39

NCBI Description (AL049751) putative protein [Arabidopsis thaliana]

Seq. No. 138533

Seq. ID LIB23-007-Q1-E1-D12

Method BLASTN
NCBI GI g3252804
BLAST score 263
E value 1.0e-146
Match length 346
% identity 69

NCBI Description Arabidopsis thaliana chromosome II BAC F26C24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138534

Seq. ID LIB23-007-Q1-E1-D3

Method BLASTN
NCBI GI g3451055
BLAST score 312
E value 1.0e-175
Match length 350
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20

(ESSAII project)

Seq. No. 138535

Seq. ID LIB23-007-Q1-E1-D5

Method BLASTX
NCBI GI g99741
BLAST score 372
E value 8.0e-36
Match length 114
% identity 46

NCBI Description P-glycoprotein pgpl - Arabidopsis thaliana

Seq. No. 138536

Seq. ID LIB23-007-Q1-E1-D7

Method BLASTX
NCBI GI g2281697
BLAST score 169
E value 6.0e-12
Match length 96
% identity 41

NCBI Description (AF010138) transcription factor [Mus musculus]

Seq. No. 138537

Seq. ID LIB23-007-Q1-E1-E8

Method BLASTN
NCBI GI g3128136
BLAST score 424
E value 0.0e+00
Match length 427
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K1F13, complete sequence [Arabidopsis thaliana]

Seq. No. 138538

```
Seq. ID
                   LIB23-007-Q1-E1-F3
Method
                  BLASTX
NCBI GI
                   q4522012
BLAST score
                   251
E value
                   1.0e-21
Match length
                   95
% identity
                   49
NCBI Description
                  (AC007069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  138539
Seq. ID
                  LIB23-007-Q1-E1-F9
Method
                  BLASTN
NCBI GI
                  q2760165
BLAST score
                  298
                  1.0e-167
E value
Match length
                  330
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAC9, complete sequence [Arabidopsis thaliana]
                  138540
Seq. No.
Seq. ID
                  LIB23-007-Q1-E1-H10
Method
                  BLASTN
NCBI GI
                  g2245073
BLAST score
                  103
                  3.0e-51
E value
Match length
                  124
% identity
                  94
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  138541
Seq. ID
                  LIB23-007-Q1-E1-H12
Method
                  BLASTN
NCBI GI
                  g2656025
                  320
BLAST score
E value
                  1.0e-180
Match length
                  389
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MCD7
Seq. No.
                  138542
Seq. ID
                  LIB23-007-Q1-E1-H7
Method
                  BLASTX
NCBI GI
                  g2673920
BLAST score
                  425
E value
                  4.0e-42
Match length
                  83
% identity
                  100
                   (AC002561) similar to Drosophila couch potato protein
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 138543

Seq. ID LIB23-008-Q1-E1-A12

Method BLASTX NCBI GI g3219858



BLAST score 389 E value 9.0e-38 Match length 105 % identity 84

NCBI Description DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE

>gi_2129724_pir__S71204 RNA polymerase II 13.6 kDa chain Arabidopsis thaliana >gi_881501 (U28048) RNA polymerase II

13.6 kDa subunit [Arabidopsis thaliana]

>gi_4678938_emb_CAB41329.1_ (AL049711) DNA-directed RNA

polymerase II 13.6K chain [Arabidopsis thaliana]

Seq. No. 138544

Seq. ID LIB23-008-Q1-E1-A3

Method BLASTX
NCBI GI g2129727
BLAST score 195
E value 6.0e-15
Match length 75
% identity 60

NCBI Description RNA-binding protein 37 - Arabidopsis thaliana >gi 1174153

(U44134) RNA-binding protein [Arabidopsis thaliana]

Seq. No. 138545

Seq. ID LIB23-008-Q1-E1-A7

Method BLASTX
NCBI GI g1854445
BLAST score 499
E value 1.0e-50
Match length 117
% identity 78

NCBI Description (D83971) CPRD14 protein [Vigna unguiculata]

Seq. No. 138546

Seq. ID LIB23-008-Q1-E1-C2

Method BLASTN
NCBI GI g2252848
BLAST score 277
E value 1.0e-154
Match length 415
% identity 60

NCBI Description Arabidopsis thaliana BAC TM018A10

Seq. No. 138547

Seq. ID LIB23-008-Q1-E1-C4

Method BLASTN
NCBI GI g4159709
BLAST score 426
E value 0.0e+00
Match length 429
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MLN21, complete sequence

Seq. No. 138548

Seq. ID LIB23-008-Q1-E1-C5

Method BLASTN NCBI GI g2980787



```
BLAST score
                  0.0e+00
E value
Match length
                  424
% identity
                  99
NCBI Description
                 Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2
                  (ESSAII project)
                  138549
Seq. No.
                  LIB23-008-Q1-E1-D5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3168605
                  80
BLAST score
E value
                  6.0e-37
Match length
                  376
% identity
                  83
NCBI Description
                 Arabidopsis thaliana catalase 3 (CAT3) and catalase 1
                  (CAT1) genes, complete cds
                  138550
Seq. No.
Seq. ID
                  LIB23-008-Q1-E1-E2
Method
                  BLASTN
                  g4249393
NCBI GI
BLAST score
                  184
E value
                  4.0e-99
                  354
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T9J23 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138551
Seq. ID
                  LIB23-008-Q1-E1-F9
                  BLASTX
Method
NCBI GI
                  g2760839
BLAST score
                  186
                  6.0e-14
E value
Match length
                  129
% identity
                  35
NCBI Description
                 (AC003105) putative receptor kinase [Arabidopsis thaliana]
Seq. No.
                  138552
Seq. ID
                  LIB23-008-Q1-E1-G4
Method
                  BLASTX
NCBI GI
                  g3540185
BLAST score
                  355
E value
                  1.0e-33
Match length
                  119
% identity
NCBI Description
                  (AC004122) Highly Similar to branched-chain amino acid
                  aminotransferase [Arabidopsis thaliana]
```

Seq. No. 138553

Seq. ID LIB23-008-Q1-E1-G6

Method BLASTX NCBI GI g4467128 BLAST score 743 3.0e-79 E value Match length 141

% identity NCBI Description (AL035538) putative protein [Arabidopsis thaliana] 138554 Seq. No. LIB23-008-Q1-E1-H11 Seq. ID Method BLASTN NCBI GI q4199934 BLAST score 191 E value 1.0e-103 Match length 277 % identity 100 NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana] Seq. No. 138555 LIB23-008-Q1-E1-H7 BLASTN

Seq. ID LIB23-008-Q1-E1-H Method BLASTN

NCBI GI g472870

BLAST score 114

E value 3.0e-57

Match length 286
% identity 94

NCBI Description A.thaliana gene for methyltransferase

Seq. No. 138556 Seq. ID LIB23-009-Q1-E1-F2 Method BLASTX NCBI GI q4678301 BLAST score 276 E value 2.0e-24 Match length 87 % identity 62

NCBI Description (AL049655) pectate lyase-like protein [Arabidopsis

thaliana]

Seq. No. 138557

Seq. ID LIB23-009-Q1-E1-F8

Method BLASTN
NCBI GI g4115352
BLAST score 189
E value 1.0e-102
Match length 306
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC T15J14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138558

Seq. ID LIB23-009-Q1-E1-G3

Method BLASTN
NCBI GI g2618602
BLAST score 283
E value 1.0e-158
Match length 379
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSJ1, complete sequence [Arabidopsis thaliana]



Seq. No. 138559

Seq. ID LIB23-009-Q1-E1-H8

Method BLASTX g2894574 NCBI GI BLAST score 314 2.0e-29 E value Match length 61 % identity 98

NCBI Description (AL021890) peroxidase prxrl [Arabidopsis thaliana]

>gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1

[Arabidopsis thaliana]

Seq. No. 138560

Seq. ID LIB23-009-Q1-E2-A7

Method BLASTN NCBI GI q3297806 BLAST score 131 E value 8.0e-68 Match length 171 94 % identity

Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 NCBI Description

(ESSA project)

Seq. No. 138561

Seq. ID LIB23-009-Q1-E2-C5

Method BLASTN NCBI GI g2924733 BLAST score 66 E value 3.0e-29 Match length 122 % identity 89

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MUF9, complete sequence [Arabidopsis thaliana]

Seq. No. 138562

Seq. ID LIB23-009-Q1-E2-D2

Method BLASTN NCBI GI g3128143 BLAST score 65 E value 3.0e-28 Match length 197 91 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTI20, complete sequence [Arabidopsis thaliana]

138563

Seq. No. Seq. ID LIB23-009-Q1-E2-D7

Method BLASTN NCBI GI g4159706 BLAST score 53 2.0e-21 E value Match length 105 % identity 91

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MGL6, complete sequence

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Tangara Tangar
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 Seq. ID
 LIB23-009-Q1-E2-E6

 Method
 BLASTN

 NCBI GI
 q2618683

BLAST score 130 E value 8.0e-67 Match length 274 % identity 89

NCBI Description Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138565

Seq. ID LIB23-009-Q1-E2-G10

Method BLASTN
NCBI GI g1490552
BLAST score 118
E value 4.0e-60
Match length 142
% identity 96

NCBI Description Arabidopsis thaliana S-adenosylmethionine decarboxylase

(SAMdc) mRNA, complete cds

Seq. No. 138566

Seq. ID LIB23-010-Q1-E1-A8

Method BLASTX
NCBI GI g4104058
BLAST score 248
E value 4.0e-21
Match length 106
% identity 47

NCBI Description (AF031195) blue copper-binding protein homolog [Triticum

aestivum]

Seq. No. 138567

Seq. ID LIB23-010-Q1-E1-B7

Method BLASTN
NCBI GI g3046855
BLAST score 182
E value 8.0e-98
Match length 374
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MSL1, complete sequence [Arabidopsis thaliana]

Seq. No. 138568

Seq. ID LIB23-010-Q1-E2-A11

Method BLASTX
NCBI GI g2921158
BLAST score 591
E value 2.0e-61
Match length 142
% identity 61

NCBI Description (AF022909) ClpC [Arabidopsis thaliana]

Seq. No. 138569

Seq. ID LIB23-010-Q1-E2-C12

Method BLASTN NCBI GI g4760411



BLAST score 364 E value 0.0e+00 Match length 368 % identity 100

NCBI Description Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,

complete sequence

Seq. No. 138570

Seq. ID LIB23-010-Q1-E2-D12

Method BLASTN
NCBI GI g2828278
BLAST score 346
E value 0.0e+00
Match length 349
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16

(ESSAII project)

Seq. No. 138571

Seq. ID LIB23-010-Q1-E2-G5

Method BLASTX
NCBI GI g2341034
BLAST score 619
E value 1.0e-64
Match length 124
% identity 100

NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No. 138572

Seq. ID LIB23-010-Q1-E2-H2

Method BLASTX
NCBI GI g1944575
BLAST score 360
E value 2.0e-34
Match length 72
% identity 86

NCBI Description (Z94058) pectinesterase [Lycopersicon esculentum]

Seq. No. 138573

Seq. ID LIB23-010-Q1-E2-H9

Method BLASTX
NCBI GI g1168529
BLAST score 760
E value 4.0e-81
Match length 149
% identity 96

NCBI Description SERINE/THREONINE-PROTEIN KINASE ASK1 >gi_541890_pir_S36944

probable serine/threonine-specific protein kinase (EC 2.7.1.-) (clone ASK1) - Arabidopsis thaliana >gi_166882 (M91548) serine/threonine kinase [Arabidopsis thaliana] >gi_1931648 (U95973) Ser/Thr kinase [Arabidopsis thaliana]

Seq. No. 138574

Seq. ID LIB23-011-Q1-E1-A9

Method BLASTX
NCBI GI g3152558
BLAST score 424



E value 4.0e-42
Match length 80
% identity 96

NCBI Description (AC002986) Similar to M. tuberculosis gene gb_Z96072 and M.

leprae gene gb_400019. [Arabidopsis thaliana]

Seq. No. 138575

Seq. ID LIB23-011-Q1-E1-B1

Method BLASTN
NCBI GI 94757410
BLAST score 108
E value 5.0e-54
Match length 203
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MVE11, complete sequence

Seq. No. 138576

Seq. ID LIB23-011-Q1-E1-B4

Method BLASTX
NCBI GI g1663724
BLAST score 359
E value 3.0e-34
Match length 115
% identity 57

NCBI Description (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No. 138577

Seq. ID LIB23-011-Q1-E1-D2

Method BLASTN
NCBI GI g4337186
BLAST score 333
E value 0.0e+00
Match length 368
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T28I24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138578

Seq. ID LIB23-011-Q1-E1-F4

Method BLASTX
NCBI GI g2708750
BLAST score 341
E value 4.0e-32
Match length 101
% identity 64

NCBI Description (AC003952) putative physical impedence protein [Arabidopsis

thaliana]

Seq. No. 138579

Seq. ID LIB23-011-Q1-E1-G2

Method BLASTX
NCBI GI g4538923
BLAST score 430
E value 1.0e-42
Match length 89
% identity 98



NCBI Description (AL049483) predicted protein destination factor [Arabidopsis thaliana] Seq. No. 138580 LIB23-011-Q1-E1-H7 Seq. ID Method BLASTX NCBI GI q421826 BLAST score 574 E value 2.0e-59 Match length 133 % identity NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana] Seq. No. 138581 Seq. ID LIB23-012-Q1-E1-A10 Method BLASTX NCBI GI g267073 BLAST score 463 E value 2.0e-46 Match length 85 % identity 100 TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin NCBI Description beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana] Seq. No. 138582 Seq. ID LIB23-012-Q1-E1-A3 Method BLASTN NCBI GI q4185120 BLAST score 81 E value 1.0e-37 Match length 370 % identity 98 NCBI Description Arabidopsis thaliana chromosome 1 BAC F5F19 sequence, complete sequence [Arabidopsis thaliana] Seq. No. 138583 LIB23-012-Q1-E1-A6 Seq. ID Method BLASTN g3420042 68 8.0e-30 167 89

NCBI GI BLAST score E value Match length % identity

NCBI Description Arabidopsis thaliana chromosome II BAC T13E15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138584

Seq. ID LIB23-012-Q1-E1-A7 Method

BLASTN NCBI GI g2252639 BLAST score 244 E value 1.0e-135 Match length 340

% identity NCBI Description Genomic sequence of Arabidopsis BAC F8A5, complete sequence [Arabidopsis thaliana] Seq. No. 138585 LIB23-012-Q1-E1-C11 Seq. ID Method BLASTN NCBI GI g2924732 BLAST score 96 E value 9.0e-47 Match length 217 96 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA2, complete sequence [Arabidopsis thaliana] 138586 Seq. No. LIB23-012-Q1-E1-C6 Seq. ID Method BLASTN NCBI GI g3241926 BLAST score 372 0.0e+00E value Match length 404 98 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana] 138587 Seq. No. Seq. ID LIB23-012-Q1-E1-D9 Method BLASTN NCBI GI q4733952 BLAST score 127 4.0e-65 E value Match length 298 % identity 95 Arabidopsis thaliana chromosome I BAC F23H11 genomic NCBI Description sequence, complete sequence Seq. No. 138588 Seq. ID LIB23-012-Q1-E1-E8 Method BLASTX NCBI GI q4559366 BLAST score 508 E value 9.0e-52 Match length 106 % identity 91

% identity 91
NCBI Description (AC006585) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No. 138589

Seq. ID LIB23-012-Q1-E1-G1

Method BLASTX
NCBI GI g3063446
BLAST score 449
E value 5.0e-45
Match length 89
% identity 98

NCBI Description (AC003981) F22013.8 [Arabidopsis thaliana]

% identity

NCBI Description



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Seq. No.
                  138590
Seq. ID
                  LIB23-012-Q1-E1-H6
Method
                  BLASTN
NCBI GI
                  q3337347
BLAST score
                  35
E value
                  3.0e-10
Match length
                  203
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13P17 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138591
Seq. ID
                  LIB23-013-Q1-E1-B10
Method
                  BLASTX
NCBI GI
                  q2832625
BLAST score
                  193
E value
                  1.0e-14
Match length
                  74
                  45
% identity
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  138592
Seq. ID
                  LIB23-013-Q1-E1-D6
Method
                  BLASTX
NCBI GI
                  q531829
BLAST score
                  172
E value
                  2.0e-12
Match length
                  77
                  48
% identity
NCBI Description
                  (U12390) beta-galactosidase alpha peptide [cloning vector
                  pSport1]
                  138593
Seq. No.
Seq. ID
                  LIB23-013-Q1-E1-D8
Method
                  BLASTX
NCBI GI
                  g1711572
BLAST score
                  141
E value
                  2.0e-51
Match length
                  129
% identity
                  83
                  SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN PRECURSOR
NCBI Description
                   (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA)
                  >gi 1076415 pir S30579 succinate--CoA ligase (GDP-forming)
                   (EC 6.2.1.4) alpha chain - Arabidopsis thaliana (fragment)
                  >gi 16510 emb CAA48891 (X69138) succinate--CoA ligase
                   (GDP-forming) [Arabidopsis thaliana]
Seq. No.
                  138594
Seq. ID
                  LIB23-013-Q1-E1-F4
Method
                  BLASTX
NCBI GI
                  q4220514
BLAST score
                  296
                  7.0e-27
E value
                  71
Match length
                  79
```

16693

(AL035356) putative protein [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                  LIB23-013-Q1-E1-F8
Method
                  BLASTX
NCBI GI
                  q1174498
BLAST score
                  482
E value
                  1.0e-48
Match length
                  94
                  98
% identity
                  SYNAPTOBREVIN-RELATED PROTEIN >gi 600710 (M90418) formerly
NCBI Description
                  called HAT24; synaptobrevin-related protein [Arabidopsis
                  thaliana]
                  138596
Seq. No.
Seq. ID
                  LIB23-013-Q1-E1-H5
Method
                  BLASTN
NCBI GI
                  g2828182
BLAST score
                  418
                  0.0e + 00
E value
                  422
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOJ9, complete sequence [Arabidopsis thaliana]
                  138597
Seq. No.
Seq. ID
                  LIB23-014-Q1-E1-A1
Method
                  BLASTN
NCBI GI
                  q4092471
BLAST score
                  71
E value
                   6.0e-32
Match length
                  79
% identity
                   97
NCBI Description
                  Arabidopsis thaliana BAC F9M13 from chromosome IV near 21.5
                  cM, complete sequence
Seq. No.
                   138598
Seq. ID
                  LIB23-014-Q1-E1-B6
Method
                  BLASTN
NCBI GI
                   q4455321
BLAST score
                   161
E value
                   1.0e-85
Match length
                   172
% identity
                   99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10
                   (ESSAII project)
Seq. No.
                   138599
Seq. ID
                  LIB23-014-Q1-E1-C10
Method
                  BLASTX
NCBI GI
                  q2911049
BLAST score
                   312
                   8.0e-29
E value
Match length
                  104
                   57
% identity
                   (AL021961) glucosyltransferase -like protein [Arabidopsis
NCBI Description
                   thaliana]
```



```
138600
Seq. No.
Seq. ID
                  LIB23-014-Q1-E1-C6
Method
                  BLASTX
NCBI GI
                  q2961388
BLAST score
                  416
                  6.0e-41
E value
Match length
                  104
% identity
                  81
                  (AL022141) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  138601
Seq. ID
                  LIB23-014-Q1-E1-D2
Method
                  BLASTN
NCBI GI
                  g4490291
BLAST score
                  147
E value
                  5.0e-77
Match length
                  295
                  100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5
                  (ESSA project)
Seq. No.
                  138602
Seq. ID
                  LIB23-014-Q1-E1-D3
Method
                  BLASTX
NCBI GI
                  g2924781
BLAST score
                  143
E value
                  2.0e-09
Match length
                  34
% identity
                  76
NCBI Description
                  (AC002334) putative cellulose synthase [Arabidopsis
                  thaliana]
Seq. No.
                  138603
                  LIB23-014-Q1-E1-D9
Seq. ID
Method
                  BLASTX
                  g2335108
NCBI GI
BLAST score
                  428
E value
                  2.0e-42
Match length
                  97
% identity
                  81
NCBI Description
                  (AC002339) putative isulinase [Arabidopsis thaliana]
Seq. No.
                  138604
Seq. ID
                  LIB23-014-Q1-E1-E5
Method
                  BLASTX
NCBI GI
                  g4512620
BLAST score
                  206
E value
                  1.0e-16
Match length
                  47
% identity
                  91
                   (AC004793) Identical to qb X71364 gene for aspartate kinase
NCBI Description
                  homoserine dehydrogenase from Arabidopsis thaliana
```

Seq. No. 138605

Seq. ID LIB23-014-Q1-E1-G8

Method BLASTX NCBI GI g3170230



BLAST score 439 E value 1.0e-43 Match length 137 % identity 62

NCBI Description (AF041848) fructose-6-phosphate 2-kinase

/fructose-2,6-bisphosphatase [Spinacia oleracea]

Seq. No. 138606

Seq. ID LIB23-015-Q1-E1-A5

Method BLASTX
NCBI GI g2492519
BLAST score 215
E value 1.0e-17
Match length 44
% identity 95

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT

7) >gi 1395191 dbj BAA13021 (D86121) 26S proteasome ATPase

subunit [Spinacia oleracea]

Seq. No. 138607

Seq. ID LIB23-015-Q1-E1-B2

Method BLASTX
NCBI GI g3928543
BLAST score 581
E value 3.0e-60
Match length 128
% identity 84

NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 138608

Seq. ID LIB23-015-Q1-E1-B5

Method BLASTN
NCBI GI g3420043
BLAST score 43
E value 4.0e-15
Match length 71
% identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC F23F1 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138609

Seq. ID LIB23-015-Q1-E1-B8

Method BLASTX
NCBI GI g2738248
BLAST score 639
E value 5.0e-67
Match length 120
% identity 100

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No. 138610

Seq. ID LIB23-015-Q1-E1-B9

Method BLASTX NCBI GI g115783 BLAST score 409

Method

NCBI GI

E value

BLAST score

BLASTX

q170354

4.0e-63

606



```
E value
                    3.0e-40
 Match length
                    79
 % identity
                    97
 NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                    (CAB-140) (LHCP) >gi_16376_emb_CAA27543 (X03909)
                   chlorophyll a/b binding protein (LHCP \overline{AB} 140) [Arabidopsis
                    thaliana]
 Seq. No.
                    138611
                   LIB23-015-Q1-E1-C3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3293582
BLAST score
                   125
E value
                   6.0e-64
Match length
                   226
% identity
                   100
NCBI Description Arabidopsis thaliana BAC T15F16
Seq. No.
                   138612
Seq. ID
                   LIB23-015-Q1-E1-C4
Method
                   BLASTX
NCBI GI
                   g2829899
BLAST score
                   676
E value
                   2.0e-71
Match length
                   132
% identity
                   100
NCBI Description
                   (AC002311) similar to ripening-induced protein,
                   gp_AJ001449_2465015 and major#latex protein,
                   gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                   138613
Seq. ID
                   LIB23-015-Q1-E1-C6
Method
                   BLASTX
NCBI GI
                   g3004551
BLAST score
                   170
E value
                   5.0e-12
Match length
                   98
% identity
                   44
NCBI Description
                   (AC003673) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   138614
Seq. ID
                   LIB23-015-Q1-E1-D6
Method
                   BLASTX
NCBI GI
                   g3461818
BLAST score
                   187
E value
                   2.0e-14
Match length
                   54
% identity
                   70
NCBI Description
                  (AC004138) putative glutathione S-transferase [Arabidopsis
                   thaliana]
Seq. No.
                  138615
Seq. ID
                  LIB23-015-Q1-E1-E4
```

Match length 22 % identity (M74156) pentameric polyubiquitin [Nicotiana sylvestris] NCBI Description 138616 Seq. No. LIB23-015-Q1-E1-E8 Seq. ID Method BLASTX NCBI GI g2462929 BLAST score 661 1.0e-69 E value 127 Match length 100 % identity (Y12295) glutathione transferase [Arabidopsis thaliana] NCBI Description Seq. No. 138617 LIB23-015-Q1-E1-F1 Seq. ID Method BLASTX q4099090 NCBI GI BLAST score 482 E value 1.0e-48 138 Match length 74 % identity (U83178) unknown [Arabidopsis thaliana] NCBI Description 138618 Seq. No. LIB23-015-Q1-E1-G8 Seq. ID Method BLASTX g115767 NCBI GI BLAST score 156 6.0e-11 E value Match length 34 97 % identity CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 138619

LIB23-015-Q1-E1-H3 Seq. ID

Method BLASTX NCBI GI q3096947 BLAST score 708 4.0e-75 E value Match length 137 % identity 99

(Y16327) putative cyclic nucleotide-regulated ion channel NCBI Description

[Arabidopsis thaliana]

138620 Seq. No.

Seq. ID LIB23-016-Q1-E1-B5

Method BLASTX NCBI GI g166867 BLAST score 649 E value 4.0e-68



Match length % identity 88 (J05216) ribosomal protein S11 (probable start codon at bp NCBI Description 67) [Arabidopsis thaliana] 138621 Seq. No. Seq. ID LIB23-016-Q1-E1-B7 Method BLASTN g2088638 NCBI GI 303 BLAST score E value 1.0e-170 Match length 355 % identity 95 Arabidopsis thaliana chromosome II BAC T28M21 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138622 Seq. ID LIB23-016-Q1-E1-D11

Method BLASTX NCBI GI g1841355 BLAST score 261 7.0e-23 E value Match length 66 % identity 65

(D85381) cytochrome c oxidase subunit Vb precursor [Oryza NCBI Description

sativa]

138623 Seq. No.

Seq. ID LIB23-016-Q1-E1-E11

Method BLASTN NCBI GI g3327922 BLAST score 286 E value 1.0e-160 Match length 286 % identity 100

Arabidopsis thaliana chromosome II BAC T31E10 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138624

Seq. ID LIB23-016-Q1-E1-E12

Method BLASTX NCBI GI g4757796 BLAST score 251 E value 1.0e-21 Match length 106 % identity 46

NCBI Description arsA (bacterial) arsenite transporter, ATP-binding, homolog

1 >gi 1616741 (U60276) hASNA-I [Homo sapiens]

Seq. No. 138625

Seq. ID LIB23-016-Q1-E1-E2

BLASTX Method g2506276 NCBI GI BLAST score 313 8.0e-29 E value 76 Match length 84 % identity



NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60

KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)

>gi_2129561_pir__\$71235_chaperonin-60_alpha_chain -

Arabidopsis thaliana >gi_1223910 (U49357) chaperonin-60

alpha subunit [Arabidopsis thaliana]

>gi_4510416_gb_AAD21502.1_ (AC006929) putative rubisco binding protein alpha subunit [Arabidopsis thaliana]

Seq. No. 138626

Seq. ID LIB23-016-Q1-E1-F10

Method BLASTN
NCBI GI g4757678
BLAST score 162
E value 6.0e-86
Match length 370
% identity 99

NCBI Description Arabidopsis thaliana chromosome I BAC F9H16 genomic

sequence, complete sequence

Seq. No. 138627

Seq. ID LIB23-016-Q1-E1-F4

Method BLASTN
NCBI GI g4589445
BLAST score 288
E value 1.0e-161
Match length 288
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWL2, complete sequence

Seq. No. 138628

Seq. ID LIB23-016-Q1-E1-H1

Method BLASTX
NCBI GI 94249386
BLAST score 498
E value 2.0e-50
Match length 97
% identity 100

NCBI Description (AC005966) Strong similarity to gb AF061286 gamma-adaptin 1

from Arabidopsis thaliana. EST gb H37393 comes from this

gene. [Arabidopsis thaliana]

Seq. No. 138629

Seq. ID LIB23-016-Q1-E1-H2

Method BLASTN
NCBI GI g402903
BLAST score 38
E value 2.0e-12
Match length 158
% identity 94

NCBI Description Arabidopsis thaliana Columbia laminin receptor-like protein

mRNA, complete cds

Seq. No. 138630

Seq. ID LIB23-017-Q1-E1-A7

Method BLASTX NCBI GI g2894574



BLAST score 485 E value 4.0e-49 Match length 93 % identity 99

NCBI Description (AL021890) peroxidase prxr1 [Arabidopsis thaliana]

>gi 2961341 emb CAA18099.1 (AL022140) peroxidase prxr1

[Arabidopsis thaliana]

Seq. No. 138631

Seq. ID LIB23-017-Q1-E1-B11

Method BLASTX
NCBI GI g300264
BLAST score 198
E value 2.0e-15
Match length 73
% identity 58

NCBI Description (S59747) HSP68=68 kda heat-stress DnaK homolog [Solanum

tuberosum=potatoes, Peptide Mitochondrial, 682 aa] [Solanum

tuberosum]

Seq. No. 138632

Seq. ID LIB23-017-Q1-E1-B9

Method BLASTX
NCBI GI g2494116
BLAST score 322
E value 6.0e-30
Match length 57
% identity 98

NCBI Description (AC002376) Similar to Synechocystis hypothetical protein

(gb_D90915). [Arabidopsis thaliana]

Seq. No. 138633

Seq. ID LIB23-017-Q1-E1-C12

Method BLASTN
NCBI GI g2564047
BLAST score 377
E value 0.0e+00
Match length 377
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJB21, complete sequence [Arabidopsis thaliana]

Seq. No. 138634

Seq. ID LIB23-017-Q1-E1-D5

Method BLASTX
NCBI GI g3695385
BLAST score 390
E value 8.0e-38
Match length 104
% identity 80

NCBI Description (AF096370) similar to Medicago truncatula MtN21

(GB:Y15293) [Arabidopsis thaliana]

Seq. No. 138635

Seq. ID LIB23-017-Q1-E1-E3

Method BLASTN NCBI GI g4159704



BLAST score 394 E value 0.0e+00 Match length 394 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MCB17, complete sequence

Seq. No. 138636

Seq. ID LIB23-017-Q1-E1-F6

Method BLASTX
NCBI GI g115783
BLAST score 231
E value 1.0e-19
Match length 58
% identity 79

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 138637

Seq. ID LIB23-017-Q1-E1-F7

Method BLASTX
NCBI GI g3834328
BLAST score 487
E value 2.0e-49
Match length 105
% identity 100

NCBI Description (AC005679) Strong similarity to glycoprotein EP1 gb_L16983

Daucus carota and a member of S locus glycoprotein family

PF_00954. [Arabidopsis thaliana]

Seq. No. 138638

Seq. ID LIB23-017-Q1-E1-G8

Method BLASTN
NCBI GI g2980757
BLAST score 197
E value 1.0e-107
Match length 284
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18

(ESSAII project)

Seq. No. 138639

Seq. ID LIB23-017-Q1-E1-H12

Method BLASTX
NCBI GI g1352243
BLAST score 596
E value 4.0e-62
Match length 118
% identity 99

NCBI Description LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1

>gi_625972_pir__A54841 DET1 protein - Arabidopsis thaliana >gi_510275 (L33695) DET1 [Arabidopsis thaliana] >gi_3695414 (AF096373) Arabidopsis thaliana light-mediated development

protein DET1 (SP:P48732) [Arabidopsis thaliana]

>gi_4538982_emb_CAB39770.1 (AL049487) Deetiolated1 (DET1)

% identity

30



light signal transduction protein [Arabidopsis thaliana]

Seq. No. 138640 Seq. ID LIB23-018-Q1-E1-B10 Method BLASTX NCBI GI q1170555 BLAST score 218 E value 1.0e-17 Match length 121 % identity 44 NCBI Description MYO-INOSITOL 4-O-METHYLTRANSFERASE >gi 282822 pir S22696 methyltransferase - common ice plant >gi 167262 (M87340) myo-inositol O-methyl transferase [Mesembryanthemum crystallinum] >gi 1488237 (U63634) inositol methyltransferase [Mesembryanthemum crystallinum] Seq. No. 138641 Seq. ID LIB23-018-Q1-E1-E10 Method BLASTX NCBI GI q2864623 BLAST score 548 E value 2.0e-56 Match length 124 % identity 90 NCBI Description (AL021811) putative protein [Arabidopsis thaliana] 138642 Seq. No. LIB23-018-Q1-E1-E7 Seq. ID Method BLASTX NCBI GI g259447 BLAST score 178 E value 2.0e-13 30 Match length % identity 93 NCBI Description (S47409) glycine-rich protein, atGRP {clone atGRP-3} [Arabidopsis thaliana, C24, Peptide, 145 aa] [Arabidopsis thaliana] Seq. No. 138643 Seq. ID LIB23-018-Q1-E1-F12 Method BLASTX NCBI GI g3600058 BLAST score 548 2.0e-56 E value Match length 112 % identity NCBI Description (AF080120) similar to vacuolar ATPases [Arabidopsis thaliana] Seq. No. 138644 LIB23-018-Q1-E1-F2 Seq. ID Method BLASTX NCBI GI g2459445 BLAST score 283 2.0e-25 E value Match length 80



NCBI Description (AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No. 138645

Seq. ID LIB23-018-Q1-E1-G1

Method BLASTX
NCBI GI g3047104
BLAST score 374
E value 4.0e-36
Match length 109
% identity 67

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 138646

Seq. ID LIB23-018-Q1-E1-H1

Method BLASTN
NCBI GI g4589421
BLAST score 132
E value 3.0e-68
Match length 228
% identity 55

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K5K13, complete sequence

Seq. No. 138647

Seq. ID LIB23-018-Q1-E1-H9

Method BLASTN
NCBI GI g2618599
BLAST score 164
E value 2.0e-87
Match length 172
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBD2, complete sequence [Arabidopsis thaliana]

Seq. No. 138648

Seq. ID LIB23-019-Q1-E1-A1

Method BLASTX
NCBI GI g1707011
BLAST score 208
E value 2.0e-16
Match length 37
% identity 100

NCBI Description (U78721) auxin-repressed protein isolog [Arabidopsis

thaliana]

Seq. No. 138649

Seq. ID LIB23-019-Q1-E1-A2

Method BLASTX
NCBI GI g2746341
BLAST score 360
E value 2.0e-34
Match length 74
% identity 85

NCBI Description (AF037590) ATA27 [Arabidopsis thaliana]

Seq. No. 138650



Seq. ID LIB23-019-Q1-E1-B6

Method BLASTN
NCBI GI g3985957
BLAST score 321
E value 0.0e+00
Match length 365
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

MYN8, complete sequence [Arabidopsis thaliana]

Seq. No. 138651

Seq. ID LIB23-019-Q1-E1-D3

Method BLASTX
NCBI GI g2832642
BLAST score 144
E value 6.0e-09
Match length 84
% identity 20

NCBI Description (AL021710) putative protein [Arabidopsis thaliana]

Seq. No. 138652

Seq. ID LIB23-019-Q1-E1-E6

Method BLASTX
NCBI GI g1432083
BLAST score 546
E value 4.0e-56
Match length 124
% identity 88

NCBI Description (U60981) homolog to Skp1p, an evolutionarily conserved

kinetochore protein in budding yeast [Arabidopsis thaliana] >gi 3068807 (AF059294) Skp1 homolog [Arabidopsis thaliana]

>gi_3719209 (U97020) UIP1 [Arabidopsis thaliana]

Seq. No. 138653

Seq. ID LIB23-019-Q1-E1-E7

Method BLASTN
NCBI GI g4678371
BLAST score 444
E value 0.0e+00
Match length 444
% identity 72

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15

(ESSA project)

Seq. No. 138654

Seq. ID LIB23-019-Q1-E1-F10

Method BLASTN
NCBI GI g3869075
BLAST score 351
E value 0.0e+00
Match length 406
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXK3, complete sequence [Arabidopsis thaliana]

Seq. No. 138655

Seq. ID LIB23-019=Q1-E1-G4



Method BLASTN
NCBI GI g3046855
BLAST score 46
E value 1.0e-16
Match length 110
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MSL1, complete sequence [Arabidopsis thaliana]

Seq. No. 138656

Seq. ID LIB23-019-Q1-E1-H10

Method BLASTX
NCBI GI g2462929
BLAST score 673
E value 6.0e-71
Match length 131
% identity 99

NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No. 138657

Seq. ID LIB23-019-Q1-E1-H4

Method BLASTN
NCBI GI g2833627
BLAST score 251
E value 1.0e-139
Match length 263
% identity 99

NCBI Description Arabidopsis thaliana chromosome 1 BAC F1707 complete

sequence [Arabidopsis thaliana]

Seq. No. 138658

Seq. ID LIB23-020-Q1-E1-B5

Method BLASTN
NCBI GI g2749918
BLAST score 236
E value 1.0e-130
Match length 240
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F316 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138659

Seq. ID LIB23-020-Q1-E1-C4

Method BLASTN
NCBI GI g2244991
BLAST score 340
E value 0.0e+00
Match length 340
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 138660

Seq. ID LIB23-020-Q1-E1-D6

Method BLASTX
NCBI GI g1518540
BLAST score 530



```
E value
                   3.0e-54
Match length
                   110
% identity
                   91
NCBI Description
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
                  138661
Seq. No.
Seq. ID
                  LIB23-020-Q1-E1-E10
Method
                  BLASTN
NCBI GI
                  q3738088
BLAST score
                  92
E value
                  2.0e-44
Match length
                   217
% identity
                  97
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T30L20 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  138662
Seq. No.
Seq. ID
                  LIB23-020-Q1-E1-E4
Method
                  BLASTN
NCBI GI
                  g3449313
BLAST score
                  348
E value
                  0.0e+00
Match length
                  348
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21P3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138663
Seq. ID
                  LIB23-020-Q1-E1-E5
Method
                  BLASTX
                  g2497886
NCBI GI
BLAST score
                  300
E value
                  3.0e-27
Match length
                  54
                  100
% identity
NCBI Description
                  METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B)
                  >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis
                  thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis
                  thaliana]
Seq. No.
                  138664
Seq. ID
                  LIB23-021-Q2-E1-C12
Method
                  BLASTX
NCBI GI
                  g3935138
BLAST score
                  540
E value
                  2.0e-55
                  123
% identity
                  85
                  (AC005106) T25N20.2 [Arabidopsis thaliana]
NCBI Description
```

Match length

Seq. No. 138665

Seq. ID LIB23-021-Q2-E1-D1

Method BLASTX NCBI GI g3402751 BLAST score 701 E value 3.0e-74 Match length 129

NCBI Description



% identity NCBI Description (AL031187) putative protein [Arabidopsis thaliana] 138666 Seq. No. Seq. ID LIB23-021-Q2-E1-E1 Method BLASTN NCBI GI q4206766 BLAST score 58 7.0e-24 E value Match length 58 % identity 100 NCBI Description Arabidopsis thaliana glycine-rich protein 3 short isoform (GRP3S) mRNA, complete cds Seq. No. 138667 Seq. ID LIB23-021-Q2-E1-E5 Method BLASTX NCBI GI g3342802 BLAST score 440 E value 1.0e-43 Match length 113 76 % identity (AF061838) putative cytosolic 6-phosphogluconate NCBI Description dehydrogenase [Zea mays] Seq. No. 138668 Seq. ID LIB23-021-Q2-E1-F1 Method BLASTX NCBI GI q2623962 BLAST score 593 E value 1.0e-61 Match length 137 % identity 80 NCBI Description (Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens] Seq. No. 138669 Seq. ID LIB23-021-Q2-E1-F12 Method BLASTX NCBI GI a2262167 BLAST score 595 E value 7.0e-62 Match length 114 99 % identity NCBI Description (AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana] Seq. No. 138670 Seq. ID LIB23-021-Q2-E1-G10 Method BLASTN NCBI GI q2281081 BLAST score 343 E value 0.0e + 00Match length 367 % identity 98

16708

Arabidopsis thaliana chromosome II BAC F18019 genomic

sequence, complete sequence [Arabidopsis thaliana]



Seq. No. 138671

Seq. ID LIB23-021-Q2-E1-H3

Method BLASTN
NCBI GI g2760167
BLAST score 195
E value 1.0e-105
Match length 378
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCO15, complete sequence [Arabidopsis thaliana]

Seq. No. 138672

Seq. ID LIB23-022-Q2-E1-C11

Method BLASTX
NCBI GI 94757880
BLAST score 153
E value 5.0e-10
Match length 113
% identity 28

NCBI Description BUB3 (budding uninhibited by benzimidazoles 3, yeast)

homolog >gi_2921873 (AF047472) spleen mitotic checkpoint BUB3 [Homo sapiens] >gi_2981231_gb_AAC06258_ (AF053304)

mitotic checkpoint component Bub3 [Homo sapiens]

>gi 3639060 (AF081496) kinetochore protein BUB3 [Homo

sapiens]

Seq. No. 138673

Seq. ID LIB23-022-Q2-E1-C6

Method BLASTN
NCBI GI g4580454
BLAST score 297
E value 1.0e-166
Match length 373
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC T2G17 genomic

sequence, complete sequence

Seq. No. 138674

Seq. ID LIB23-022-Q2-E1-C7

Method BLASTN
NCBI GI g3426033
BLAST score 144
E value 1.0e-75
Match length 168
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC F12C20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138675

Seq. ID LIB23-022-Q2-E1-E1

Method BLASTX
NCBI GI g1888357
BLAST score 244
E value 8.0e-21
Match length 66
% identity 71



(X98130) alpha-mannosidase [Arabidopsis thaliana]

>gi 1890154 emb CAA72432 (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. 138676

NCBI Description

Seq. ID LIB23-022-Q2-E1-F10

Method BLASTX
NCBI GI g2924786
BLAST score 689
E value 7.0e-73
Match length 134
% identity 99

NCBI Description (AC002334) similar to disease resistance protein

[Arabidopsis thaliana]

Seq. No. 138677

Seq. ID LIB23-022-Q2-E1-F5

Method BLASTN
NCBI GI g560770
BLAST score 249
E value 1.0e-138
Match length 310
% identity 85

NCBI Description Arabidopsis thaliana rd22 gene, complete cds

Seq. No. 138678

Seq. ID LIB23-022-Q2-E1-G9

Method BLASTX
NCBI GI g3859592
BLAST score 667
E value 2.0e-70
Match length 119
% identity 100

NCBI Description (AF104919) contains similarity to expansins [Arabidopsis

thaliana]

Seq. No. 138679

Seq. ID LIB23-022-Q2-E1-H2

Method BLASTN
NCBI GI g2564050
BLAST score 280
E value 1.0e-156
Match length 375
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUA22, complete sequence [Arabidopsis thaliana]

Seq. No. 138680

Seq. ID LIB23-022-Q2-E1-H3

Method BLASTX
NCBI GI g4063734
BLAST score 285
E value 1.0e-25
Match length 107
% identity 55

NCBI Description (AC006259) putative P450 [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                  LIB23-022-Q2-E1-H7
Method
                  BLASTX
NCBI GI
                  g4415942
BLAST score
                   568
E value
                   9.0e - 59
Match length
                  110
                  100
% identity
NCBI Description
                  (AC006418) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB23-023-Q1-E1-A4
Method
                  BLASTX
NCBI GI
                  q3850621
BLAST score
                  531
E value
                  1.0e-54
Match length
                  105
% identity
                  100
                  (Y15382) putative RNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  138683
Seq. No.
Seq. ID
                  LIB23-023-Q1-E1-B4
Method
                  BLASTX
                  g2464901
NCBI GI
BLAST score
                  181
                  2.0e-13
E value
Match length
                  76
% identity
                  51
NCBI Description
                  (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                  138684
Seq. ID
                  LIB23-023-Q1-E1-C2
Method
                  BLASTN
NCBI GI
                  g2656032
BLAST score
                  219
E value
                   1.0e-120
Match length
                  219
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MZF18
Seq. No.
                  138685
Seq. ID
                  LIB23-023-Q1-E1-E1
Method
                  BLASTX
NCBI GI
                  g120667
BLAST score
                  145
E value
                  3.0e-09
Match length
                  27
                  100
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
```

>gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis

thaliana >gi 166706 (M64116) cystolic

glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate

dehydrogenase [Arabidopsis thaliana]

Method

BLASTN



```
Seq. No.
                   138686
Seq. ID
                  LIB23-023-Q1-E1-E3
Method
                  BLASTX
NCBI GI
                   g2894600
                   156
BLAST score
E value
                   1.0e-10
                   79
Match length
                   37
% identity
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   138687
Seq. ID
                   LIB23-023-Q1-E1-F1
Method
                   BLASTX
                   q1684857
NCBI GI
                   447
BLAST score
E value
                   1.0e-44
Match length
                   90
% identity
                   37
                  (U77940) polyubiquitin [Phaseolus vulgaris]
NCBI Description
                   138688
Seq. No.
                   LIB23-023-Q1-E1-F10
Seq. ID
Method
                   BLASTN
                   q2160155
NCBI GI
                   352
BLAST score
                   0.0e + 00
E value
                   364
Match length
                   99
% identity
                   Sequence of BAC F21M12 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   138689
                   LIB23-023-Q1-E1-F9
Method
                   BLASTN
                   q4589437
NCBI GI
BLAST score
                   99
                   2.0e-48
E value
Match length
                   181
% identity
                   100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MPN9, complete sequence
Seq. No.
                   138690
                   LIB23-023-Q1-E1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2980774
BLAST score
                   213
                   3.0e-17
E value
Match length
                   41
% identity
                   100
                   (AL022198) leucyl aminopeptidase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   138691
Seq. ID
                   LIB23-025-Q1-E1-A1
```



```
NCBI GI
                  q3449316
BLAST score
                  47
                  2.0e-17
E value
Match length
                  63
% identity
                  94
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9D7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138692
Seq. ID
                  LIB23-025-Q1-E1-A6
Method
                  BLASTX
NCBI GI
                  g4704613
BLAST score
                  445
E value
                  2.0e-44
Match length
                  101
% identity
                  88
NCBI Description
                  (AF109695) monodehydroascorbate reductase [Brassica juncea]
Seq. No.
                  138693
                  LIB23-025-Q1-E1-A8
Seq. ID
Method
                  BLASTX
                  g1076763
NCBI GI
BLAST score
                  88
E value
                  1.0e-02
Match length
                  80
% identity
                  AWJL218 protein - wheat >gi 551212 emb CAA57134 (X81369)
NCBI Description
                  AWJL218 [Triticum aestivum]
Seq. No.
                  138694
Seq. ID
                  LIB23-025-Q1-E1-B10
Method
                  BLASTN
NCBI GI
                  g2351069
BLAST score
                  306
E value
                  1.0e-172
Match length
                  310
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSH12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138695
Seq. ID
                  LIB23-025-Q1-E1-C2
Method
                  BLASTX
NCBI GI
                  g4567271
BLAST score
                  420
                  2.0e-41
E value
Match length
                  126
% identity
                  71
                  (AC006841) putative kinesin protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  138696
Seq. ID
                  LIB23-025-Q1-E1-C4
```

Method BLASTX
NCBI GI g3928103
BLAST score 411
E value 2.0e-40
Match length 93



% identity

NCBI Description (AC005770) putative water channel protein [Arabidopsis

thaliana]

138697 Seq. No.

Seq. ID LIB23-025-Q1-E1-D11

Method BLASTN NCBI GI q2182289 BLAST score 387 0.0e+00 E value Match length 387 % identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F11P17 genomic

sequence, complete sequence [Arabidopsis thaliana]

138698 Seq. No.

Seq. ID LIB23-025-01-E1-D3

Method BLASTX NCBI GI g3831452 BLAST score 680 E value 7.0e-72 Match length 123 100 % identity

NCBI Description (AC005700) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 138699

Seq. ID LIB23-025-Q1-E1-D6

Method BLASTX NCBI GI q3785991 BLAST score 407 E value 3.0e-40 Match length 81

% identity 86

NCBI Description (AC005560) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 138700

Seq. ID LIB23-025-Q1-E1-D7

Method BLASTX NCBI GI q4558549 BLAST score 445 E value 1.0e-44 Match length 87 % identity 100

NCBI Description (AC007138) putative SecA-type chloroplast protein transport

factor [Arabidopsis thaliana]

Seq. No. 138701

Seq. ID LIB23-025-Q1-E1-E4

Method BLASTN NCBI GI g2623294 BLAST score 91 E value 9.0e-44 Match length 248 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T20B5 genomic

sequence, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                  138702
Seq. ID
                  LIB23-025-Q1-E1-F4
Method
                  BLASTN
NCBI GI
                  g3319339
BLAST score
                  57
E value
                  3.0e-23
Match length
                  69
% identity
                  96
NCBI Description Arabidopsis thaliana BAC F9D12
                  138703
Seq. No.
                  LIB23-025-Q1-E1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2315362
BLAST score
                  153
E value
                  8.0e-38
Match length
                  120
                  33
% identity
NCBI Description
                  (AF016441) contains similarity to multiple TPR domains
                  [Caenorhabditis elegans]
Seq. No.
                  138704
Seq. ID
                  LIB23-025-Q1-E1-H8
Method
                  BLASTN
NCBI GI
                  g2104523
BLAST score
                  221
E value
                  1.0e-121
Match length
                  281
% identity
                  95
                  Arabidopsis thaliana BAC T10M13 from chromosome IV, from
NCBI Description
                  10.8 cM to 11.6 cM, complete sequence
Seq. No.
                  138705
Seq. ID
                  LIB23-026-Q1-E1-A11
Method
                  BLASTN
NCBI GI
                  g2564048
BLAST score
                  126
E value
                  1.0e-64
                  294
Match length
                  98
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MKD15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138706
                  LIB23-026-Q1-E1-A12
Seq. ID
Method
                  BLASTN
```

NCBI GI g16228 BLAST score 66 E value 7.0e-29 98 Match length % identity 92

NCBI Description A.thaliana cor47 mRNA

Seq. No. 138707

Seq. ID LIB23-026-Q1-E1-A2

Method BLASTX NCBI GI g2914706



```
BLAST score
E value
                   4.0e-49
Match length
                   125
                   73
% identity
NCBI Description
                  (AC003974) putative homeobox protein [Arabidopsis thaliana]
Seq. No.
                   138708
Seq. ID
                  LIB23-026-Q1-E1-B8
Method
                  BLASTX
NCBI GI
                   g4455199
BLAST score
                   534
E value
                   9.0e-55
Match length
                  118
% identity
                   89
NCBI Description
                  (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  138709
Seq. ID
                  LIB23-026-Q1-E1-C10
Method
                  BLASTX
NCBI GI
                   g2739386
BLAST score
                   253
                   4.0e-22
E value
Match length
                  87
% identity
                   61
NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
                  138710
Seq. No.
Seq. ID
                  LIB23-026-Q1-E1-D1
Method
                  BLASTX
NCBI GI
                   q4539460
BLAST score
                   222
E value
                   3.0e-18
Match length
                  116
% identity
NCBI Description (AL049500) putative protein [Arabidopsis thaliana]
Seq. No.
                   138711
Seq. ID
                  LIB23-026-Q1-E1-D8
Method
                  BLASTX
NCBI GI
                  q419760
BLAST score
                   476
                   3.0e-48
E value
                  94
Match length
% identity
                   50
                  P-glycoprotein atpgp1 - Arabidopsis thaliana
NCBI Description
                  >gi_3849833 emb_CAA43646 (X61370) P-glycoprotein
                   [Arabidopsis thaliana]
                  138712
Seq. No.
Seq. ID
                  LIB23-026-Q1-E1-E9
Method
                  BLASTX
NCBI GI
                  q730456
BLAST score
                  332
E value
                  3.0e-31
                  79
Match length
                  75
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S19
```



Seq. No. 138713 Seq. ID LIB23-026-Q1-E1-F6 Method BLASTN NCBI GI g2618602 BLAST score 331 E value 0.0e + 00Match length 335 100 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MSJ1, complete sequence [Arabidopsis thaliana] Seq. No. 138714 LIB23-026-Q1-E1-G1 Seq. ID Method BLASTX NCBI GI a3287693 BLAST score 550 E value 1.0e-56 117 Match length 86 % identity (AC003979) Similar to LIM17 gene product gb 1653769 from NCBI Description the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana] 138715 Seq. No. Seq. ID LIB23-026-Q1-E1-H2 Method BLASTX NCBI GI q2317911 BLAST score 442 E value 5.0e-44 Match length 105 85 % identity NCBI Description (U89959) similar to GTP-binding protein [Arabidopsis thaliana] Seq. No. 138716 Seq. ID LIB23-026-Q1-E1-H3

Method BLASTN NCBI GI q4678291 233 BLAST score 1.0e-128 E value 346 Match length % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10

(ESSA project)

Seq. No. 138717

Seq. ID LIB23-026-Q1-E1-H9

Method BLASTN NCBI GI g4733952 BLAST score 223 1.0e-122 E value Match length 251 97 % identity

Arabidopsis thaliana chromosome I BAC F23H11 genomic NCBI Description

sequence, complete sequence



```
Seq. No.
                   138718
Seq. ID
                  LIB23-027-Q1-E1-A12
Method
                  BLASTN
NCBI GI
                  q4757401
BLAST score
                  86
E value
                  1.0e-40
Match length
                  183
% identity
                  91
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGH6, complete sequence
Seq. No.
                  138719
Seq. ID
                  LIB23-027-Q1-E1-A3
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  20
E value
                  1.8e-01
Match length
                  48
                  31
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  138720
Seq. ID
                  LIB23-027-Q1-E1-A8
Method
                  BLASTN
NCBI GI
                  q3402745
BLAST score
                  260
E value
                  1.0e-144
Match length
                  374
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5
NCBI Description
                   (ESSAII project)
Seq. No. Seq. ID
                  138721
                  LIB23-027-Q1-E1-A9
Method
                  BLASTX
                  q3021270
NCBI GI
BLAST score
                  471
E value
                  2.0e-47
Match length
                  104
% identity
                  87
NCBI Description
                   (AL022347) serine/threonine kinase -like protein
                   [Arabidopsis thaliana]
Seq. No.
                  138722
Seq. ID
                  LIB23-027-Q1-E1-B8
                  BLASTX
```

Method NCBI GI g1170203 BLAST score 647 E value 6.0e-68 Match length 128 % identity 99

GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi 454359 NCBI Description

(U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]

Seq. No. 138723

Seq. ID LIB23-027-Q1-E1-C10

Method BLASTX



```
NCBI GI
                  q2435514
BLAST score
                  550
E value
                  1.0e-56
Match length
                  123
% identity
                  84
                  (AF024504) Similar to serine/threonine protein kinase;
NCBI Description
                  coded for by A. thaliana cDNA T20930; coded for by A.
                  thaliana cDNA T43472 [Arabidopsis thaliana]
Seq. No.
                  138724
                  LIB23-027-Q1-E1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220527
BLAST score
                  481
                  1.0e-48
E value
                  122
Match length
% identity
                  66
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  138725
                  LIB23-027-Q1-E1-C3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2564046
BLAST score
                  148
E value
                  1.0e-77
Match length
                  281
% identity
                  96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MGI19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138726
                  LIB23-027-Q1-E1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2895510
BLAST score
                  451
E value
                  5.0e-45
Match length
                  121
% identity
                  77
NCBI Description
                  (AF033204) putative pectin methylesterase [Arabidopsis
                  thaliana]
Seq. No.
                  138727
Seq. ID
                  LIB23-027-Q1-E1-D8
Method
                  BLASTX
NCBI GI
                  g541816
BLAST score
                  525
E value
                  1.0e-53
Match length
                  125
% identity
                  74
```

NCBI Description protein kinase - common ice plant >gi_457689_emb_CAA82990_

(Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No. 138728

Seq. ID LIB23-027-Q1-E1-E11

Method BLASTX NCBI GI g4309697 BLAST score 482

```
1.0e-48
E value
Match length
                   95
% identity
                   94
                   (AC006266) putative DNA-directed RNA polymerase subunit
NCBI Description
                   [Arabidopsis thaliana]
                  138729
Seq. No.
                  LIB23-027-Q1-E1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1931647
BLAST score
                   473
                  1.0e-47
E value
Match length
                   88
% identity
                   98
                  (U95973) endomembrane protein EMP70 precusor isolog
NCBI Description
                   [Arabidopsis thaliana]
                   138730
Seq. No.
Seq. ID
                  LIB23-027-Q1-E1-F10
Method
                  BLASTX
                   g4455160
NCBI GI
BLAST score
                   316
                   4.0e-29
E value
Match length
                   92
% identity
                   77
                   (AL031187) kinesin-related protein katA (fragment)
NCBI Description
                   [Arabidopsis thaliana]
                   138731
Seq. No.
Seq. ID
                  LIB23-027-Q1-E1-F3
Method
                  BLASTX
                   g2894607
NCBI GI
BLAST score
                   194
                   7.0e-15
E value
Match length
                   60
                   60
% identity
                  (AL021889) NAM (no apical meristem) - like protein
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 138732

LIB23-027-Q1-E1-G6 Seq. ID

Method BLASTX g1170089 NCBI GI 651 BLAST score E value 2.0e-68 Match length 128 % identity 100

GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) NCBI Description

>gi_481822_pir__S39542 probable glutathione transferase (EC

2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789 dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione

S-transferase [Arabidopsis thaliana]

Seq. No. 138733

Seq. ID LIB23-027-Q1-E1-H9

Method BLASTN



```
NCBI GI
BLAST score
                  202
E value
                  1.0e-110
Match length
                  369
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRG7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138734
Seq. ID
                  LIB23-028-Q1-E1-A3
Method
                  BLASTN
NCBI GI
                  q2264310
BLAST score
                  267
                  1.0e-148
E value
Match length
                  312
% identity
                  95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MKP11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138735
                  LIB23-028-Q1-E1-A8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3241923
BLAST score
                  269
E value
                  1.0e-150
Match length
                  373
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MMN10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138736
Seq. ID
                  LIB23-028-Q1-E1-C9
Method
                  BLASTN
NCBI GI
                  g4753645
BLAST score
                  50
                  1.0e-19
E value
Match length
                  135
                  90
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18
                   (ESSA project)
Seq. No.
                  138737
Seq. ID
                  LIB23-028-Q1-E1-E6
Method
                  BLASTX
NCBI GI
                  g3036819
BLAST score
                  575
E value
                  1.0e-59
Match length
                  111
% identity
                  100
NCBI Description
                  (AJ000058) MCM3 homolog [Arabidopsis thaliana]
Seq. No.
                  138738
```

Seq. ID LIB23-028-Q1-E1-E8

Method BLASTX
NCBI GI g1169422
BLAST score 210
E value 9.0e-17



Match length 52 % identity 79

NCBI Description DIHYDROFOLATE REDUCTASE 1 / THYMIDYLATE SYNTHASE 1

(DHFR-TS) >gi_289193 (L08593) dihydrofolate

reductase-thymidylate synthase [Arabidopsis thaliana]

Seq. No. 138739

Seq. ID LIB23-028-Q1-E1-F12

Method BLASTN
NCBI GI g2098816
BLAST score 350
E value 0.0e+00
Match length 350
% identity 100

NCBI Description Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No. 138740

Seq. ID LIB23-028-Q1-E1-F3

Method BLASTX
NCBI GI g4455209
BLAST score 421
E value 1.0e-41
Match length 84
% identity 98

NCBI Description (AL035440) putative Proline synthetase associated protein

[Arabidopsis thaliana]

Seq. No. 138741

Seq. ID LIB23-028-Q1-E1-G10

Method BLASTX
NCBI GI g1531762
BLAST score 195
E value 5.0e-15
Match length 51
% identity 75

NCBI Description (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis

thaliana]

Seq. No. 138742

Seq. ID LIB23-029-Q1-E1-A8

Method BLASTX
NCBI GI g2454184
BLAST score 484
E value 1.0e-64
Match length 129
% identity 92

NCBI Description (U80186) pyruvate dehydrogenase El beta subunit

[Arabidopsis thaliana]

Seq. No. 138743

Seq. ID LIB23-029-Q1-E1-B11

Method BLASTX
NCBI GI g4455273
BLAST score 334
E value 1.0e-31
Match length 81
% identity 80



NCBI Description (AL035527) subtilisin proteinase-like [Arabidopsis thaliana]

Seq. No. 138744

Seq. ID LIB23-029-Q1-E1-B9

Method BLASTX
NCBI GI g2494175
BLAST score 596
E value 5.0e-62
Match length 114
% identity 100

NCBI Description GLUTAMATE DECARBOXYLASE 2 (GAD 2) >gi_1184960 (U46665)

glutamate decarboxylase 2 [Arabidopsis thaliana]

>gi_1236619 (U49937) glutamate decarboxylase [Arabidopsis

thaliana]

Seq. No. 138745

Seq. ID LIB23-029-Q1-E1-C5

Method BLASTN
NCBI GI g2281081
BLAST score 65
E value 3.0e-28
Match length 187
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC F18019 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138746

Seq. ID LIB23-029-Q1-E1-D2

Method BLASTN
NCBI GI g3176695
BLAST score 285
E value 1.0e-159
Match length 285
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F14J9 genomic

sequence contains phyA marker, complete sequence

[Arabidopsis thaliana]

Seq. No. 138747

Seq. ID LIB23-029-Q1-E1-D8

Method BLASTN
NCBI GI g2738757
BLAST score 199
E value 1.0e-108
Match length 199
% identity 100

NCBI Description Arabidopsis thaliana 5'-adenylylsulfate reductase (APR2)

gene, complete cds

Seq. No. 138748

Seq. ID LIB23-029-Q1-E1-E1

Method BLASTN
NCBI GI g3869065
BLAST score 87
E value 2.0e-41
Match length 253



% identity 72

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K24M7, complete sequence [Arabidopsis thaliana]

Seq. No. 138749

Seq. ID LIB23-029-Q1-E1-E2

Method BLASTN
NCBI GI g2828278
BLAST score 51
E value 2.0e-20
Match length 51

Match length 51 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16

(ESSAII project)

Seq. No. 138750

Seq. ID LIB23-029-Q1-E1-F3

Method BLASTX
NCBI GI g2702276
BLAST score 514
E value 1.0e-52
Match length 97
% identity 99

NCBI Description (AC003033) putative beta-glucosidase [Arabidopsis thaliana]

Seq. No. 138751

Seq. ID LIB23-029-Q1-E1-G1

Method BLASTX
NCBI GI g1076366
BLAST score 587
E value 5.0e-61
Match length 113
% identity 97

NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis

thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi_992643 (U32186)

cyclophilin [Arabidopsis thaliana]

>gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase

[Arabidopsis thaliana]

Seq. No. 138752

Seq. ID LIB23-030-Q1-E1-A11

Method BLASTN
NCBI GI g4218109
BLAST score 124
E value 2.0e-63
Match length 274
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16

(ESSAII project)

Seq. No. 138753

Seq. ID LIB23-030-Q1-E1-A3

Method BLASTN NCBI GI g2924651 BLAST score 129 E value 1.0e-66



Match length 129 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No. 138754

Seq. ID LIB23-030-Q1-E1-A5

Method BLASTN
NCBI GI g3821780
BLAST score 34
E value 1.0e-09
Match length 34
% identity 59

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 138755

Seq. ID LIB23-030-Q1-E1-B7

Method BLASTN
NCBI GI g2702261
BLAST score 356
E value 0.0e+00
Match length 356
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T21L14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138756

Seq. ID LIB23-030-Q1-E1-D5

Method BLASTX
NCBI GI 94415933
BLAST score 610
E value 1.0e-63
Match length 117
% identity 98

NCBI Description (AC006418) putative cellular apoptosis susceptibility

protein [Arabidopsis thaliana]

>gi_4559390_gb_AAD23050.1_AC006526_15 (AC006526) putative
cellular apoptosis susceptibility protein [Arabidopsis

thaliana]

Seq. No. 138757

Seq. ID LIB23-030-Q1-E1-F3

Method BLASTN
NCBI GI 94220468
BLAST score 141
E value 8.0e-74
Match length 157
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC T8011 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138758

Seq. ID LIB23-031-Q1-E1-B3

Method BLASTN
NCBI GI g2832639
BLAST score 219
E value 1.0e-120



Match length 275 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12

(ESSAII project)

Seq. No. 138759

Seq. ID LIB23-031-Q1-E1-B4

Method BLASTX
NCBI GI g4455351
BLAST score 362
E value 1.0e-34
Match length 94
% identity 71

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 138760

Seq. ID LIB23-031-Q1-E1-C6

Method BLASTX
NCBI GI g115783
BLAST score 512
E value 3.0e-52
Match length 96
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 138761

Seq. ID LIB23-031-Q1-E1-C8

Method BLASTN
NCBI GI g4220628
BLAST score 323
E value 0.0e+00
Match length 344
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K24C1, complete sequence [Arabidopsis thaliana]

Seq. No. 138762

Seq. ID LIB23-031-Q1-E1-D10

Method BLASTN
NCBI GI g2979540
BLAST score 200
E value 1.0e-108
Match length 306
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F17K2 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138763

Seq. ID LIB23-031-Q1-E1-E10

Method BLASTN
NCBI GI g4510392
BLAST score 346
E value 0.0e+00
Match length 350



% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T17D12 genomic

sequence, complete sequence

Seq. No. 138764

Seq. ID LIB23-031-Q1-E1-F1

Method BLASTX
NCBI GI g2244750
BLAST score 484
E value 6.0e-49
Match length 106
% identity 90

NCBI Description (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]

>gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase

[Arabidopsis thaliana]

Seq. No. 138765

Seq. ID LIB23-031-Q1-E1-F3

Method BLASTN
NCBI GI g3980374
BLAST score 41
E value 6.0e-14
Match length 41
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F16P2 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138766

Seq. ID LIB23-031-Q1-E1-F5

Method BLASTX
NCBI GI g115767
BLAST score 499
E value 9.0e-51
Match length 95
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir_A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 138767

Seq. ID LIB23-031-Q1-E1-F7

Method BLASTN
NCBI GI g2828186
BLAST score 398
E value 0.0e+00
Match length 398
% identity 77

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18I23, complete sequence [Arabidopsis thaliana]

Seq. No. 138768

Seq. ID LIB23-031-Q1-E1-G11

Method BLASTX

NCBI GI

BLAST score

g4417296

151



```
q4678939
NCBI GI
BLAST score
                  172
                  3.0e-12
E value
Match length
                  61
                  56
% identity
                  (AL049711) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  138769
                  LIB23-031-Q1-E1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4218535
BLAST score
                  335
E value
                  2.0e-31
Match length
                  88
                  65
% identity
                  (AJ010829) GRAB1 protein [Triticum sp.]
NCBI Description
                  138770
Seq. No.
Seq. ID
                  LIB23-032-Q1-E1-F1
Method
                  BLASTN
                  g2564046
NCBI GI
BLAST score
                  261
E value
                  1.0e-145
Match length
                  261
% identity
                  100
NCBI Description
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MGI19, complete sequence [Arabidopsis thaliana]
                  138771
Seq. No.
Seq. ID
                  LIB23-032-Q1-E1-F11
Method
                  BLASTX
NCBI GI
                  g1699023
BLAST score
                  455
E value
                  2.0e-45
Match length
                  84
% identity
                  100
                  (U78866) putative arginine-aspartate-rich RNA binding
NCBI Description
                  protein [Arabidopsis thaliana] >gi 1699051 (U78867)
                  putative aspartate-arginine-rich mRNA binding protein
                   [Arabidopsis thaliana]
Seq. No.
                  138772
Seq. ID
                  LIB23-032-Q1-E1-H12
Method
                  BLASTX
NCBI GI
                  q4689473
BLAST score
                  263
E value
                   6.0e-23
Match length
                  133
% identity
NCBI Description
                   (AC007213) putative receptor protein kinase [Arabidopsis
                  thaliana]
                  138773
Seq. No.
Seq. ID
                  LIB23-032-Q1-E1-H5
Method
                  BLASTX
```



E value 2.0e-36
Match length 92
% identity 59

NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]

>gi 4587592 gb AAD25820.1_AC007232_10 (AC007232) unknown

protein [Arabidopsis thaliana]

Seq. No. 138774

Seq. ID LIB23-033-Q1-E1-B5

Method BLASTN
NCBI GI g3763915
BLAST score 192
E value 1.0e-104
Match length 404
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F14B2 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138775

Seq. ID LIB23-033-Q1-E1-C4

Method BLASTX
NCBI GI g1171978
BLAST score 369
E value 2.0e-35
Match length 91
% identity 35

NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)

(PABP 2) >gi 304109 (L19418) poly(A)-binding protein

[Arabidopsis thaliana] >gi 2911051 emb_CAA17561_ (AL021961)

poly(A)-binding protein [Arabidopsis thaliana]

Seq. No. 138776

Seq. ID LIB23-033-Q1-E1-D8

Method BLASTX
NCBI GI g4176545
BLAST score 256
E value 4.0e-22
Match length 114
% identity 43

NCBI Description (AL035259) strong similarity to human leukotriene a-4

hydrolase [Schizosaccharomyces pombe]

Seq. No. 138777

Seq. ID LIB23-033-Q1-E1-E4

Method BLASTX
NCBI GI g115783
BLAST score 479
E value 2.0e-48
Match length 90
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >qi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 138778

Seq. ID LIB23-033-Q1-E1-E6



Method BLASTX
NCBI GI g1903021
BLAST score 630
E value 6.0e-66
Match length 125
% identity 100

NCBI Description (Y10216) hypothetical 3-isopropylmalate dehydrogenase

[Arabidopsis thaliana]

Seq. No. 138779

Seq. ID LIB23-033-Q1-E1-F6

Method BLASTX
NCBI GI g115783
BLAST score 479
E value 3.0e-48
Match length 90
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 138780

Seq. ID LIB23-033-Q1-E1-G1

Method BLASTX
NCBI GI g2244852
BLAST score 121
E value 1.0e-43
Match length 91
% identity 99

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 138781

Seq. ID LIB23-033-Q1-E1-G10

Method BLASTN
NCBI GI g3449329
BLAST score 292
E value 1.0e-163
Match length 448
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDH9, complete sequence [Arabidopsis thaliana]

Seq. No. 138782

Seq. ID LIB23-034-Q1-E1-D2

Method BLASTX
NCBI GI g4049344
BLAST score 365
E value 5.0e-35
Match length 71
% identity 97

NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 138783

Seq. ID LIB23-034-Q1-E1-D6

Method BLASTX NCBI GI g4049344



BLAST score 286 E value 6.0e-26 Match length 69 % identity 84

NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 138784

Seq. ID LIB23-034-Q1-E1-F10

Method BLASTX
NCBI GI g2262113
BLAST score 789
E value 2.0e-84
Match length 150
% identity 99

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 138785

Seq. ID LIB23-034-Q1-E1-F8

Method BLASTX
NCBI GI g3757518
BLAST score 750
E value 5.0e-80
Match length 142
% identity 100

NCBI Description (AC005167) putative immediate-early salicylate-induced

glucosyltransferase [Arabidopsis thaliana]

Seq. No. 138786

Seq. ID LIB23-034-Q1-E1-G4

Method BLASTX
NCBI GI g2499616
BLAST score 491
E value 9.0e-50
Match length 117
% identity 77

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG NTF6 (P43)

>gi_1076639_pir__S51320 mitogen-activated protein kinase 6
(EC 2.7.1.-) - common tobacco >gi_2129967_pir__S68189
serine/threonine protein kinase p43 - common tobacco
>gi_634068_emb_CAA58760_ (X83879) p43Nft6 serine/threonine

protein kinase [Nicotiana tabacum]

Seq. No. 138787

Seq. ID LIB23-034-Q1-E1-H7

Method BLASTX
NCBI GI g2118045
BLAST score 352
E value 2.0e-33
Match length 59
% identity 97

NCBI Description beta-fructofuranosidase (EC 3.2.1.26) - Arabidopsis

thaliana (fragment) >gi_899153_emb_CAA61624_ (X89454)

beta-fructofuranosidase [Arabidopsis thaliana]

Seq. No. 138788

Seq. ID LIB23-034-Q1-E1-H8

Method BLASTN



```
q3335356
NCBI GI
BLAST score .
                  305
                  1.0e-171
E value
                  490
Match length
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F16M14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  138789
Seq. No.
                  LIB23-035-Q1-E1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351014
BLAST score
                  193
                  7.0e-15
E value
                  78
Match length
                  54
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902_dbj BAA07207_ (D38010)
                  ribosomal protein S8 [Oryza sativa]
                  138790
Seq. No.
                  LIB23-035-Q1-E1-H9
Seq. ID
                  BLASTX
Method
                  q4455223
NCBI GI
BLAST score
                  275
                  8.0e-26
E value
Match length
                  109
                  27
% identity
                  (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  138791
Seq. No.
                  LIB23-035-Q1-E112-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4519194
                  90
BLAST score
E value
                  2.0e-43
Match length
                  185
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHM17, complete sequence
                  138792
Seq. No.
                  LIB23-035-Q1-E112-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2464913
BLAST score
                  648
E value
                  4.0e-68
Match length
                  126
% identity
NCBI Description
                  (Z99708) sugar transporter like protein [Arabidopsis
                  thaliana]
                  138793
Seq. No.
```

Seq. ID LIB23-035-Q1-E112-A7

Method BLASTX
NCBI GI g2688299
BLAST score 321



```
E value
                   9.0e-30
Match length
                  117
% identity
NCBI Description
                  (AE001145) prolyl-tRNA synthetase (proS) [Borrelia
                  burgdorferi]
Seq. No.
                  138794
Seq. ID
                  LIB23-035-Q1-E112-B8
Method
                  BLASTX
NCBI GI
                  q1175467
BLAST score
                  153
E value
                  4.0e-10
Match length
                  86
% identity
                  38
                  HYPOTHETICAL 69.5 KD PROTEIN C22G7.05 IN CHROMOSOME I
NCBI Description
                  >gi_2130326_pir__S62449 hypothetical protein SPAC22G7.05 -
                   fission yeast (Schizosaccharomyces pombe)
                  >gi_1009455_emb_CAA91129.1_ (Z54328) hypothetical protein
                   [Schizosaccharomyces pombe]
Seq. No.
                  138795
Seq. ID
                  LIB23-035-Q1-E112-D4
Method
                  BLASTX
NCBI GI
                  g2506139
BLAST score
                   385
E value
                   3.0e-37
Match length
                  92
                  83
% identity
                  COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
NCBI Description
                   (ARCHAIN) >gi 1314049 emb CAA91901 (Z67962)
                   archain/delta-COP [Oryza sativa]
Seq. No.
                   138796
Seq. ID
                   LIB23-035-Q1-E112-D7
Method
                   BLASTN
NCBI GI
                   q2262135
BLAST score
                   166
                   3.0e-88
E value
                   426
Match length
% identity
                   99
                  Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
NCBI Description
                   cM, complete sequence
                   138797
Seq. No.
Seq. ID
                   LIB23-035-Q1-E112-E5
Method
                   BLASTX
NCBI GI
                   q4581146
BLAST score
                   425
E value
                   6.0e-42
Match length
                   88
% identity
                   (AC006919) putative fructose-bisphosphate aldolase,
NCBI Description
                   cytoplasmic [Arabidopsis thaliana]
```

Cycop

Seq. No.

Seq. ID LIB23-035-Q1-E112-G5

138798

Method BLASTX



```
q166834
NCBI GI
BLAST score
                  150
E value
                  1.0e-29
Match length
                  68
                  100
% identity
                  (M86720) ribulose bisphosphate carboxylase/oxygenase
NCBI Description
                  activase [Arabidopsis thaliana] >gi 2642155 (AC003000)
                  Rubisco activase [Arabidopsis thaliana]
                  138799
Seq. No.
                  LIB23-036-Q1-E1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g99696
BLAST score
                  295
                  9.0e-27
E value
Match length
                  81
                  75
% identity
NCBI Description
                  glutamate--ammonia ligase (EC 6.3.1.2) precursor,
                  chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana
                  >gi 240070 bbs 69728 (S69727) light-regulated glutamine
                  synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430
                  aa] [Arabidopsis thaliana] >gi 228453 prf 1804333A Gln
                  synthetase [Arabidopsis thaliana]
Seq. No.
                  138800
                  LIB23-036-Q1-E1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4490717
                  200
BLAST score
E value
                  1.0e-108
Match length
                  269
                  93
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone
NCBI Description
                  project)
Seq. No.
                  138801
Seq. ID
                  LIB23-036-Q1-E1-C6
Method
                  BLASTX
                  g1173218
NCBI GI
BLAST score
                  471
                  2.0e-47
E value
Match length
                  92
                  100
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.
                  138802
Seq. ID
                  LIB23-036-Q1-E1-D12
Method
                  BLASTX
NCBI GI
                  q3850569
```

Method BLASTX
NCBI GI g3850569
BLAST score 273
E value 4.0e-24
Match length 112
% identity 44

NCBI Description (AC005278) ESTs gb_T21276, gb_T45403, and gb_AA586113 come

from this gene. [Arabidopsis thaliana]



```
138803
Seq. No.
                  LIB23-036-Q1-E1-E6
Seq. ID
Method
                  BLASTN
                  g2252823
NCBI GI
                  204
BLAST score
                  1.0e-111
E value
                  290
Match length
                  96
% identity
NCBI Description Arabidopsis thaliana BAC IG005I10
                  138804
Seq. No.
                  LIB23-036-Q1-E1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827537
                  413
BLAST score
                  1.0e-40
E value
                  125
Match length
% identity
                   66
                   (AL021633) putative zinc finger protein [Arabidopsis
NCBI Description
                   thalianaJ
                   138805
Seq. No.
                  LIB23-036-Q1-E1-F1
Seq. ID
                  BLASTX
Method
                   g4204849
NCBI GI
BLAST score
                   316
                   3.0e-29
E value
Match length
                   80
                   75
% identity
                  (U55875) protein kinase [Arabidopsis thaliana]
NCBI Description
                   138806
Seq. No.
                   LIB23-036-Q1-E1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3335337
BLAST score
                   545
E value
                   5.0e-56
                   110
Match length
                   99
% identity
                  (AC004512) Similar to acyl carrier protein, mitochondrial
NCBI Description
                   precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD
                   subunit (MYACP-1), gb_L23574 from A. thaliana.
                   gb Z30712, gb Z30713, gb Z26204, gb N37975 and gb N96330
                   come from this gene
                   138807
Seq. No.
                   LIB23-036-Q1-E1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q461550
BLAST score
                   393
```

Method BLASTX
NCBI GI g461550
BLAST score 393
E value 3.0e-38
Match length 113
% identity 73

NCBI Description ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR

>gi_81635_pir__B39732 H+-transporting ATP synthase (EC

3.6.1.34) gamma-1 chain precursor, chloroplast -



Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana]

Seq. No. 138808

Seq. ID LIB23-036-Q1-E1-G1

Method BLASTX
NCBI GI g4467099
BLAST score 461
E value 3.0e-46
Match length 90
% identity 100

NCBI Description (AL035538) glycine hydroxymethyltransferase like protein

[Arabidopsis thaliana]

Seq. No. 138809

Seq. ID LIB23-036-Q1-E1-H2

Method BLASTX
NCBI GI g3142303
BLAST score 428
E value 3.0e-42
Match length 126
% identity 33

NCBI Description (AC002411) Strong similarity to MRP-like ABC transporter

gb_U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No. 138810

Seq. ID LIB23-036-Q1-E1-H8

Method BLASTX
NCBI GI g2344890
BLAST score 153
E value 4.0e-10
Match length 41
% identity 71

NCBI Description (AC002388) TINY transcription factor isolog [Arabidopsis

thaliana]

Seq. No. 138811

Seq. ID LIB23-037-Q1-E1-A10

Method BLASTX
NCBI GI g4586021
BLAST score 509
E value 7.0e-52
Match length 112
% identity 90

NCBI Description (AC007170) putative cytoplasmic aconitate hydratase

[Arabidopsis thaliana]

Seq. No. 138812

Seq. ID LIB23-037-Q1-E1-A12

Method BLASTX
NCBI GI g115783
BLAST score 512
E value 3.0e-52
Match length 96
% identity 100



```
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  138813
Seq. No.
                  LIB23-037-Q1-E1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4159708
BLAST score
                  374
                  0.0e+00
E value
Match length
                  374
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MKP6, complete sequence
Seq. No.
                  138814
                  LIB23-037-Q1-E1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2749918
BLAST score
                  190
E value
                  1.0e-103
Match length
                  238
% identity
                  100
                  Arabidopsis thaliana chromosome I BAC F3I6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138815
Seq. ID
                  LIB23-037-Q1-E1-B5
Method
                  BLASTN
NCBI GI
                  g1022779
BLAST score
                  116
                  7.0e-59
E value
Match length
                  147
% identity
                  93
NCBI Description Arabidopsis thaliana GF14 Kappa isoform mRNA, complete cds
Seq. No.
                  138816
                  LIB23-037-Q1-E1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3128141
BLAST score
                  213
E value
                  1.0e-116
Match length
                  382
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQD22, complete sequence [Arabidopsis thaliana]
                  138817
Seq. No.
Seq. ID
                  LIB23-037-Q1-E1-D12
Method
                  BLASTN
```

NCBI GI g3449313 BLAST score 259 E value 1.0e-144 Match length 388

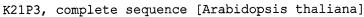
100

% identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

Seq. ID





```
Seq. No.
                  138818
                  LIB23-037-Q1-E1-D2
Seq. ID
                  BLASTX
Method
                  g4559333
NCBI GI
BLAST score
                  396
                  1.0e-38
E value
                  115
Match length
                  43
% identity
                  (AC007087) unknown protein [Arabidopsis thaliana]
NCBI Description
                  138819
Seq. No.
Seq. ID
                  LIB23-037-Q1-E1-D5
Method
                  BLASTN
                  g2244829
NCBI GI
BLAST score
                  128
                   4.0e-66
E value
                  132
Match length
% identity
                  99
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  138820
Seq. No.
Seq. ID
                  LIB23-037-Q1-E1-E7
                  BLASTN
Method
                   g3600062
NCBI GI
BLAST score
                   346
                   0.0e + 00
E value
Match length
                   358
                   99
% identity
NCBI Description Arabidopsis thaliana BAC T25C13
                   138821
Seq. No.
                   LIB23-037-Q1-E1-F2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4191760
BLAST score
                   171
                   3.0e-91
E value
Match length
                   377
                   99
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F17F8,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   138822
                   LIB23-037-Q1-E1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4467134
BLAST score
                   247
E value
                   1.0e-21
Match length
                   47
                   100
% identity
                   (AL035540) protein kinase like protein [Arabidopsis
NCBI Description
                   thaliana]
                   138823
Seq. No.
```

16738

LIB23-037-Q1-E1-G10

NCBI GI

BLAST score



```
Method
                  BLASTN
                  g3869075
NCBI GI
BLAST score
                  241
                  1.0e-133
E value
                  356
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXK3, complete sequence [Arabidopsis thaliana]
                  138824
Seq. No.
                  LIB23-037-Q1-E1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g99742
BLAST score
                  563
E value
                  4.0e-58
Match length
                  126
                  88
% identity
                  2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 1
NCBI Description
                  - Arabidopsis thaliana
Seq. No.
                  138825
                  LIB23-037-Q1-E1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3482929
BLAST score
                  369
                  2.0e-35
E value
Match length
                  87
                  74
% identity
                   (AC003970) Putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                  138826
Seq. No.
                  LIB23-037-Q1-E1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g541816
BLAST score
                   293
                   5.0e-27
E value
Match length
                   57
                  95
% identity
                  protein kinase - common ice plant >gi_457689_emb_CAA82990_
NCBI Description
                   (Z30329) protein kinase [Mesembryanthemum crystallinum]
Seq. No.
                   138827
Seq. ID
                  LIB23-038-Q1-E1-C3
Method
                  BLASTX
                   g4038352
NCBI GI
BLAST score
                   335
                   2.0e-31
E value
Match length
                   132
% identity
                   45
NCBI Description
                  (AF098951) breast cancer resistance protein [Homo sapiens]
Seq. No.
                   138828
Seq. ID
                  LIB23-038-Q1-E1-D1
Method
                   BLASTN
```

16739

g3821780



E value 1.0e-08
Match length 36
% identity 97

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No.

138829

Seq. ID

LIB23-038-Q1-E1-D10

Method BLASTN
NCBI GI g2351065
BLAST score 318
E value 1.0e-179
Match length 434
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MHF15, complete sequence [Arabidopsis thaliana]

Seq. No. 138830

Seq. ID LIB23-038-Q1-E1-E12

Method BLASTX
NCBI GI g120667
BLAST score 493
E value 5.0e-50
Match length 95
% identity 97

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis

thaliana >gi_166706 (M64116) cystolic

glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi 166710 (M64119) glyceraldehyde-3-phosphate

dehydrogenase [Arabidopsis thaliana]

Seq. No. 138831

Seq. ID LIB23-038-Q1-E1-E4

Method BLASTN
NCBI GI g2564044
BLAST score 388
E value 0.0e+00
Match length 404
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19P17, complete sequence [Arabidopsis thaliana]

Seq. No. 138832

Seq. ID LIB23-038-Q1-E1-F10

Method BLASTN
NCBI GI g4760411
BLAST score 189
E value 1.0e-102
Match length 390
% identity 99

NCBI Description Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,

complete sequence

Seq. No. 138833

Seq. ID LIB23-038-Q1-E1-G10

Method BLASTN

Match length



```
q3299824
NCBI GI
BLAST score
                   189
E value
                  1.0e-102
Match length
                   379
                  99
% identity
                  Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,
NCBI Description
                  near 17 cM, complete sequence [Arabidopsis thaliana]
                  138834
Seq. No.
Seq. ID
                  LIB23-038-Q1-E1-G3
Method
                  BLASTX
NCBI GI
                  g2462746
BLAST score
                  571
E value
                  5.0e-59
Match length
                  116
                  96
% identity
                   (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                  thaliana]
                  138835
Seq. No.
Seq. ID
                  LIB23-038-Q1-E1-G5
Method
                  BLASTN
NCBI GI
                  g4220644
BLAST score
                  374
E value
                  0.0e+00
Match length
                  374
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MXL8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   138836
Seq. ID
                  LIB23-038-Q1-E1-H7
Method
                  BLASTX
NCBI GI
                   g2244878
BLAST score
                   275
                   3.0e-24
E value
Match length
                  70
                   59
% identity
NCBI Description
                  (Z97338) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   138837
Seq. ID
                  LIB23-039-Q1-E1-C3
Method
                   BLASTX
NCBI GI
                   q3046815
BLAST score
                   258
E value
                   1.0e-22
Match length
                   56
% identity
                   84
NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   138838
Seq. ID
                   LIB23-039-Q1-E1-E1
Method
                  BLASTN
NCBI GI
                   g2392894
BLAST score
                   289
E value
                   1.0e-162
```



```
% identity
                  Arabidopsis thaliana brassinosteroid insensitive 1 (BRI1)
NCBI Description
                  gene, complete cds
                  138839
Seq. No.
                  LIB23-040-Q1-E1-C3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2924731
BLAST score
                  157
                  3.0e-83
E value
                  224
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSI17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138840
                  LIB23-040-Q1-E1-E2
Seq. ID
Method
                  BLASTN
                  g3859590
NCBI GI
BLAST score
                  92
                  3.0e-44
E value
                  297
Match length
                  93
% identity
                  Arabidopsis thaliana BAC T15B16
NCBI Description
Seq. No.
                  138841
                  LIB23-040-Q1-E1-E9
Seq. ID
                  BLASTX
Method
                  q2388585
NCBI GI
BLAST score
                  321
                  1.0e-29
E value
Match length
                  83
                  80
% identity
                  (AC000098) Similar to Caenorhabditis unknown protein
NCBI Description
                  T03F1.1 (gb U88169). [Arabidopsis thaliana]
                  138842
Seq. No.
                  LIB23-040-Q1-E1-G12
Seq. ID
Method
                  BLASTX
                  g1168470
NCBI GI
                  503
BLAST score
E value
                  4.0e-51
Match length
                  127
                  74
% identity
                  PROTEIN KINASE APK1A >gi 282877 pir S28615 protein kinase,
NCBI Description
                  tyrosine/serine/threonine-specific (EC 2.7.1.-) -
                  Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522)
                  protein tyrosine-serine-threonine kinase [Arabidopsis
                  thaliana]
```

Seq. No. 138843

Seq. ID LIB23-040-Q1-E1-H3

Method BLASTN NCBI GI g2564049 BLAST score 274 E value 1.0e-153 Match length 300

% identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MLE2, complete sequence [Arabidopsis thaliana] 138844 Seq. No. LIB23-041-Q1-E1-B11 Seq. ID Method BLASTN NCBI GI q2673901 BLAST score 391 0.0e + 00E value 391 Match length 100 % identity Arabidopsis thaliana chromosome II BAC T24P15 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 138845 Seq. No. LIB23-041-Q1-E1-B9 Seq. ID BLASTX Method g320552 NCBI GI 583 BLAST score 2.0e-60 E value 129 Match length 89 % identity anthranilate synthase (EC 4.1.3.27) alpha-1 chain -NCBI Description Arabidopsis thaliana 138846 Seq. No. LIB23-041-Q1-E1-D12 Seq. ID Method BLASTX NCBI GI q2497702 BLAST score 205

4.0e-16 E value Match length 117 44 % identity

OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR NCBI Description

> >gi_2121019_pir__I40710 outer membrane lipoprotein -Citrobacter freundii >gi_717136 (U21727) lipocalin

precursor [Citrobacter freundii]

Seq. No. 138847

LIB23-041-01-E1-E1 Seq. ID

Method BLASTX NCBI GI q2367392 BLAST score 252 E value 8.0e-22 Match length 92 % identity

NCBI Description (U82513) random slug cDNA25 protein [Dictyostelium

discoideum]

Seq. No. 138848

Seq. ID LIB23-041-Q1-E1-F10

Method BLASTN NCBI GI g4585952 BLAST score 406 0.0e + 00E value Match length 406

NCBI Description



```
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F26F24,
NCBI Description
                  complete sequence
                  138849
Seq. No.
Seq. ID
                  LIB23-041-Q1-E1-F9
Method
                  BLASTX
NCBI GI
                  g4115931
BLAST score
                  554
                  5.0e-57
E value
Match length
                  137
% identity
                  79
NCBI Description
                  (AF118223) contains similarity to Guillardia theta ABC
                  transporter (GB:AF041468) [Arabidopsis thaliana]
                  138850
Seq. No.
                  LIB23-041-Q1-E1-G9
Seq. ID
Method
                  BLASTX
                  g3688175
NCBI GI
BLAST score
                  560
                  9.0e-58
E value
Match length
                  126
                   84
% identity
NCBI Description
                   (AL031804) gamma-VPE (vacuolar processing enzyme)
                   [Arabidopsis thaliana]
                  138851
Seq. No.
Seq. ID
                  LIB23-041-Q1-E1-H6
Method
                  BLASTX
NCBI GI
                  q2829896
                   238
BLAST score
                   4.0e-20
E value
Match length
                  103
% identity
                   50
                   (AC002311) highly similar to auxin-regulated protein GH3,
NCBI Description
                  gp_X60033_18591 [Arabidopsis thaliana]
Seq. No.
                   138852
Seq. ID
                  LIB23-041-Q1-E1-H7
Method
                  BLASTN
NCBI GI
                  q413731
BLAST score
                   296
E value
                   1.0e-166
Match length
                   321
% identity
                   98
NCBI Description
                  Arabidopsis thaliana phytoene synthase mRNA, complete cds
Seq. No.
                  138853
Seq. ID
                  LIB23-042-Q1-E1-C9
Method
                  BLASTN
NCBI GI
                  g2564048
BLAST score
                   380
E value
                   0.0e+00
                   420
Match length
% identity
                   99
```

16744

MKD15, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



```
Seq. No.
                  138854
Seq. ID
                  LIB23-042-Q1-E1-D1
Method
                  BLASTX
NCBI GI
                  q2914703
                  243
BLAST score
E value
                  1.0e-20
                  52
Match length
                  87
% identity
                  (AC003974) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  138855
Seq. ID
                  LIB23-042-Q1-E1-D12
Method
                  BLASTN
NCBI GI
                  g4519188
BLAST score
                  257
                  1.0e-142
E value
Match length
                  446
% identity
                  100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K21L19, complete sequence
                  138856
Seq. No.
Seq. ID
                  LIB23-042-Q1-E1-D2
Method
                  BLASTX
                  g2809252
NCBI GI
BLAST score
                  495
E value
                  2.0e-50
Match length
                  98
% identity
                  99
NCBI Description
                  (AC002560) F21B7.21 [Arabidopsis thaliana]
Seq. No.
                  138857
Seq. ID
                  LIB23-042-Q1-E1-D6
Method
                  BLASTX
NCBI GI
                  q3687445
BLAST score
                  222
E value
                  3.0e-18
Match length
                  105
% identity
                  37
NCBI Description
                  (AL022398) dJ434014.5 (novel PUTATIVE protein similar to
                  YIL091C yeast hypoyhetical 84 kD protein from SGA1-KTR7
                  intergenic region) [Homo sapiens]
Seq. No.
                  138858
Seq. ID
                  LIB23-042-Q1-E1-E1
Method
                  BLASTN
NCBI GI
                  q3128136
BLAST score
                  173
E value
                  1.0e-92
Match length
                  320
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K1F13, complete sequence [Arabidopsis thaliana]
```

LIB23-042-Q1-E1-H4

138859

Seq. No. Seq. ID

Seq. ID

Method



```
Method
                   BLASTX
NCBI GI
                   g1370152
BLAST score
                   264
E value
                   4.0e-23
Match length
                   62
                   79
% identity
NCBI Description
                   (Z73954) RAB11F [Lotus japonicus]
Seq. No.
                   138860
Seq. ID
                   LIB23-043-Q1-E1-A5
Method
                   BLASTX
NCBI GI
                   q2492784
BLAST score
                   166
                   1.0e-11
E value
                   54
Match length
                   57
% identity
                   2-ISOPROPYLMALATE SYNTHASE (ALPHA-ISOPROPYLMALATE SYNTHASE)
NCBI Description
                   (ALPHA-IPM SYNTHETASE) >gi_1770069_emb_CAA99531_ (Z75208) 2-isopropylmalate synthase [Bacillus subtilis]
                   >gi 2635293 emb CAB14788 (Z99118) 2-isopropylmalate
                   synthase [Bacillus subtilis]
Seq. No.
                   138861
Seq. ID
                   LIB23-043-Q1-E1-B5
Method
                   BLASTN
NCBI GI
                   q4220643
BLAST score
                   219
E value
                   1.0e-120
Match length
                   412
                   100
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MWD22, complete sequence [Arabidopsis thaliana]
Seq. No.
                   138862
Seq. ID
                   LIB23-043-Q1-E1-C11
Method
                   BLASTX
NCBI GI
                   q2281090
BLAST score
                   574
E value
                   2.0e-59
Match length
                   132
% identity
                   89
                   (AC002333) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   138863
Seq. ID
                   LIB23-043-Q1-E1-D7
                   BLASTN
Method
NCBI GI
                   q4159704
BLAST score
                   216
E value
                   1.0e-118
Match length
                   356
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MCB17, complete sequence
Seq. No.
                   138864
```

16746

LIB23-043-Q1-E1-E6

BLASTX



q2194127 NCBI GI BLAST score 662 1.0e-69 E value 126 Match length 100 % identity

(AC002062) Strong similarity to Arabidopsis receptor-like NCBI Description

protein kinase (gb_ATLECGENE) and F20P5.16. [Arabidopsis

thaliana]

138865 Seq. No.

Seq. ID LIB23-043-Q1-E1-F12

Method BLASTX g4262186 NCBI GI BLAST score 419 1.0e-41 E value 84 Match length 98 % identity

(AC005508) Highly similar to cullin 3 [Arabidopsis NCBI Description

thaliana]

138866 Seq. No.

LIB23-043-Q1-E1-F6 Seq. ID

Method BLASTN NCBI GI g2511585 BLAST score 246 E value 1.0e-136 Match length 246 100 % identity

NCBI Description Arabidopsis thaliana mRNA for proteasome subunit prc2b

138867 Seq. No.

LIB23-043-Q1-E1-F8 Seq. ID

Method BLASTN NCBI GI g2264315 BLAST score 161 E value 2.0e-85 Match length 373 % identity 100

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MRN17, complete sequence [Arabidopsis thaliana]

138868 Seq. No.

LIB23-043-Q1-E1-G3 Seq. ID

Method BLASTN NCBI GI g3451055 BLAST score 149 E value 3.0e-78 Match length 343 % identity 97

Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 NCBI Description

(ESSAII project)

Seq. No. 138869

Seq. ID LIB23-043-Q1-E1-G4

Method BLASTX NCBI GI g3582333 BLAST score 279

Match length

% identity

120

93



```
6.0e-25
E value
Match length
                  118
% identity
                  44
                   (AC005496) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  138870
Seq. No.
                  LIB23-043-Q1-E1-H11
Seq. ID
Method
                  BLASTX
                  g1076348
NCBI GI
                  397
BLAST score
                  1.0e-38
E value
                  92
Match length
                  82
% identity
NCBI Description
                  myosin MYA1, class V - Arabidopsis thaliana
                  >gi 433663 emb CAA82234 (Z28389) myosin [Arabidopsis
                  thaliana]
                  138871
Seq. No.
Seq. ID
                  LIB23-044-Q1-E2-B12
Method
                  BLASTN
NCBI GI
                  g3985934
BLAST score
                  406
                  0.0e+00
E value
                   406
Match length
% identity
                   100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJE7, complete sequence [Arabidopsis thaliana]
                   138872
Seq. No.
                   LIB23-044-Q1-E2-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2618699
BLAST score
                   208
E value
                   2.0e-16
Match length
                   118
                   38
% identity
                  (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
                   138873
Seq. No.
Seq. ID
                   LIB23-044-Q1-E2-E2
Method
                   BLASTX
NCBI GI
                   q3080412
BLAST score
                   337
                   8.0e-32
E value
Match length
                   99
                   63
% identity
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   138874
Seq. ID
                   LIB23-044-Q1-E2-F8
Method
                   BLASTN
NCBI GI
                   q1419389
BLAST score
                   80
E value
                   1.0e-37
```

16748

NCBI Description A.thaliana mRNA for thylakoid-bound ascorbate peroxidase



```
Seq. No.
                  138875
                  LIB23-044-Q1-E2-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220468
                  79
BLAST score
                  9.0e-37
E value
                  139
Match length
% identity
                  89
                  Arabidopsis thaliana chromosome II BAC T8011 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  138876
Seq. No.
Seq. ID
                  LIB23-044-Q1-E2-G8
Method
                  BLASTX
NCBI GI
                  q3096918
BLAST score
                  549
                  2.0e-56
E value
Match length
                  132
% identity
                  86
NCBI Description
                  (AL023094) putative cyclase associated protein CAP
                   [Arabidopsis thaliana] >gi 3169136 dbj BAA28621 (AB014759)
                  Atcapl [Arabidopsis thaliana]
Seq. No.
                  138877
                  LIB23-044-Q1-E2-H12
Seq. ID
Method
                  BLASTN
                  g836939
NCBI GI
BLAST score
                  149
E value
                  1.0e-78
                  149
Match length
                  100
% identity
                  Arabidopsis thaliana calcium-dependent protein kinase
NCBI Description
                  (CDPK6) mRNA, complete cds
Seq. No.
                  138878
                  LIB23-044-Q1-E2-H5
Seq. ID
Method
                  BLASTX
                  g2708741
NCBI GI
BLAST score
                  354
E value
                  4.0e-34
Match length
                  75
                  93
% identity
NCBI Description
                  (AC003952) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  138879
                  LIB23-044-Q1-E2-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3152590
BLAST score
                  627
E value
                  1.0e-65
```

Match length 127 100 % identity

NCBI Description (AC002986) Similar to protein serine/threonine kinase NPK15

gb D31737 from Nicotiana tabacum. [Arabidopsis thaliana]

Seq. No. 138880



```
LIB23-044-Q1-E2-H9
Seq. ID
Method
                  BLASTN
                  g4159712
NCBI GI
                  247
BLAST score
                  1.0e-136
E value
                  375
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MWI23, complete sequence
                  138881
Seq. No.
Seq. ID
                  LIB23-045-Q1-E1-A11
Method
                  BLASTN
                  g3386593
NCBI GI
BLAST score
                  190
E value
                  1.0e-103
Match length
                  213
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F4I18 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  138882
Seq. No.
                  LIB23-045-Q1-E1-A2
Seq. ID
Method
                  BLASTX
                  q4584832
NCBI GI
BLAST score
                   218
                   6.0e-18
E value
                   78
Match length
                   51
% identity
                  (AL031764) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                   138883
Seq. No.
                  LIB23-045-Q1-E1-A3
Seq. ID
Method
                  BLASTX
                   g1702872
NCBI GI
BLAST score
                   478
E value
                   2.0e-48
Match length
                   94
                   100
% identity
NCBI Description
                   (Y09667) ferredoxin-dependent glutamate synthase
                   [Arabidopsis thaliana]
Seq. No.
                   138884
Seq. ID
                   LIB23-045-Q1-E1-A7
Method '
                   BLASTN
NCBI GI
                   q4455339
BLAST score
                   230
E value
                   1.0e-126
Match length
                   284
% identity
                   100
```

Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 NCBI Description

(ESSAII project)

138885

Seq. No.

Seq. ID LIB23-045-Q1-E1-A9 BLASTX Method

NCBI GI g115767



BLAST score 447

E value 8.0e-45

Match length 85

identity 100

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir_A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_(X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

 Seq. No.
 138886

 Seq. ID
 LIB23-045-Q1-E1-B10

 Method
 BLASTX

 NCBI GI
 g1172977

 BLAST score
 404

 E value
 9.0e-40

E value 9.0e
Match length 83
% identity 99

NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

 Seq. No.
 138887

 Seq. ID
 LIB23-045-Q1-E1-B12

 Method
 BLASTX

 NCBI GI
 q2507422

NCBI GI g2507422
BLAST score 173
E value 7.0e-13
Match length 35
% identity 100

NCBI Description CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS)

(O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi 3293261 (AF039206)

cystathionine gamma-synthase precursor [Arabidopsis

thaliana]

Seq. No. 138888

Seq. ID LIB23-045-Q1-E1-B2

Method BLASTX
NCBI GI g4406816
BLAST score 444
E value 2.0e-44
Match length 84
% identity 100

NCBI Description (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No. 138889

Seq. ID LIB23-045-Q1-E1-B8

Method BLASTN
NCBI GI g4544405
BLAST score 281
E value 1.0e-157
Match length 281
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F2818 genomic

sequence, complete sequence

Seq. ID

Method

NCBI GI



```
Seq. No.
                  138890
Seq. ID
                  LIB23-045-Q1-E1-C11
Method
                  BLASTX
NCBI GI
                  g3269287
BLAST score
                  367
                  1.0e-36
E value
Match length
                  93
% identity
                  90
                  (AL030978) GH3 like protein [Arabidopsis thaliana]
NCBI Description
                  138891
Seq. No.
Seq. ID
                  LIB23-045-Q1-E1-C12
Method
                  BLASTX
NCBI GI
                  g3123745
BLAST score
                  238
E value
                  3.0e-20
Match length
                  92
                  52
% identity
NCBI Description
                  (AB013447) aluminum-induced [Brassica napus]
                  138892
Seq. No.
                  LIB23-045-Q1-E1-C2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2642427
BLAST score
                  284
E value
                  1.0e-159
Match length
                  284
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T20D16 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138893
Seq. ID
                  LIB23-045-Q1-E1-C3
Method
                  BLASTX
NCBI GI
                  g2281635
BLAST score
                  274
                  2.0e-24
E value
                  80
Match length
% identity
                  71
NCBI Description
                   (AF003098) AP2 domain containing protein RAP2.5
                   [Arabidopsis thaliana]
Seq. No.
                  138894
Seq. ID
                  LIB23-045-Q1-E1-C6
Method
                  BLASTX
NCBI GI
                  g3152606
BLAST score
                  220
E value
                  3.0e-18
Match length
                  54
% identity
                  70
NCBI Description
                  (AC004482) putative ring zinc finger protein [Arabidopsis
                  thaliana]
Seq. No.
                  138895
```

16752

LIB23-045-Q1-E1-D10

BLASTX

g166867



```
BLAST score
                  3.0e-26
E value
                  74
Match length
                  85
% identity
                  (J05216) ribosomal protein S11 (probable start codon at bp
NCBI Description
                  67) [Arabidopsis thaliana]
                  138896
Seq. No.
                  LIB23-045-Q1-E1-D6
Seq. ID
                  BLASTX
Method
                  g232031
NCBI GI
                  280
BLAST score
                  3.0e-25
E value
Match length
                  76
% identity
                   64
                  ELONGATION FACTOR 1 BETA' >gi 322851_pir__S29224
NCBI Description
                  translation elongation factor eEF-1 beta chain - rice
                   >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
                   [Oryza sativa]
Seq. No.
                  138897
                  LIB23-045-Q1-E1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2088654
BLAST score
                   315
                   2.0e-29
E value
Match length
                   69
                   90
% identity
                   (AF002109) 60S acidic ribosomal protein P0 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   138898
Seq. No.
                  LIB23-045-Q1-E1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4314378
BLAST score
                   361
                   1.0e-34
E value
Match length
                   89
                   75
% identity
NCBI Description
                  (AC006232) putative lipase [Arabidopsis thaliana]
                   138899
Seq. No.
                   LIB23-045-Q1-E1-E10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2088638
                   253
BLAST score
E value
                   1.0e-140
Match length
                   253
% identity
                   100
```

NCBI Description Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138900

Seq. ID LIB23-045-Q1-E1-E3

Method BLASTX
NCBI GI g2129759
BLAST score 464



```
9.0e-47
E value
Match length
                  94
% identity
NCBI Description
                  UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana
                  >qi 1143392 emb CAA90941 (Z54214) uridine diphosphate
                  glucose epimerase [Arabidopsis thaliana]
Seq. No.
                  138901
                  LIB23-045-Q1-E1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4210334
BLAST score
                  355
E value
                  5.0e - 34
Match length
                  88
% identity
                  82
                   (AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit
NCBI Description
                   [Arabidopsis thaliana]
                  138902
Seq. No.
Seq. ID
                  LIB23-045-Q1-E1-F2
Method
                  BLASTN
NCBI GI
                  g3420043
BLAST score
                  285
                  1.0e-159
E value
Match length
                  285
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F23F1 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  138903
Seq. No.
                  LIB23-045-Q1-E1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3169569
BLAST score
                  155
E value
                   4.0e-27
                   69
Match length
                   97
% identity
                   (AF062589) 3-keto-acyl-CoA thiolase 2 [Arabidopsis
NCBI Description
                   thaliana] >gi_3220237 (AF062591) peroxisomal
                   3-keto-acyl-CoA thiolase 2 precursor [Arabidopsis thaliana]
Seq. No.
                   138904
                  LIB23-045-Q1-E1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4587989
BLAST score
                   241
                   1.0e-20
E value
                   70
Match length
```

% identity 74

(AF085279) hypothetical Cys-3-His zinc finger protein NCBI Description

[Arabidopsis thaliana]

Seq. No. 138905

Seq. ID LIB23-045-Q1-E1-G10

Method BLASTX g4678924 NCBI GI BLAST score 140

E value Match length



```
8.0e-09
E value
Match length
                  62
% identity
                  42
                  (AL049711) putative protein [Arabidopsis thaliana]
NCBI Description
                  138906
Seq. No.
                  LIB23-045-Q1-E1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169598
BLAST score
                  198
E value
                  1.0e-15
Match length
                  48
                  75
% identity
                  OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   (DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  138907
Seq. ID
                  LIB23-045-Q1-E1-G3
Method
                  BLASTX
NCBI GI
                  q2829869
BLAST score
                  497
E value
                  1.0e-50
                  93
Match length
                  100
% identity
                  (AC002396) pyruvate dehydrogenase E1 alpha subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  138908
Seq. ID
                  LIB23-045-Q1-E1-G4
Method
                  BLASTX
NCBI GI
                   q16245
BLAST score
                   484
E value
                   4.0e-49
Match length
                   93
% identity
                   100
                  (X51514) precursor acetolactate synthase (670 AA)
NCBI Description
                   [Arabidopsis thaliana]
                   138909
Seq. No.
                   LIB23-045-Q1-E1-G5
Seq. ID
Method
                   BLASTN
                   q3449317
NCBI GI
                   43
BLAST score
                   4.0e-15
E value
Match length
                   59
                   93
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MKM21, complete sequence [Arabidopsis thaliana]
                   138910
Seq. No.
                   LIB23-045-Q1-E1-G8
Seq. ID
Method
                   BLASTX
                   g115783
NCBI GI
BLAST score
                   324
```

16755

2.0e-30



```
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  138911
Seq. No.
Seq. ID
                  LIB23-045-Q1-E1-G9
Method
                  BLASTN
NCBI GI
                  g1532270
BLAST score
                  253
                  1.0e-140
E value
Match length
                  265
% identity
                  99
NCBI Description
                  Arabidopsis thaliana mRNA for
                  deltal-pyrroline-5-carboxylate synthase, complete cds
Seq. No.
                  138912
                  LIB23-045-Q1-E1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2894574
BLAST score
                  407
                  4.0e-40
E value
Match length
                  77
% identity
                  100
                  (AL021890) peroxidase prxrl [Arabidopsis thaliana]
NCBI Description
                  >gi 2961341 emb CAA18099.1 (AL022140) peroxidase prxr1
                  [Arabidopsis thaliana]
Seq. No.
                  138913
                  LIB23-045-Q1-E1-H6
Seq. ID
Method
                  BLASTX
                  g3176714
NCBI GI
BLAST score
                  304
                  5.0e-28
E value
Match length
                  89
% identity
                  69
                  (AC002392) putative tRNA-splicing endonuclease positive
NCBI Description
                  effector [Arabidopsis thaliana]
Seq. No.
                  138914
                  LIB23-046-Q1-E1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2358139
BLAST score
                  169
                  4.0e-90
E value
Match length
                  387
% identity
                  98
NCBI Description
                  Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete
                  sequence [Arabidopsis thaliana]
```

Seq. No. 138915

Seq. ID LIB23-046-Q1-E1-C6

Method BLASTX
NCBI GI g4741940
BLAST score 529
E value 4.0e-54



```
Match length
                  96
% identity
                  64
                  (AF134120) Lhca2 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  138916
                  LIB23-046-Q1-E1-D12
Seq. ID
Method
                  BLASTN
                  q4455168
NCBI GI
BLAST score
                  40
                  1.0e-13
E value
Match length
                  72
                  89
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10
NCBI Description
                   (ESSAII project)
Seq. No.
                  138917
Seq. ID
                  LIB23-046-Q1-E1-E2
Method
                  BLASTN
NCBI GI
                  g3702315
BLAST score
                  218
E value
                  1.0e-119
Match length
                  406
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC T3F17 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138918
Seq. ID
                  LIB23-046-Q1-E1-E7
Method
                  BLASTN
NCBI GI
                  q3869069
BLAST score
                  206
                  1.0e-112
E value
                  396
Match length
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MEB5, complete sequence [Arabidopsis thaliana]
                  138919
Seq. No.
Seq. ID
                  LIB23-046-Q1-E1-F1
Method
                  BLASTX
NCBI GI
                  g322492
BLAST score
                  677
E value
                  2.0e-71
Match length
                  131
                  100
% identity
NCBI Description
                  photomorphogenesis repressor COP1 - Arabidopsis thaliana
                  138920
Seq. No.
                  LIB23-046-Q1-E1-F5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220645
BLAST score
                  256
E value
                  1.0e-142
Match length
                   386
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
```

MYA6, complete sequence [Arabidopsis thaliana]



```
138921
Seq. No.
Seq. ID
                  LIB23-046-Q1-E1-F9
Method
                  BLASTX
NCBI GI
                  g2961357
BLAST score
                  207
                  2.0e-16
E value
Match length
                  55
                  75
% identity
                  (AL022140) putative protein [Arabidopsis thaliana]
NCBI Description
                  138922
Seq. No.
                  LIB23-046-Q1-E1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  569
                  8.0e-59
E value
                  108
Match length
                  99
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  138923
                  LIB23-046-Q1-E1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2351067
BLAST score
                  262
E value
                  1.0e-146
                  274
Match length
                  59
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MPO12, complete sequence [Arabidopsis thaliana]
                  138924
Seq. No.
Seq. ID
                  LIB23-046-Q1-E1-H4
Method
                  BLASTX
NCBI GI
                  q3668093
BLAST score
                  249
                  2.0e-21
E value
Match length
                  83
% identity
                   63
                  (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
                  138925
Seq. No.
Seq. ID
                  LIB23-046-Q1-E1-H7
Method
                  BLASTX
NCBI GI
                  q2894574
BLAST score
                  614
E value
                   4.0e-64
Match length
                  116
                  100
% identity
NCBI Description
                   (AL021890) peroxidase prxr1 [Arabidopsis thaliana]
```

[Arabidopsis thaliana]

>gi_2961341_emb_CAA18099.1 (AL022140) peroxidase prxr1

% identity

NCBI Description

47

thaliana]



```
Seq. No.
                  138926
                  LIB23-047-Q1-E1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2642158
BLAST score
                  310
                  1.0e-28
E value
                  75
Match length
                  75
% identity
NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]
                  138927
Seq. No.
                  LIB23-047-Q1-E1-A6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g115783
BLAST score
                  605
E value
                  4.0e-63
Match length
                  114
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi 16376 emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  138928
Seq. No.
Seq. ID
                  LIB23-047-Q1-E1-D2
Method
                  BLASTN
                  g3510347
NCBI GI
BLAST score
                  41
                  9.0e-14
E value
Match length
                  184
                  86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSJ11, complete sequence [Arabidopsis thaliana]
                  138929
Seq. No.
Seq. ID
                  LIB23-047-Q1-E1-D7
Method
                  BLASTX
                  q1710581
NCBI GI
BLAST score
                  500
E value
                  7.0e-51
                  100
Match length
% identity
                  60S RIBOSOMAL PROTEIN L9 >gi 2129720 pir S71255 ribosomal
NCBI Description
                  protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_
                   (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]
                  138930
Seq. No.
Seq. ID
                  LIB23-047-Q1-E1-F5
Method
                  BLASTX
NCBI GI
                   q4455319
BLAST score
                  171
                   3.0e-12
E value
Match length
                  70
```

(AL035528) putative disease resistance protein [Arabidopsis



```
Seq. No.
                  138931
                  LIB23-047-Q1-E1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4249386
BLAST score
                  571
E value
                  3.0e-59
Match length
                  114
                  100
% identity
                  (AC005966) Strong similarity to gb AF061286 gamma-adaptin 1
NCBI Description
                  from Arabidopsis thaliana. EST gb H37393 comes from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  138932
Seq. ID
                  LIB23-047-Q1-E1-G12
Method
                  BLASTX
NCBI GI
                  q2880043
BLAST score
                  473
E value
                  1.0e-47
Match length
                  115
% identity
                  83
                  (AC002340) putative 3-hydroxyisobutyryl-coenzyme A
NCBI Description
                  hydrolase [Arabidopsis thaliana]
                  138933
Seq. No.
Seq. ID
                  LIB23-047-Q1-E1-G6
                  BLASTN
Method
NCBI GI
                  g2924651
BLAST score
                  142
E value
                  3.0e-74
Match length
                  243
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K2A18, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138934
                  LIB23-047-Q1-E1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262162
BLAST score
                  284
                  1.0e-25
E value
Match length
                  69
                  78
% identity
                   (AC005275) putative glycosylation enzyme [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  138935
                  LIB23-047-Q1-E1-H7
Seq. ID
Method
                  BLASTX
                  g3334404
NCBI GI
BLAST score
                  394
                  2.0e-38
E value
Match length
                  89
```

87 % identity

VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD NCBI Description SUBUNIT) >gi_2266990 (U65638) vacuolar type ATPase subunit

A [Arabidopsis thaliana] >gi_3834305 (AC005679) Identical to gb U65638 Arabidopsis thaliana vacuolar type ATPase



138936

subunit A mRNA. ESTs gb_N96435, gb_N96106, gb_N96189, gb_N96091, gb_AA042286, gb_F14324, gb_W43643, gb_N96027, gb_N96299, gb_R29943, gb_T43460, gb_T43544, gb_T22472

Seq. ID LIB23-048-Q1-E1-B1
Method BLASTN
NCBI GI g4510360
BLAST score 196
E value 1.0e-106
Match length 348
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic

sequence, complete sequence

Seq. No. 138937

Seq. No.

Seq. ID LIB23-048-Q1-E1-D4

Method BLASTX
NCBI GI g3492806
BLAST score 369
E value 2.0e-35
Match length 115
% identity 61

NCBI Description (AJ225045) adventitious rooting related oxygenase [Malus

domestica]

Seq. No. 138938

Seq. ID LIB23-048-Q1-E1-D7

Method BLASTX
NCBI GI g3913418
BLAST score 126
E value 1.0e-54
Match length 109
% identity 97

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi 1531763 emb CAA69073 (Y07765)

S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No. 138939

Seq. ID LIB23-048-Q1-E1-E11

Method BLASTX
NCBI GI g4512615
BLAST score 531
E value 2.0e-54
Match length 110
% identity 98

NCBI Description (AC004793) Strong similarity to gb X59970 3-isopropylmalate

dehydrogenase (IMDH) from Brassica napus. EST gb F14478

comes from this gene. [Arabidopsis thaliana]

Seq. No. 138940

Seq. ID LIB23-048-Q1-E1-F11

Method BLASTX
NCBI GI g1518388
BLAST score 273
E value 3.0e-24
Match length 85



```
% identity
NCBI Description (X91172) korean-radish isoperoxidase [Raphanus sativus]
                  138941
Seq. No.
                  LIB23-048-Q1-E1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4455309
                  195
BLAST score
                  5.0e-15
E value
Match length
                  68
% identity
                  57
NCBI Description (AL035528) hypothetical protein [Arabidopsis thaliana]
                  138942
Seq. No.
                  LIB23-048-Q1-E1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587595
                  294
BLAST score
                  5.0e-27
E value
Match length
                  56
% identity
                  98
NCBI Description
                  (AC006951) putative proline-rich protein APG [Arabidopsis
                  thaliana]
Seq. No.
                  138943
Seq. ID
                  LIB23-049-Q1-E1-A5
Method
                  BLASTX
NCBI GI
                  q3249065
BLAST score
                  369
                  2.0e-35
E value
Match length
                  74
                   97
% identity
NCBI Description
                   (ACO04473) Similar to HAK1 gb U22945 high affinity
                  potassium transporter from Schwanniomyces occidentalis.
                   [Arabidopsis thaliana]
                  138944
Seq. No.
Seq. ID
                  LIB23-049-Q1-E1-A6
Method
                  BLASTX
NCBI GI
                   g4588012
BLAST score
                   484
                   6.0e-49
E value
                   116
Match length
                   79
% identity
                   (AF085717) putative callose synthase catalytic subunit
NCBI Description
                   [Gossypium hirsutum]
Seq. No.
                   138945
Seq. ID
                  LIB23-049-Q1-E1-A8
                  BLASTX
Method
NCBI GI
                   g2494896
BLAST score
                   619
E value
                   1.0e-64
Match length
                   114
                   56
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 3 DELTA SUBUNIT
NCBI Description
```

(EIF-3 DELTA) (EIF3 P36) (TGF-BETA RECEPTOR INTERACTING



PROTEIN 1) (TRIP-1) >gi_2129749_pir__S60256 TGF-beta receptor interacting protein 1 homolog - Arabidopsis thaliana >gi 1036803 (U36765) TGF-beta receptor interacting

protein 1 homolog [Arabidopsis thaliana]

Seq. No. 138946

Seq. ID LIB23-049-Q1-E1-B5

Method BLASTN
NCBI GI g3036791
BLAST score 358
E value 0.0e+00
Match length 358
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T19K4

(ESSAII project)

Seq. No. 138947

Seq. ID LIB23-049-Q1-E1-B7

Method BLASTX
NCBI GI g3169176
BLAST score 552
E value 6.0e-57
Match length 120
% identity 91

NCBI Description (AC004401) putative protein kinase [Arabidopsis thaliana]

Seq. No. 138948

Seq. ID LIB23-049-Q1-E1-C6

Method BLASTN
NCBI GI g3869066
BLAST score 45
E value 4.0e-16
Match length 151
% identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBM17, complete sequence [Arabidopsis thaliana]

Seq. No. 138949

Seq. ID LIB23-049-Q1-E1-C8

Method BLASTN
NCBI GI g2459406
BLAST score 274
E value 1.0e-153
Match length 278
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F4P9 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138950

Seq. ID LIB23-049-Q1-E1-D10

Method BLASTX
NCBI GI g2462757
BLAST score 228
E value 2.0e-19
Match length 63
% identity 81

NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]



```
Seq. No.
                  138951
                  LIB23-049-Q1-E1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1911166
                  579
BLAST score
                  4.0e-60
E value
Match length
                  118
% identity
                  92
                  (X94400) soluble-starch-synthase [Solanum tuberosum]
NCBI Description
```

Seq. No. 138952

Seq. ID LIB23-049-Q1-E1-D4 Method BLASTX NCBI GI g115480 BLAST score 607 E value 2.0e-63 Match length 118 % identity 52

NCBI Description CALMODULIN-1 >gi 166649 (M38379) calmodulin-1 [Arabidopsis

thaliana]

NCBI GI g4539290
BLAST score 134
E value 3.0e-69
Match length 344
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19

(ESSA project)

Seq. No. 138954

Seq. ID LIB23-049-Q1-E1-G2

Method BLASTN
NCBI GI g4006885
BLAST score 213
E value 1.0e-116
Match length 327
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 138955

Seq. ID LIB23-049-Q1-E1-G5

Method BLASTN
NCBI GI 94757662
BLAST score 225
E value 1.0e-123
Match length 330
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10B6 from

chromosome I, complete sequence

Seq. No. 138956

Seq. ID LIB23-049-Q1-E1-G7



```
Method
NCBI GI
                  q4220635
BLAST score
                  205
E value
                  1.0e-111
                  350
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDB19, complete sequence [Arabidopsis thaliana]
                  138957
Seq. No.
Seq. ID
                  LIB23-049-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                  q1653767
                  243
BLAST score
                  6.0e-21
E value
                  79
Match length
                  57
% identity
NCBI Description
                  (D90916) oligopeptidase A [Synechocystis sp.]
                  138958
Seq. No.
                  LIB23-049-Q1-E1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3241922
BLAST score
                  165
E value
                  4.0e-88
Match length
                  181
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MLM24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138959
                  LIB23-049-Q1-E1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3023848
BLAST score
                  476
E value
                  5.0e-48
Match length
                  100
                  50
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                  PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA)
                  >qi 2289095 (U77381) WD-40 repeat protein [Arabidopsis
                  thaliana]
Seq. No.
                  138960
Seq. ID
                  LIB23-050-Q1-E1-F4
Method
                  BLASTX
NCBI GI
                  g3252809
BLAST score
                  296
                  4.0e-27
E value
Match length
                  84
                  38
% identity
                  (AC004705) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 138961

Seq. ID LIB23-050-Q1-E1-H8

Method BLASTX NCBI GI g4512680



BLAST score 254
E value 6.0e-22
Match length 55
% identity 96

NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]

Seq. No. 138962

Seq. ID LIB23-051-Q1-E1-A9

Method BLASTX
NCBI GI g2894574
BLAST score 491
E value 8.0e-50
Match length 93
% identity 100

NCBI Description (AL021890) peroxidase prxrl [Arabidopsis thaliana] >gi 2961341 emb CAA18099.1_ (AL022140) peroxidase prxrl

[Arabidopsis thaliana]

Seq. No. 138963

Seq. ID LIB23-051-Q1-E1-B7

Method BLASTN
NCBI GI g4587582
BLAST score 103
E value 8.0e-51
Match length 147
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T16B14 genomic

sequence, complete sequence

Seq. No. 138964

Seq. ID LIB23-051-Q1-E1-B9

Method BLASTN
NCBI GI g3873174
BLAST score 67
E value 3.0e-29
Match length 75
% identity 97

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14N23,

complete sequence [Arabidopsis thaliana]

Seq. No. 138965

Seq. ID LIB23-051-Q1-E1-C4

Method BLASTN
NCBI GI g3461810
BLAST score 121
E value 1.0e-61
Match length 232
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T17M13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138966

Seq. ID LIB23-051-Q1-E1-D10

Method BLASTX NCBI GI g133978 BLAST score 311 E value 1.0e-28



Match length % identity 57 40S RIBOSOMAL PROTEIN S6 (PHOSPHOPROTEIN NP33) NCBI Description >gi_70932_pir__R3RTS6 ribosomal protein S6 - rat
>gi_70933_pir__R3MS6 ribosomal protein S6 - mouse
>gi_319910_pir__R3HU6 ribosomal protein S6 - human
>gi_36148_emb_CAA47719__(X67309) ribosomal protein S6 [Homo sapiens] >gi_54010_emb_CAA68430__(Y00348) ribosomal protein S6 [Mus musculus] >gi_206747 (M29358) ribosomal protein S6 [Rattus norvegicus] >gi_307393 (M77232) ribosomal protein S6 [Homo sapiens] >gi_1177549_emb_CAA90936_ (Z54209) rpS6 [Mus musculus] Seq. No. 138967 LIB23-051-Q1-E1-E10 Seq. ID Method BLASTN NCBI GI g2702261 191 BLAST score E value 1.0e-103 194 Match length 99 % identity Arabidopsis thaliana chromosome II BAC T21L14 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 138968 LIB23-051-Q1-E1-E2 Seq. ID Method BLASTX g1495269 NCBI GI BLAST score 449 1.0e-44 E value 125 Match length 73 % identity (X97829) product similar to ccr protein, Citrus paradisi; NCBI Description PIR: S52663 [Arabidopsis thaliana] >gi_1550735_emb_CAA66824_ (X98130) unknown [Arabidopsis thaliana] 138969 Seq. No. LIB23-051-Q1-E1-E6 Seq. ID Method BLASTX q2252824 NCBI GI BLAST score 494 5.0e-50 E value Match length 118 % identity (AF013293) No definition line found [Arabidopsis thaliana] NCBI Description Seq. No. 138970 Seq. ID LIB23-051-Q1-E1-F6 Method BLASTN NCBI GI q4662640

Method BLASTN
NCBI GI g4662640
BLAST score 86
E value 1.0e-40
Match length 312
% identity 83

NCBI Description Arabidopsis thaliana chromosome II BAC F15K19 genomic

sequence, complete sequence



```
Seq. No.
                  138971
                  LIB23-051-Q1-E1-G6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3335331
BLAST score
                  240
                  1.0e-132
E value
Match length
                  380
                  100
% identity
                  Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  138972
Seq. ID
                  LIB23-051-Q1-E1-H4
Method
                  BLASTN
NCBI GI
                  g4732168
BLAST score
                  64
                  1.0e-27
E value
                  173
Match length
% identity
                  59
NCBI Description Arabidopsis thaliana BAC T1J24
                  138973
Seq. No.
                  LIB23-051-Q1-E1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2632252
                   153
BLAST score
                  2.0e-14
E value
Match length
                   61
                   64
% identity
                  (Y12464) serine/threonine kinase [Sorghum bicolor]
NCBI Description
                   138974
Seq. No.
Seq. ID
                   LIB23-052-Q1-E1-B1
Method
                   BLASTX
NCBI GI
                   g3241943
BLAST score
                   443
                   3.0e-44
E value
                   101
Match length
                   78
% identity
                  (AC004625) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   138975
                   LIB23-052-Q1-E1-B2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3869072
BLAST score
                   311
                   1.0e-175
E value
Match length
                   335
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MJB24, complete sequence [Arabidopsis thaliana]
```

138976 Seq. No.

Seq. ID LIB23-052-Q1-E1-C1

Method BLASTX NCBI GI g1169423



```
BLAST score
E value
                  6.0e-20
Match length
                  48
                  98
% identity
                  DIHYDROFOLATE REDUCTASE 2 / THYMIDYLATE SYNTHASE 2
NCBI Description
                  (DHFR-TS) >gi 289195 (L08594) dihydrofolate
                  reductase-thymidylate synthase [Arabidopsis thaliana]
                  >gi_3096926_emb_CAA18836.1_ (AL023094) dihydrofolate
                  reductase-thymidylate synthase [Arabidopsis thaliana]
Seq. No.
                  138977
Seq. ID
                  LIB23-052-Q1-E1-C9
Method
                  BLASTN
NCBI GI
                  q3510342
                  232
BLAST score
                  1.0e-128
E value
Match length
                  240
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MGN6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138978
Seq. ID
                  LIB23-052-Q1-E1-F8
Method
                  BLASTX
                  g3367517
NCBI GI
BLAST score
                  469
                  4.0e-47
E value
                  99
Match length
% identity
                  89
                  (ACO04392) Similar to F4I1.26 putative beta-glucosidase
NCBI Description
                  gi_3128187 from A. thaliana BAC gb_AC004521. ESTs
                  gb N97083, gb F19868 and gb_F15482 come from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  138979
                  LIB23-052-Q1-E1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4758918
BLAST score
                  165
E value
                  1.0e-11
                  83
Match length
                  40
% identity
                  phosphatidylinositol glycan, class B
NCBI Description
                  >gi 1552169 dbj BAA07709 (D42138) PIG-B [Homo sapiens]
Seq. No.
                  138980
Seq. ID
                  LIB23-052-Q1-E1-H7
```

Method BLASTX
NCBI GI g4467147
BLAST score 637
E value 7.0e-70
Match length 140
% identity 99

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 138981

Seq. ID LIB23-053-Q1-E1-B5



Method NCBI GI q115783 BLAST score 483 7.0e-49 E value 91 Match length % identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

138982 Seq. No.

Seq. ID LIB23-053-Q1-E1-B6

Method BLASTX NCBI GI g3738339 BLAST score 450 E value 5.0e-45 Match length 113 % identity 74

(AC005170) putative kinase [Arabidopsis thaliana] NCBI Description

138983 Seq. No.

Seq. ID LIB23-053-Q1-E1-C5

Method BLASTX NCBI GI q399213 599 BLAST score E value 2.0e-62 Match length 117 99 % identity

ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG NCBI Description

CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato >gi_170435 (M32604) ATP-dependent protease (CD4B)

[Lycopersicon esculentum]

138984 Seq. No.

Seq. ID LIB23-053-Q1-E1-C9

Method BLASTX NCBI GI q4630748 BLAST score 373 5.0e-36 E value Match length 90 % identity 83

(AC007236) putative anion exchange protein 3 [Arabidopsis NCBI Description

thaliana]

Seq. No. 138985

Seq. ID LIB23-053-Q1-E1-D5

Method BLASTN g2266984 NCBI GI BLAST score 159 2.0e-84 E value Match length 159 % identity 100

Arabidopsis thaliana mRNA for chloroplast and mitochondrial NCBI Description

methionyl-tRNA synthetase

Seq. No. 138986



```
Seq. ID
                  LIB23-053-Q1-E1-D6
Method
                  BLASTX
NCBI GI
                  g2191168
                  387
BLAST score
E value
                  1.0e-37
Match length
                  93
% identity
                  86
                  (AF007270) contains similarity to myosin heavy chain
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  138987
Seq. ID
                  LIB23-053-Q1-E1-D7
Method
                  BLASTX
NCBI GI
                  q1495251
BLAST score
                  329
E value
                  9.0e-31
                  66
Match length
% identity
                  95
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                  138988
Seq. No.
                  LIB23-053-Q1-E1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115783
BLAST score
                  479
                  2.0e-48
E value
                  90
Match length
% identity
                  100
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543
                                                             (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  138989
Seq. No.
Seq. ID
                  LIB23-053-Q1-E1-E5
Method
                  BLASTN
NCBI GI
                  q4589438
BLAST score
                  318
E value
                  1.0e-179
Match length
                  359
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQJ2, complete sequence
                  138990
Seq. No.
Seq. ID
                  LIB23-053-Q1-E1-H6
Method
                  BLASTX
NCBI GI
                  q115767
                  596
BLAST score
                  5.0e-62
E value
                  113
Match length
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
```

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]



>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 138991

Seq. ID LIB23-053-Q1-E1-H7

Method BLASTX
NCBI GI g3004564
BLAST score 307
E value 1.0e-31
Match length 91
% identity 73

NCBI Description (AC003673) putative receptor Ser/Thr protein kinase

[Arabidopsis thaliana]

Seq. No. 138992

Seq. ID LIB23-054-Q1-E1-A3

Method BLASTN
NCBI GI g1877523
BLAST score 221
E value 1.0e-121
Match length 345
% identity 100

NCBI Description Arabidopsis thaliana BAC T7I23, complete sequence

[Arabidopsis thaliana]

Seq. No. 138993

Seq. ID LIB23-054-Q1-E1-A5

Method BLASTX
NCBI GI g4538987
BLAST score 658
E value 3.0e-69
Match length 134
% identity 99

NCBI Description (AJ133777) gamma-adaptin 2 [Arabidopsis thaliana]

Seq. No. 138994

Seq. ID LIB23-054-Q1-E1-B8

Method BLASTX
NCBI GI g4584110
BLAST score 332
E value 5.0e-31
Match length 124
% identity 52

NCBI Description (AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No. 138995

Seq. ID LIB23-054-Q1-E1-C11

Method BLASTN
NCBI GI g2244950
BLAST score 341
E value 0.0e+00
Match length 341
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 138996

% identity

NCBI Description

100



```
LIB23-054-Q1-E1-C7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3386593
BLAST score
                  153
E value
                  2.0e-80
Match length
                  324
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC F4I18 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  138997
Seq. ID
                  LIB23-054-Q1-E1-D1
Method
                  BLASTX
NCBI GI
                  q115767
BLAST score
                  678
E value
                  1.0e-71
Match length
                  130
% identity
                  99
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  138998
                  LIB23-054-Q1-E1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3395431
BLAST score
                  266
                  2.0e-23
E value
                  118
Match length
% identity
                  46
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  138999
Seq. ID
                  LIB23-054-Q1-E1-D6
Method
                  BLASTX
NCBI GI
                  q2827714
BLAST score
                  179
E value
                  4.0e-13
Match length
                  129
% identity
NCBI Description
                  (AL021684) receptor protein kinase - like protein
                   [Arabidopsis thaliana]
Seq. No.
                  139000
Seq. ID
                  LIB23-054-Q1-E1-D7
Method
                  BLASTN
NCBI GI
                  g3337347
BLAST score
                  271
                  1.0e-151
E value
Match length
                  417
```

16773

Arabidopsis thaliana chromosome II BAC F13P17 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.

Seq. ID Method



```
139001
Seq. No.
                  LIB23-054-Q1-E1-D8
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4490717
BLAST score
                  166
                  1.0e-88
E value
                  220
Match length
% identity
                  92
                  Arabidopsis thaliana DNA chromosome 4, BAC clone
                                                                      (ESSA
NCBI Description
                  project)
                  139002
Seq. No.
Seq. ID
                  LIB23-054-Q1-E1-D9
Method
                  BLASTX
                  g2809255
NCBI GI
BLAST score
                  632
                  2.0e-66
E value
                  111
Match length
                   99
% identity
                  (AC002560) F21B7.24 [Arabidopsis thaliana]
NCBI Description
                   139003
Seq. No.
                  LIB23-054-Q1-E1-E1
Seq. ID
Method
                  BLASTN
                   g2924730
NCBI GI
BLAST score
                   262
                   1.0e-145
E value
                   294
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MPI7, complete sequence [Arabidopsis thaliana]
                   139004
Seq. No.
                   LIB23-054-Q1-E1-E2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3327922
                   156
BLAST score
                   2.0e-82
E value
Match length
                   342
% identity
                   100
                  Arabidopsis thaliana chromosome II BAC T31E10 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139005
                   LIB23-054-Q1-E1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2852447
BLAST score
                   237
E value
                   7.0e-20
Match length
                   75
                   65
% identity
                  (D88206) protein kinase [Arabidopsis thaliana]
NCBI Description
                   139006
```

16774

LIB23-054-Q1-E1-F11

BLASTN

E value Match length



```
NCBI GI
                  q3298610
BLAST score
                  136
E value
                  2.0e-70
Match length
                  276
                  100
% identity
NCBI Description Arabidopsis thaliana BAC T2H3
                  139007
Seq. No.
Seq. ID
                  LIB23-054-Q1-E1-F5
Method
                  BLASTX
NCBI GI
                  q2058504
BLAST score
                  364
E value
                  9.0e-35
Match length
                  104
                  76
% identity
                  (U76554) zinc-finger protein-1 [Brassica rapa]
NCBI Description
Seq. No.
                  139008
                  LIB23-054-Q1-E1-G1
Seq. ID
Method
                  BLASTX
                  g2213884
NCBI GI
                  182
BLAST score
E value
                  2.0e-13
Match length
                  76
% identity
                   53
                  (AF004166) 2-isopropylmalate synthase [Lycopersicon
NCBI Description
                  pennellii]
                  139009
Seq. No.
                  LIB23-054-Q1-E1-G5
Seq. ID
                  BLASTN
Method
NCBI GI
                   g3355463
BLAST score
                   201
E value
                   1.0e-109
Match length
                   397
% identity
                   99
                  Arabidopsis thaliana chromosome II BAC F12L6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139010
Seq. ID
                   LIB23-054-Q1-E1-G6
Method
                   BLASTX
                   g2947063
NCBI GI
BLAST score
                   224
                   2.0e-18
E value
Match length
                   99
% identity
                   (AC002521) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No. Seq. ID
                   139011
                   LIB23-054-Q1-E1-H11
Method
                   BLASTN
NCBI GI
                   g3873174
                   343
BLAST score
```

16775

0.0e+00



% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14N23,

complete sequence [Arabidopsis thaliana]

Seq. No. 139012

Seq. ID LIB23-055-Q1-E1-A12

Method BLASTX
NCBI GI 9480450
BLAST score 330
E value 8.0e-31
Match length 80
% identity 86

NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis

thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid

reductoisomerase [Arabidopsis thaliana]

Seq. No. 139013

Seq. ID LIB23-055-Q1-E1-A4

Method BLASTX
NCBI GI g4559384
BLAST score 206
E value 3.0e-16
Match length 59
% identity 66

NCBI Description (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No. 139014

Seq. ID LIB23-055-Q1-E1-B1

Method BLASTN
NCBI GI g2864607
BLAST score 313
E value 1.0e-176
Match length 325
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6

(ESSAII project)

Seq. No. 139015

Seq. ID LIB23-055-Q1-E1-B10

Method BLASTX
NCBI GI g4732123
BLAST score 521
E value 7.0e-57
Match length 114
% identity 95

NCBI Description (AF129087) mitogen-activated protein kinase homologue

[Medicago sativa]

Seq. No. 139016

Seq. ID LIB23-055-Q1-E1-B9

Method BLASTX
NCBI GI g1711355
BLAST score 276
E value 1.0e-24
Match length 104
% identity 58

NCBI Description SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE

% identity

99



>gi_421786_pir__S34678 short-chain alcohol dehydrogenase Norway spruce >gi_395223_emb_CAA52213_ (X74115) short-chain
alcohol dehydrogenase [Picea abies]

139017 Seq. No. Seq. ID LIB23-055-Q1-E1-C1 BLASTN Method g3492855 NCBI GI BLAST score 149 3.0e-78 E value 371 Match length 78 % identity Genomic sequence for Arabidopsis thaliana BAC F20N2, NCBI Description complete sequence [Arabidopsis thaliana] 139018 Seq. No. LIB23-055-Q1-E1-C8 Seq. ID Method BLASTX NCBI GI g2465923 BLAST score 222 4.0e-18 E value 112 Match length % identity 45 (AF024648) receptor-like serine/threonine kinase NCBI Description [Arabidopsis thaliana] Seq. No. 139019 LIB23-055-Q1-E1-D1 Seq. ID Method BLASTX g4539332 NCBI GI BLAST score 574 2.0e-59 E value 115 Match length 100 % identity (AL035539) glycosyltransferase like protein (fragment) NCBI Description [Arabidopsis thaliana] Seq. No. 139020 Seq. ID LIB23-055-Q1-E1-D12 Method BLASTN NCBI GI q4468976 BLAST score 385 E value 0.0e+00385 Match length % identity 100 Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18 NCBI Description (ESSA project) Seq. No. 139021 Seq. ID LIB23-055-Q1-E1-D4 Method BLASTX NCBI GI g115783 BLAST score 512 3.0e-52 E value Match length 97

16777

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR



(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No. 139022

Seq. ID LIB23-055-Q1-E1-E1

Method BLASTN
NCBI GI g2244829
BLAST score 154
E value 3.0e-81
Match length 309
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 139023

Seq. ID LIB23-055-Q1-E1-E7

Method BLASTX
NCBI GI g4455364
BLAST score 337
E value 1.0e-31
Match length 105
% identity 59

NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis

thaliana]

Seq. No. 139024

Seq. ID LIB23-055-Q1-E1-F5

Method BLASTN
NCBI GI g2182287
BLAST score 324
E value 0.0e+00
Match length 413
% identity 96

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T7N9,

complete sequence [Arabidopsis thaliana]

Seq. No. 139025

Seq. ID LIB23-055-Q1-E1-G7

Method BLASTN
NCBI GI g2264304
BLAST score 353
E value 0.0e+00
Match length 408
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBG8, complete sequence [Arabidopsis thaliana]

Seq. No. 139026

Seq. ID LIB23-055-Q1-E1-H3

Method BLASTX
NCBI GI g2288988
BLAST score 209
E value 1.0e-16
Match length 112
% identity 38

NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 139027 Seq. ID LIB23-055-Q1-E1-H6 Method BLASTN NCBI GI g2623294 128 BLAST score E value 1.0e-65 401 Match length 99 % identity Arabidopsis thaliana chromosome II BAC T20B5 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 139028 LIB23-056-Q1-E1-B12 Seq. ID BLASTX Method q3451071 NCBI GI BLAST score 468 E value 5.0e-47 Match length 93 100 % identity

(ALO31326) beta adaptin - like protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 139029

LIB23-056-Q1-E1-B4 Seq. ID

Method BLASTX q3152600 NCBI GI 232 BLAST score E value 2.0e-19 69 Match length % identity 71

(AC002986) Contains similarity to S. cerevisiae NCBI Description

hypothetical protein YOR197w, gb Z75105. ESTs gb_H37409,

gb_AA395290, and gb_T43907 come from this gene.

[Arabidopsis thaliana]

Seq. No. 139030

Seq. ID LIB23-056-Q1-E1-C11

Method BLASTX NCBI GI q2895510 BLAST score 302 E value 1.0e-27 Match length 110 51 % identity

(AF033204) putative pectin methylesterase [Arabidopsis NCBI Description

thaliana]

Seq. No. 139031

LIB23-056-Q1-E1-C2 Seq. ID

Method BLASTX g4734005 NCBI GI BLAST score 547 3.0e-56 E value 109 Match length % identity 100

(AC007178) hypothetical protein [Arabidopsis thaliana] NCBI Description



```
139032
Seq. No.
Seq. ID
                  LIB23-056-Q1-E1-D2
Method
                  BLASTX
NCBI GI
                  q4567245
BLAST score
                   637
                  7.0e-67
E value
Match length
                  121
% identity
                  36
                  (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
                  139033
Seq. No.
                  LIB23-056-Q1-E1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4006885
BLAST score
                  227
E value
                  1.0e-125
                  227
Match length
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                  fragment No
                  139034
Seq. No.
                  LIB23-056-Q1-E1-E1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3702733
BLAST score
                  167
E value
                   3.0e-89
Match length
                   203
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJP23, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139035
Seq. ID
                  LIB23-056-Q1-E1-E2
Method
                  BLASTX
NCBI GI
                   g1076287
BLAST score
                   427
                   3.0e-42
E value
                   107
Match length
% identity
                   78
                  amine acid permease - Arabidopsis thaliana
NCBI Description
                   >gi_510236_emb_CAA50672_ (X71787) amine acid permease
                   [Arabidopsis thaliana]
Seq. No.
                   139036
Seq. ID
                   LIB23-056-Q1-E1-F1
Method
                   BLASTX
NCBI GI
                   q4678306
BLAST score
                   195
E value
                   5.0e-15
Match length
                   46
                   76
% identity
                  (AL049655) kinesin-like protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 139037

Seq. ID LIB23-056-Q1-E1-G5

Method BLASTN

Method NCBI GI

BLAST score



```
NCBI GI
                  q3176693
BLAST score
                  117
                  4.0e-59
E value
Match length
                  348
                  97
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T27I1 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139038
Seq. ID
                  LIB23-056-Q1-E1-G6
Method
                  BLASTX
NCBI GI
                  q486784
BLAST score
                  491
E value
                  9.0e-50
Match length
                  115
                  25
% identity
NCBI Description Golgi-associated particle 102K chain - human
Seq. No.
                  139039
                  LIB23-056-Q1-E1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267079
BLAST score
                  511
E value
                  4.0e-52
Match length
                  93
                  100
% identity
                  TUBULIN BETA-6 CHAIN >gi_320187_pir__JQ1590 tubulin beta-6
NCBI Description
                  chain - Arabidopsis thaliana >gi 166904 (M84703) beta-6
                  tubulin [Arabidopsis thaliana]
Seq. No.
                  139040
                  LIB23-056-Q1-E1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1346181
BLAST score
                  175
                  9.0e-13
E value
                   45
Match length
                  80
% identity
                  GLYCINE-RICH RNA-BINDING PROTEIN GRP2A >gi 496237 (L31377)
NCBI Description
                  homology with RNA-binding proteins in meristematic tissue
                   [Sinapis alba]
                  139041
Seq. No.
Seq. ID
                  LIB23-057-Q1-E1-B11
                  BLASTX
Method
NCBI GI
                  g3935183
BLAST score
                  296
                  1.0e-31
E value
Match length
                  86
% identity
                  80
                  (AC004557) F17L21.26 [Arabidopsis thaliana]
NCBI Description
                  139042
Seq. No.
Seq. ID
                  LIB23-057-Q1-E1-C3
                  BLASTN
```

16781

g4757414



E value 1.0e-137 Match length 287 % identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYF24, complete sequence

Seq. No. 139043

Seq. ID LIB23-057-Q1-E1-D11

Method BLASTN
NCBI GI g4263694
BLAST score 107
E value 3.0e-53
Match length 208
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F22D22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139044

Seq. ID LIB23-057-Q1-E1-D7

Method BLASTX
NCBI GI g2809257
BLAST score 328
E value 1.0e-30
Match length 63
% identity 54

NCBI Description (AC002560) F21B7.26 [Arabidopsis thaliana]

Seq. No. 139045

Seq. ID LIB23-057-Q1-E1-D8

Method BLASTN
NCBI GI g2264302
BLAST score 75
E value 1.0e-34
Match length 103
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAC12, complete sequence [Arabidopsis thaliana]

Seq. No. 139046

Seq. ID LIB23-057-Q1-E1-H11

Method BLASTX
NCBI GI g115783
BLAST score 173
E value 6.0e-13
Match length 46
% identity 83

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 139047

Seq. ID LIB23-057-Q1-E1-H12

Method BLASTN
NCBI GI g4587641
BLAST score 129
E value 2.0e-66



Match length 208 % identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic

sequence, complete sequence

Seq. No. 139048

Seq. ID LIB23-057-Q1-E1-H6

Method BLASTX
NCBI GI g114421
BLAST score 386
E value 1.0e-37
Match length 81
% identity 93

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR

>gi_82133_pir__A24355 H+-transporting ATP synthase (EC
3.6.1.34) beta-1 chain, mitochondrial - curled-leaved
tobacco >gi 19685 emb CAA26620 (X02868) ATP synthase beta

subunit [Nicotiana plumbaginifolia]

Seq. No. 139049

Seq. ID LIB23-058-Q1-E1-A6

Method BLASTN
NCBI GI g3193311
BLAST score 187
E value 1.0e-101
Match length 279
% identity 100

NCBI Description Arabidopsis thaliana BAC F6N15

Seq. No. 139050

Seq. ID LIB23-058-Q1-E1-A8

Method BLASTN
NCBI GI g3128135
BLAST score 332
E value 0.0e+00
Match length 371
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19E1, complete sequence [Arabidopsis thaliana]

Seq. No. 139051

Seq. ID LIB23-058-Q1-E1-E5

Method BLASTN
NCBI GI g1946354
BLAST score 241
E value 1.0e-133
Match length 285
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC T06B20 genomic

sequence, complete sequence

Seq. No. 139052

Seq. ID LIB23-058-Q1-E1-F10

MethodBLASTNNCBI GIg2341023BLAST score372E value0.0e+00



Match length 376 % identity 100

NCBI Description Sequence of BAC F19P19 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 139053

Seq. ID LIB23-058-Q1-E1-F5

Method BLASTN
NCBI GI g1490552
BLAST score 295
E value 1.0e-165
Match length 295
% identity 100

NCBI Description Arabidopsis thaliana S-adenosylmethionine decarboxylase

(SAMdc) mRNA, complete cds

Seq. No. 139054

Seq. ID LIB23-058-Q1-E1-G7

Method BLASTN
NCBI GI g3241923
BLAST score 101
E value 5.0e-50
Match length 117
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MMN10, complete sequence [Arabidopsis thaliana]

Seq. No. 139055

Seq. ID LIB23-058-Q1-E1-H11

Method BLASTX
NCBI GI g4741197
BLAST score 647
E value 5.0e-68
Match length 120
% identity 100

NCBI Description (AL049746) aldose 1-epimerase-like protein [Arabidopsis

thaliana]

Seq. No. 139056

Seq. ID LIB23-058-Q1-E1-H7

Method BLASTN
NCBI GI g4415928
BLAST score 110
E value 4.0e-55
Match length 218
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC F13A10 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139057

Seq. ID LIB23-059-Q1-E1-A12

Method BLASTX
NCBI GI g2499608
BLAST score 258
E value 1.0e-26
Match length 81
% identity 73



NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 4 (MAP KINASE 4) (ATMPK4) >gi_2129645_pir__ S40470 mitogen-activated protein kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457400_dbj_BAA04867_ (D21840) MAP kinase [Arabidopsis thaliana]

Seq. No. 139058

Seq. ID LIB23-059-Q1-E1-B12

Method BLASTN
NCBI GI g2098816
BLAST score 201
E value 1.0e-109
Match length 205
% identity 100

NCBI Description Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No. 139059

Seq. ID LIB23-059-Q1-E1-B2

Method BLASTX
NCBI GI g132166
BLAST score 250
E value 1.0e-21
Match length 67
% identity 81

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]

Seq. No. 139060

Seq. ID LIB23-059-Q1-E1-B4

Method BLASTN
NCBI GI g2924730
BLAST score 78
E value 2.0e-36
Match length 78
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MPI7, complete sequence [Arabidopsis thaliana]

Seq. No. 139061

Seq. ID LIB23-059-Q1-E1-B6

Method BLASTX
NCBI GI g3980411
BLAST score 332
E value 2.0e-31
Match length 66
% identity 100

NCBI Description (AC004561) putative proline-rich protein [Arabidopsis

thaliana]

Seq. No. 139062

Seq. ID LIB23-059-Q1-E1-B7

Method BLASTN NCBI GI g1655481 BLAST score 276

% identity

100



```
1.0e-154
E value
Match length
                  276
                  100
% identity
                  Arabidopsis thaliana mRNA for delta subunit of
NCBI Description
                  mitochondrial F1-ATPase, complete cds
                  139063
Seq. No.
                  LIB23-059-Q1-E1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4512668
BLAST score
                  167
                  4.0e-12
E value
Match length
                  75
                  52
% identity
                  (AC006931) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  139064
                  LIB23-059-Q1-E1-C2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3449327
BLAST score
                  161
                  2.0e-85
E value
                  282
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCA23, complete sequence [Arabidopsis thaliana]
                  139065
Seq. No.
                  LIB23-059-Q1-E1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q401169
BLAST score
                  267
                  1.0e-23
E value
                  51
Match length
                  100
% identity
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
Seq. No.
                  139066
                  LIB23-059-Q1-E1-E8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2828183
BLAST score
                  117
E value
                   3.0e-59
Match length
                  287
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MPL12, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139067
Seq. ID
                  LIB23-059-Q1-E1-F1
Method
                  BLASTN
NCBI GI
                   q2618601
BLAST score
                   259
E value
                   1.0e-144
Match length
                   259
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: 16786





MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No. 139068

Seq. ID LIB23-059-Q1-E1-F2

Method BLASTN
NCBI GI g4713943
BLAST score 222
E value 1.0e-122
Match length 273
% identity 97

NCBI Description Arabidopsis thaliana chromosome 1 BAC T8K14 sequence,

complete sequence

Seq. No. 139069

Seq. ID LIB23-059-Q1-E1-F4

Method BLASTX
NCBI GI g115767
BLAST score 524
E value 8.0e-54
Match length 95
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 139070

Seq. ID LIB23-059-Q1-E1-F5

Method BLASTX
NCBI GI g400976
BLAST score 455
E value 9.0e-46
Match length 91
% identity 100

NCBI Description RAS-RELATED PROTEIN RHA1 >gi_478671_pir__S23727 GTP-binding

protein RHA1 - Arabidopsis thaliana >gi_16484_emb_CAA41863_

(X59152) RHA1 [Arabidopsis thaliana]

>gi_397594_emb_CAA80534_ (Z22958) GTP-binding protein

[Arabidopsis thaliana]

Seq. No. 139071

Seq. ID LIB23-059-Q1-E1-F6

Method BLASTX
NCBI GI 9464707
BLAST score 375
E value 2.0e-36
Match length 76
% identity 100

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi_434343 emb_CAA82273 (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi 434345 emb CAA82274 (Z28702) S18 ribosomal protein



[Arabidopsis thaliana] >gi 434906 emb CAA82275 (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi 4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No. Seq. ID LIB23-059-Q1-E1-G1 Method BLASTX NCBI GI q2306917 BLAST score 466 E value 5.0e-47 Match length 88 100 % identity

(AF003728) plasma membrane intrinsic protein [Arabidopsis] NCBI Description

thaliana]

139072

139073 Seq. No.

LIB23-059-Q1-E1-G10 Seq. ID

Method BLASTX NCBI GI g115783 BLAST score 219 2.0e-18 E value Match length 52 83 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

139074 Seq. No.

Seq. ID LIB23-059-Q1-E1-G12

Method BLASTX NCBI GI q1703386 BLAST score 156 E value 6.0e-11 Match length 59 49 % identity

ACETYLORNITHINE DEACETYLASE (ACETYLORNITHINASE) (AO) NCBI Description

(N-ACETYLORNITHINASE) (NAO) >gi_763048 (U23957)

N-acetylornithine deacetylase [Dictyostelium discoideum]

Seq. No. 139075

Seq. ID LIB23-059-Q1-E1-G2

Method BLASTX NCBI GI g4455273 BLAST score 484 E value 4.0e-49 Match length 95 100 % identity

(AL035527) subtilisin proteinase-like [Arabidopsis NCBI Description

thaliana]



```
      Seq. No.
      139076

      Seq. ID
      LIB23-059-Q1-E1-G3

      Method
      BLASTN

      NCBI GI
      q3355463
```

BLAST score 281 E value 1.0e-157 Match length 289 % identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139077

Seq. ID LIB23-059-Q1-E1-G8

Method BLASTN
NCBI GI g3046856
BLAST score 148
E value 1.0e-77
Match length 277
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXI22, complete sequence [Arabidopsis thaliana]

Seq. No. 139078

Seq. ID LIB23-059-Q1-E1-H12

Method BLASTN
NCBI GI g3241920
BLAST score 119
E value 1.0e-60
Match length 191
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAE1, complete sequence [Arabidopsis thaliana]

Seq. No. 139079

Seq. ID LIB23-059-Q1-E1-H3

Method BLASTX
NCBI GI 94099092
BLAST score 480
E value 1.0e-48
Match length 90
% identity 100

NCBI Description (U83179) unknown [Arabidopsis thaliana]

Seq. No. 139080

Seq. ID LIB23-059-Q1-E1-H6

Method BLASTX
NCBI GI g2809246
BLAST score 284
E value 1.0e-25
Match length 95
% identity 56

NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]

Seq. No. 139081

Seq. ID LIB23-059-Q1-E1-H8

Method BLASTX NCBI GI g4417278

E value

Match length

1.0e-37

73



```
BLAST score
E value
                  2.0e-20
                  57
Match length
% identity
                  72
                  (AC007019) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  139082
Seq. No.
                  LIB23-060-Q1-E1-A10
Seq. ID
Method
                  BLASTN
                  g2760173
NCBI GI
BLAST score
                  257
                  1.0e-143
E value
                  273
Match length
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYH19, complete sequence [Arabidopsis thaliana]
                  139083
Seq. No.
Seq. ID
                  LIB23-060-Q1-E1-A11
Method
                  BLASTX
                  g4455210
NCBI GI
BLAST score
                  267
                  6.0e-24
E value
                  73
Match length
                  78
% identity
                   (AL035440) putative aspartate-tRNA ligase [Arabidopsis
NCBI Description
                  thaliana]
                  139084
Seq. No.
                  LIB23-060-Q1-E1-A2
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2924733
BLAST score
                   231
                   1.0e-127
E value
                   313
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUF9, complete sequence [Arabidopsis thaliana]
                   139085
Seq. No.
                   LIB23-060-Q1-E1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1707412
BLAST score
                   245
E value
                   4.0e-21
Match length
                   68
                   60
% identity
                   (X95906) Cleavage and Polyadenylation Specifity Factor
NCBI Description
                   protein [Bos taurus]
Seq. No.
                   139086
                   LIB23-060-Q1-E1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1199804
BLAST score
                   386
```



```
% identity
NCBI Description (X95639) transmembrane channel protein [Brassica oleracea]
                  139087
Seq. No.
                  LIB23-060-Q1-E1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4539448
                  267
BLAST score
                  1.0e-149
E value
Match length
                  267
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23
                  (ESSA project)
                  139088
Seq. No.
                  LIB23-060-Q1-E1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1495251
BLAST score
                  236
                  4.0e-20
E value
                  47
Match length
                  94
% identity
NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]
Seq. No.
                  139089
                  LIB23-060-Q1-E1-C11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2274861
BLAST score
                  71
                  5.0e-32
E value
Match length
                  151
                  87
% identity
NCBI Description Arabidopsis thaliana Sbe2.1 gene
Seq. No.
                  139090
                  LIB23-060-Q1-E1-C5
Seq. ID
Method
                  BLASTX
                  q1161926
NCBI GI
BLAST score
                  584
E value
                  1.0e-60
                  128
Match length
                   82
% identity
                  (U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine
NCBI Description
Seq. No.
                   139091
Seq. ID
                  LIB23-060-Q1-E1-C9
Method
                  BLASTX
                   g1174162
NCBI GI
BLAST score
                   458
                   4.0e-46
E value
                  80
Match length
                   100
% identity
                   (U44976) ubiquitin-conjugating enzyme [Arabidopsis
NCBI Description
```

ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

thaliana] >gi_3746915 (AF091106) E2

```
Seq. No.
                   139092
Seq. ID
                  LIB23-060-Q1-E1-D8
Method
                  BLASTX
                  g2244765
NCBI GI
                  168
BLAST score
                  9.0e-12
E value
Match length
                  136
                  19
% identity
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  139093
Seq. No.
                  LIB23-060-Q1-E1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3158370
BLAST score
                   376
                   2.0e-36
E value
                  72
Match length
                  100
% identity
                  (AF035382) catalase 3 [Arabidopsis thaliana]
NCBI Description
                  139094
Seq. No.
                  LIB23-060-Q1-E1-E11
Seq. ID
Method
                  BLASTX
                   g2459443
NCBI GI
BLAST score
                   307
                   2.0e-28
E value
                   60
Match length
                   100
% identity
                  (AC002332) putative NAD(P)-dependent cholesterol
NCBI Description
                   dehydrogenase [Arabidopsis thaliana]
                   139095
Seq. No.
                   LIB23-060-Q1-E1-F10
Seq. ID
                   BLASTX
Method
                   g2146746
NCBI GI
                   302
BLAST score
                   8.0e-28
E value
Match length
                   59
                   97
% identity
                   protein kinase (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                   >gi_166819 (L05562) protein kinase [Arabidopsis thaliana]
                   139096
Seq. No.
                   LIB23-060-Q1-E1-F3
Seq. ID
Method
                   BLASTN
                   g3184270
NCBI GI
                   182
BLAST score
                   7.0e-98
E value
Match length
                   405
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC T8K22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139097
```

LIB23-060-Q1-E1-F9

Method BLASTN NCBI GI g4263753

Seq. ID

Seq. No.

Seq. ID

Method



```
BLAST score
E value
                    1.0e-122
Match length
                   249
                   96
% identity
                   Arabidopsis thaliana chromosome V map near 60.5 cM,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   139098
Seq. ID
                   LIB23-060-Q1-E1-G11
Method
                   BLASTX
NCBI GI
                   g4455351
BLAST score
                   199
E value
                   1.0e-15
Match length
                    68
% identity
                    54
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   139099
Seq. No.
Seq. ID
                   LIB23-060-Q1-E1-G12
Method
                   BLASTX
NCBI GI
                   g4741952
BLAST score
                   372
                    5.0e-36
E value
Match length
                   71
% identity
                   100
                   (AF134126) Lhcb3 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   139100
                   LIB23-060-Q1-E1-G2
Seq. ID
Method
                   BLASTN
                    g4376087
NCBI GI
BLAST score
                    252
                    1.0e-139
E value
Match length
                    382
% identity
                    100
                   Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                    fragment No
Seq. No.
                    139101
Sea. ID
                    LIB23-060-Q1-E1-G9
Method
                    BLASTX
NCBI GI
                    q120667
BLAST score
                    349
E value
                    2.0e-33
Match length
                    68
% identity
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
thaliana >gi_166706 (M64116) cystolic
                    glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                    thaliana] >gi 166710 (M64119) glyceraldehyde-3-phosphate
                    dehydrogenase [Arabidopsis thaliana]
                    139102
```

16793

LIB23-060-Q1-E1-H11

BLASTN



```
q3894179
NCBI GI
BLAST score
                  268
                  1.0e-149
E value
Match length
                  268
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13H10 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139103
                  LIB23-060-Q1-E1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173151
BLAST score
                  379
E value
                  1.0e-36
Match length
                  77
                  99
% identity
                  DNA-DIRECTED RNA POLYMERASE BETA CHAIN
NCBI Description
                  >gi 629607 pir S48842 DNA-directed RNA polymerase (EC
                  2.7.7.6) beta chain - white mustard chloroplast
                  >gi 563343 emb CAA57814 (X82417) RNA polymerase subunit
                  beta [Sinapis alba]
Seq. No.
                  139104
Seq. ID
                  LIB23-060-Q1-E1-H5
Method
                  BLASTX
                  g2827663
NCBI GI
BLAST score
                  165
E value
                  2.0e-11
Match length
                  89
% identity
                  8
NCBI Description
                  (AL021637) membrane-associated salt-inducible-like protein
                   [Arabidopsis thaliana]
Seq. No.
                  139105
Seq. ID
                  LIB23-060-Q1-E1-H7
Method
                  BLASTX
NCBI GI
                  g4835225
BLAST score
                  442
E value
                  3.0e-44
Match length
                  84
                  99
% identity
NCBI Description
                   (AL049862) UTP-glucose glucosyltransferase like protein
                   [Arabidopsis thaliana]
Seq. No.
                  139106
Seq. ID
                  LIB23-060-Q1-E1-H9
Method
                  BLASTX
NCBI GI
                  q3158370
BLAST score
                  457
E value
                  5.0e-46
Match length
                  91
% identity
                  98
                  (AF035382) catalase 3 [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 139107

Seq. ID LIB23-061-Q1-E1-A10

Method BLASTN



```
NCBI GI
                  q2264312
BLAST score
                  129
E value
                  2.0e-66
                  200
Match length
                  92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOK16, complete sequence [Arabidopsis thaliana]
                  139108
Seq. No.
Seq. ID
                  LIB23-061-Q1-E1-A9
Method
                  BLASTN
NCBI GI
                  g2398848
BLAST score
                  125
E value
                  2.0e-64
Match length
                  125
                  100
% identity
                  Arabidopsis thaliana SIG1 mRNA for plastid RNA polymerase
NCBI Description
                  sigma-subunit, complete cds
Seq. No.
                  139109
Seq. ID
                  LIB23-061-Q1-E1-B7
Method
                  BLASTN
NCBI GI
                  g2708736
BLAST score
                  251
E value
                  1.0e-139
Match length
                  275
                  97
% identity
NCBI Description
                  Arabidopsis thaliana BAC T13L16 from chromosome II, near 33
                  cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139110
                  LIB23-061-Q1-E1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3894190
BLAST score
                  244
E value
                  8.0e-21
Match length
                   67
                  70
% identity
NCBI Description
                  (AC005662) putative RNA polymerase [Arabidopsis thaliana]
Seq. No.
                  139111
Seq. ID
                  LIB23-061-Q1-E1-F7
Method
                  BLASTN
NCBI GI
                  g4584387
BLAST score
                  94
E value
                  5.0e-46
Match length
                  98
                  99
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7
```

(ESSA project)

Seq. No. 139112

Seq. ID LIB23-061-Q1-E1-H7

Method BLASTX
NCBI GI g4538947
BLAST score 277
E value 8.0e-25

% identity

63



77 Match length % identity 36 NCBI Description (AL049483) putative mitochondrial carrier protein [Arabidopsis thaliana] Seq. No. 139113 Seq. ID LIB23-061-Q1-E1-H9 Method BLASTN g3293582 NCBI GI BLAST score 38 E value 6.0e-12 Match length 46 % identity 96 NCBI Description Arabidopsis thaliana BAC T15F16 139114 Seq. No. LIB23-062-Q1-E1-A10 Seq. ID Method BLASTX g2623298 NCBI GI BLAST score 525 1.0e-53 E value Match length 134 79 % identity NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis thaliana] Seq. No. 139115 LIB23-062-Q1-E1-A11 Seq. ID Method BLASTX g2160188 NCBI GI BLAST score 153 E value 7.0e-58 Match length 118 % identity 98 NCBI Description (AC000132) Similar to Vicia sucrose transport protein (gb_Z93774). [Arabidopsis thaliana] Seq. No. 139116 Seq. ID LIB23-062-Q1-E1-A5 Method BLASTX NCBI GI q4586061 BLAST score 294 E value 4.0e-27 Match length 54 % identity 100 NCBI Description (AC007020) putative BOP1 protein [Arabidopsis thaliana] Seq. No. 139117 Seq. ID LIB23-062-Q1-E1-B6 Method BLASTX NCBI GI q4585976 BLAST score 439 E value 2.0e-43 Match length 140

16796

NCBI Description (AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No.

Seq. ID

139123

LIB23-062-Q1-E1-F9



```
139118
Seq. No.
Seq. ID
                  LIB23-062-Q1-E1-C10
Method
                  BLASTX
NCBI GI
                  q1279640
BLAST score
                  319
                  2.0e-29
E value
                  93
Match length
                  60
% identity
                  (X92204) NAM [Petunia x hybrida]
NCBI Description
                  139119
Seq. No.
                  LIB23-062-Q1-E1-C11
Seq. ID
Method
                  BLASTN
                  g2832667
NCBI GI
BLAST score
                  282
E value
                  1.0e-157
Match length
                  338
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14
NCBI Description
                  (ESSAII project)
Seq. No.
                  139120
Seq. ID
                  LIB23-062-Q1-E1-C7
Method
                  BLASTN
NCBI GI
                  g3449318
BLAST score
                  423
                  0.0e+00
E value
Match length
                  423
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLF18, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139121
                  LIB23-062-Q1-E1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2271485
BLAST score
                  741
                  6.0e-79
E value
Match length
                  142
                  100
% identity
                  (AF009647) arginine decarboxylase [Arabidopsis thaliana]
NCBI Description
                  >gi 3096940 emb CAA18850.1 (AL023094) arginine
                  decarboxylase SPE2 [Arabidopsis thaliana]
                  139122
Seq. No.
                  LIB23-062-Q1-E1-E10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2656028
BLAST score
                  194
                  1.0e-105
E value
Match length
                  385
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNF13
```



```
Method
                  BLASTN
NCBI GI
                  g3033373
BLAST score
                  233
E value
                  1.0e-128
                  305
Match length
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC F19I3 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139124
                  LIB23-063-Q1-E1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2924728
BLAST score
                  74
                  2.0e-33
E value
                  129
Match length
% identity
                  91
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXH1, complete sequence [Arabidopsis thaliana]
                  139125
Seq. No.
                  LIB23-063-Q1-E1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1350768
BLAST score
                  390
E value
                  8.0e-38
Match length
                  93
% identity
                  84
NCBI Description 60S RIBOSOMAL PROTEIN L7A
                  139126
Seq. No.
                  LIB23-063-Q1-E1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4580454
BLAST score
                  47
                  2.0e-17
E value
Match length
                  143
% identity
                  87
                  Arabidopsis thaliana chromosome II BAC T2G17 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  139127
Seq. ID
                  LIB23-063-Q1-E1-A5
Method
                  BLASTN
                  g4519190
NCBI GI
BLAST score
                  323
E value
                  0.0e + 00
Match length
                  323
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K6A12, complete sequence
Seq. No.
                  139128
```

Seq. ID LIB23-063-Q1-E1-A9

Method BLASTX
NCBI GI g3461836
BLAST score 532



```
2.0e-54
E value
Match length
                  101
                  100
% identity
                  (AC005315) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  >gi_3927841 (AC005727) putative protein kinase [Arabidopsis
                  thaliana]
                  139129
Seq. No.
                  LIB23-063-Q1-E1-B10
Seq. ID
                  BLASTX
Method
                  g1531762
NCBI GI
                  195
BLAST score
                  6.0e-15
E value
Match length
                  51
% identity
                  75
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
                  139130
Seq. No.
                  LIB23-063-Q1-E1-B8
Seq. ID
Method
                  BLASTN
                  g2264306
NCBI GI
BLAST score
                  164
                  3.0e-87
E value
Match length
                  315
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBK5, complete sequence [Arabidopsis thaliana]
                  139131
Seq. No.
                  LIB23-063-Q1-E1-D1
Seq. ID
Method
                  BLASTX
                   q3335332
NCBI GI
BLAST score
                   417
                   4.0e-41
E value
                   78
Match length
                   100
% identity
                   (AC004512) Contains similarity to S-receptor kinase
NCBI Description
                   gb D88193 from Brassica rapa. [Arabidopsis thaliana]
Seq. No.
                   139132
                   LIB23-063-Q1-E1-D9
Seq. ID
Method
                   BLASTX
                   g1946369
NCBI GI
BLAST score
                   351
                   3.0e-33
E value
                   99
Match length
                   67
% identity
                  (U93215) unknown protein [Arabidopsis thaliana]
NCBI Description
                   139133
Seq. No.
Seq. ID
                   LIB23-063-Q1-E1-E11
                   BLASTX
Method
                   g3309086
NCBI GI
BLAST score
                   351
                   3.0e-33
E value
Match length
                   68
```

% identity NCBI Description (AF076253) calcineurin B-like protein 3 [Arabidopsis thaliana] 139134 Seq. No. Seq. ID LIB23-063-Q1-E1-G5 Method BLASTX g2961358 NCBI GI BLAST score 676 E value 2.0e-71 133 Match length % identity 100 NCBI Description (AL022140) serine/threonine protein kinase like protein [Arabidopsis thaliana] Seq. No. 139135 LIB23-063-Q1-E1-H3 Seq. ID Method BLASTN NCBI GI g3128136 BLAST score 152 5.0e-80 E value Match length 381 96 % identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K1F13, complete sequence [Arabidopsis thaliana] Seq. No. 139136 LIB23-063-Q1-E1-H5 Seq. ID Method BLASTX g3287863 415 9.0e-41 71 100 % identity NCBI Description

NCBI GI BLAST score E value Match length

PUTATIVE TRYPSIN INHIBITOR T01024.29 PRECURSOR >gi 2288993

(ACO02335) trypsin inhibitor isolog [Arabidopsis thaliana]

Seq. No. 139137

Seq. ID LIB23-063-Q1-E1-H8

Method BLASTN NCBI GI g2618599 BLAST score 373 E value 0.0e+00Match length 373 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBD2, complete sequence [Arabidopsis thaliana]

Seq. No. 139138

Seq. ID LIB23-064-Q1-E1-B12

Method BLASTX q1172872 NCBI GI BLAST score 382 E value 5.0e-37 Match length 74 % identity 100

NCBI Description CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718



drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi 435618 dbj BAA02373 (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No. 139139 Seq. ID LIB23-064-Q1-E1-H11 Method BLASTX g1800307 NCBI GI BLAST score 201 E value 6.0e-16 Match length 80 % identity 55

(U83883) p105 coactivator [Rattus norvegicus] NCBI Description

139140 Seq. No.

LIB23-065-Q1-E1-A2 Seq. ID

Method BLASTN NCBI GI q4558586 BLAST score 174 2.0e-93 E value Match length 178 99 % identity

NCBI Description Arabidopsis thaliana chromosome 1 BAC T518 sequence,

complete sequence

Seq. No. 139141

LIB23-065-Q1-E1-A3 Seq. ID

Method BLASTX NCBI GI g266989 BLAST score 393 E value 2.0e-38 Match length 74 % identity 100

NCBI Description GTP-BINDING PROTEIN SAR1B >gi_322517_pir__S28603 GTP-binding protein - Arabidopsis thaliana >gi_166734

(M95795) GTP-binding protein [Arabidopsis thaliana]

Seq. No. 139142

LIB23-065-Q1-E1-A6 Seq. ID

Method BLASTN NCBI GI q4454022 BLAST score 231 E value 1.0e-127 Match length 239 % identity 99

Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 NCBI Description

(ESSAII project)

Seq. No. 139143

Seq. ID LIB23-065-Q1-E1-A7

Method BLASTX NCBI GI g421836 BLAST score 278 5.0e-25 E value Match length 57

% identity NCBI Description G-box-binding factor GF14 - Arabidopsis thaliana >qi 553040 (M96855) GF14 [Arabidopsis thaliana] Seq. No. 139144 Seq. ID LIB23-065-Q1-E1-A8 Method BLASTX NCBI GI g2352923 BLAST score 352 E value 1.0e-33 Match length 91 % identity 79 NCBI Description (AF012863) cytosolic glucose-6-phosphate dehydrogenase 2 [Petroselinum crispum] Seq. No. 139145 Seq. ID LIB23-065-Q1-E1-B2 Method BLASTN NCBI GI q3985934 BLAST score 115 E value 5.0e-58 Match length 257 % identity 100 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana] Seq. No. 139146 Seq. ID LIB23-065-Q1-E1-B3 Method BLASTN NCBI GI q2828183 BLAST score 277 E value 1.0e-154 Match length 277 % identity 100 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana] Seq. No. 139147 Seq. ID LIB23-065-Q1-E1-B4 Method BLASTN NCBI GI g2245073 BLAST score 278 1.0e-155 E value Match length 278 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 139148

Seq. ID LIB23-065-Q1-E1-B6

Method BLASTN NCBI GI g2564050 BLAST score 258 E value 1.0e-143 Match length 280 99 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



MUA22, complete sequence [Arabidopsis thaliana]

Seq. No. 139149 Seq. ID LIB23-065-Q1-E1-B8 Method BLASTX NCBI GI g4490329 BLAST score 199 E value 1.0e-15 Match length 85 % identity 53 NCBI Description (AL035656) extensin-like protein [Arabidopsis thaliana] Seq. No. 139150 Seq. ID LIB23-065-Q1-E1-C7 Method BLASTX g266989 NCBI GI BLAST score 385 E value 1.0e-37 Match length 73 % identity 100 NCBI Description GTP-BINDING PROTEIN SAR1B >gi 322517_pir___\$28603 GTP-binding protein - Arabidopsis thaliana >gi_166734 (M95795) GTP-binding protein [Arabidopsis thaliana] Seq. No. 139151 Seq. ID LIB23-065-Q1-E1-C8 Method BLASTX g2795809 NCBI GI BLAST score 237 E value 3.0e-20 Match length 50 % identity 82 NCBI Description (AC003674) putative expansin [Arabidopsis thaliana] Seq. No. 139152 Seq. ID LIB23-065-Q1-E1-D12 Method BLASTX NCBI GI g2739389 BLAST score 392 E value 4.0e-38 Match length 125 % identity 21 NCBI Description (AC002505) Cf-2.2 like protein [Arabidopsis thaliana] Seq. No. 139153 Seq. ID LIB23-065-Q1-E1-D3 Method BLASTX NCBI GI q2213882 BLAST score 250 E value 1.0e-21 Match length 92 % identity 49 NCBI Description (AF004165) 2-isopropylmalate synthase [Lycopersicon pennellii]

Seq. No.

Seq. ID LIB23-065-Q1-E1-D5

139154



```
Method
                   BLASTX
NCBI GI
                   a4741948
BLAST score
                   399
                   3.0e-39
E value
Match length
                   76
% identity
                   100
NCBI Description (AF134124) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                   139155
Seq. ID
                   LIB23-065-Q1-E1-E1
Method ~
                   BLASTX
NCBI GI
                   q1709535
BLAST score
                   474
                   6.0e-48
E value
Match length
                   93
% identity
                   100
NCBI Description
                   DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B)
                   [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK);
                   GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR)
                   (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE)
                   (GLUTAMYL-GAMMA-SEMIALDE... >gi_887388_emb_CAA60447
                   (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis
                   thaliana] >gi_1669658_emb_CAA70527_ (Y09355)
pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]
Seq. No.
                   139156
Seq. ID
                   LIB23-065-Q1-E1-E6
Method
                   BLASTX
NCBI GI
                   q3024526
BLAST score
                   311
E value
                   7.0e-29
Match length
                   62
% identity
                   100
NCBI Description
                   RAS-RELATED PROTEIN RAB11 >gi_2118459_pir__S59942 small
                   GTP-binding protein Rab11 - Arabidopsis thaliana >gi 451860
                   (L18883) small GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                   139157
Seq. ID
                   LIB23-065-Q1-E1-E7
Method
                   BLASTX
NCBI GI
                   g2213584
BLAST score
                   412
E value
                   1.0e-40
Match length
                   79
% identity
                   100
NCBI Description (AC000348) T7N9.4 [Arabidopsis thaliana]
Seq. No.
                   139158
Seq. ID
                   LIB23-065-Q1-E1-E8
Method
                   BLASTX
NCBI GI
                   q3927836
BLAST score
                   270
E value
                   5.0e-24
Match length
                   74
% identity
```

16804

(AC005727) unknown protein [Arabidopsis thaliana]

66

NCBI Description



```
Seq. No.
                   139159
Seq. ID
                  LIB23-065-Q1-E1-E9
Method
                  BLASTX
NCBI GI
                  q619747
BLAST score
                   360
E value
                  2.0e-34
Match length
                  70
                  100
% identity
                   (U18968) phosphoribosylanthranilate isomerase [Arabidopsis
NCBI Description
Seq. No.
                  139160
Seq. ID
                  LIB23-065-Q1-E1-F10
Method
                  BLASTN
NCBI GI
                  q4757678
BLAST score
                  363
E value
                  0.0e+00
Match length
                  363
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F9H16 genomic
                  sequence, complete sequence
Seq. No.
                  139161
Seq. ID
                  LIB23-065-Q1-E1-F2
Method
                  BLASTN
NCBI GI
                  g4519193
BLAST score
                  173
E value
                  1.0e-92
Match length
                  281
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MDC11, complete sequence
Seq. No.
                  139162
Seq. ID
                  LIB23-065-Q1-E1-F4
Method
                  BLASTN
NCBI GI
                  q2529657
BLAST score
                  39
E value
                  1.0e-12
Match length
                  103
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T30B22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139163
Seq. ID
                  LIB23-065-Q1-E1-F5
Method
                  BLASTX
NCBI GI
                  q3288821
BLAST score
                  312
E value
                  6.0e-29
```

Match length 74 % identity 80

NCBI Description (AF063901) alanine:glyoxylate aminotransferase;

transaminase [Arabidopsis thaliana]

>gi 4733989 gb AAD28669.1_AC007209_5 (AC007209)

alanine-glyoxylate aminotransferase [Arabidopsis thaliana]



```
Seq. No.
                   139164
Seq. ID
                   LIB23-065-Q1-E1-F6
Method
                   BLASTX
NCBI GI
                   g3775987
BLAST score
                   463
E value
                   1.0e-46
Match length
                   93
% identity
                   100
NCBI Description
                  (AJ010457) RNA helicase [Arabidopsis thaliana]
Seq. No.
                   139165
Seq. ID
                   LIB23-065-Q1-E1-F8
Method
                   BLASTX
NCBI GI
                   q2829899
BLAST score
                   240
E value
                   2.0e-20
Match length
                   70
% identity
                   63
NCBI Description
                   (AC002311) similar to ripening-induced protein,
                   gp AJ001449 2465015 and major#latex protein,
                   gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                  139166
Seq. ID
                  LIB23-065-Q1-E1-G1
Method
                  BLASTX
NCBI GI
                  q4680192
BLAST score
                   304
E value
                   5.0e-28
Match length
                  87
% identity
                   69
                   (AF111710) hypothetical protein [Oryza sativa subsp.
NCBI Description
                   indica]
Seq. No.
                  139167
Seq. ID
                  LIB23-065-Q1-E1-G10
Method
                  BLASTN
NCBI GI
                  q4580365
BLAST score
                  160
E value
                   9.0e-85
Match length
                  372
% identity
                  97
                  Arabidopsis thaliana chromosome I BAC F3F20 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  139168
Seq. ID
                  LIB23-065-Q1-E1-G2
Method
                  BLASTX
NCBI GI
                  g1346526
BLAST score
                  353
E value
                  9.0e-34
Match length
                  69
% identity
                  96
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
```

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
>gi_1076533_pir__S52218 methionine adenosyltransferase (EC 2.5.1.6) - garden pea >gi_609225_emb_CAA57581_ (X82077)
methionine adenosyltransferase [Pisum_sativum] >gi_609559





(L36681) S-adenosylmethionine synthase [Pisum sativum]

139169 Seq. No. Seq. ID LIB23-065-Q1-E1-G6 Method BLASTX g2462738 NCBI GI BLAST score 186 E value 3.0e-14 Match length 47 % identity 98 (AC002292) similar to "Mx" GTP binding proteins NCBI Description [Arabidopsis thaliana] Seq. No. 139170 Seq. ID LIB23-065-Q1-E1-G7 Method BLASTN NCBI GI g633027 BLAST score 226 E value 1.0e-124 Match length 226

NCBI Description Arabidopsis thaliana mRNA for protein phosphatase 2C

139171 Seq. No.

% identity

Seq. ID LIB23-065-Q1-E1-G8

100

Method BLASTX NCBI GI g4753651 BLAST score 429 1.0e-42 E value Match length 81 100 % identity

NCBI Description (AL049751) ribosomal protein L13a like protein [Arabidopsis

thaliana]

Seq. No. 139172

Seq. ID LIB23-065-Q1-E1-G9

Method BLASTX NCBI GI g2959767 BLAST score 530 E value 3.0e-54 Match length 121 85 % identity

(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi 3738292 NCBI Description

(AC005309) glutathione-conjugate transporter AtMRP4

[Arabidopsis thaliana]

Seq. No. 139173

Seq. ID LIB23-065-Q1-E1-H10

Method BLASTN NCBI GI q2828278 BLAST score 34 E value 1.0e-09 Match length 66 % identity 85

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16

(ESSAII project)



```
Seq. No.
                  139174
Seq. ID
                  LIB23-065-Q1-E1-H2
Method
                  BLASTX
NCBI GI
                  g2506443
BLAST score
                  404
E value
                  9.0e-40
Match length
                  80
                  100
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                  CHLOROPLAST >gi_2117520_pir__JQ1285
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde
                  3-phosphate dehydrogenase [Arabidopsis thaliana]
                  >gi_1402885_emb_CAA66816_ (X98130)
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) [Arabidopsis thaliana]
Seq. No.
                  139175
Seq. ID
                  LIB23-065-Q1-E1-H6
Method
                  BLASTN
NCBI GI
                  q4454447
BLAST score
                  40
                  2.0e-13
E value
Match length
                  68
% identity
                  90
                  Arabidopsis thaliana chromosome II BAC F5H14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  139176
Seq. No.
Seq. ID
                  LIB23-066-Q1-E1-A2
Method
                  BLASTX
NCBI GI
                  g2194125
BLAST score
                  230
E value
                  4.0e-19
Match length
                  59
% identity
NCBI Description
                  (AC002062) ESTs gb R30459, gb N38441 come from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  139177
Seq. ID
                  LIB23-066-Q1-E1-A6
Method
                  BLASTX
NCBI GI
                  g3142300
BLAST score
                  451
E value
                  5.0e-45
Match length
                  125
% identity
                  69
NCBI Description
                  (AC002411) Contains similarity to pre-mRNA processing
                  protein PRP39 gb L29224 from S. cerevisiae. ESTs gb R64908
                  and gb T88158, gb N38703 and gb AA651043 come from this
                  gene. [Arabidopsis thaliana]
```

Seq. No. 139178

LIB23-066-Q1-E1-B1 Seq. ID

BLASTX Method NCBI GI g4585977



```
BLAST score
                  410
E value
                  2.0e-40
Match length
                  89
                  80
% identity
NCBI Description
                  (AC005287) Unknown protein [Arabidopsis thaliana]
                  139179
Seq. No.
Seq. ID
                  LIB23-066-Q1-E1-B11
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  328
E value
                  1.0e-30
Match length
                  80
% identity
                  78
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  139180
Seq. ID
                  LIB23-066-Q1-E1-B3
Method
                  BLASTX
NCBI GI
                  g4049354
BLAST score
                  527
E value
                  5.0e-54
Match length
                  101
% identity
                  99
NCBI Description
                  (AL034567) glycine hydroxymethyltransferase (EC
                  2.1.2.1)-like protein [Arabidopsis thaliana]
                  139181
Seq. No.
                  LIB23-066-Q1-E1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2623294
BLAST score
                  397
E value
                  0.0e + 00
Match length
                  397
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC T20B5 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139182
Seq. ID
                  LIB23-066-Q1-E1-C8
Method
                  BLASTX
NCBI GI
                  g124224
BLAST score
                  176
E value
                  8.0e-13
Match length
                  41
% identity
                  80
NCBI Description
                  INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
```

>gi_100345_pir__S21060 translation initiation factor eIF-5A

- common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No. 139183

Seq. ID LIB23-066-Q1-E1-D7

Method BLASTX

Method

NCBI GI



```
NCBI GI
                  q4584527
BLAST score
                  208
                  1.0e-16
E value
                  108
Match length
                  42
% identity
NCBI Description
                  (AL049607) putative protein [Arabidopsis thaliana]
Seq. No.
                  139184
Seq. ID
                  LIB23-066-Q1-E1-E9
Method
                  BLASTX
NCBI GI
                  q399091
BLAST score
                  391
                  6.0e-38
E value
Match length
                  101
% identity
                  78
NCBI Description
                  PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP
                  (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)
                  (H+-PPASE) >gi_282878_pir__A38230 inorganic pyrophosphatase
                  (EC 3.6.1.1), H+-translocating pyrophosphate-energized -
                  Arabidopsis thaliana >gi_166634 (M81892) vacuolar
                  H+-phosphatase [Arabidopsis thaliana]
Seq. No.
                  139185
Seq. ID
                  LIB23-066-Q1-E1-H10
Method
                  BLASTN
NCBI GI
                  q2828278
BLAST score
                  230
E value
                  1.0e-126
Match length
                  322
% identity
                  97
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16
                  (ESSAII project)
Seq. No.
                  139186
Seq. ID
                  LIB23-066-Q1-E1-H11
Method
                  BLASTX
NCBI GI
                  g2894597
BLAST score
                  506
                  2.0e-51
E value
                  119
Match length
                  85
% identity
NCBI Description (AL021889) bHLH protein - like [Arabidopsis thaliana]
Seq. No.
                  139187
Seq. ID
                  LIB23-067-Q1-E1-A7
Method
                  BLASTN
NCBI GI
                  g897676
BLAST score
                  118
E value
                  3.0e-60
Match length
                  118
                  100
% identity
NCBI Description A.thaliana DNA for 40 kDa protein gene
Seq. No.
                  139188
Seq. ID
                  LIB23-067-Q1-E1-B1
```

BLASTN

g4757414

Match length

% identity

306

99



```
BLAST score
E value
                  1.0e-142
Match length
                  278
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MYF24, complete sequence
                  139189
Seq. No.
                  LIB23-067-Q1-E1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3281865
BLAST score
                  393
E value
                  4.0e-38
Match length
                  138
% identity
                  39
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                  139190
Seq. No.
                  LIB23-067-Q1-E1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4337011
BLAST score
                  345
                  5.0e-38
E value
Match length
                  89
% identity
                  97
                  (AF119572) zinc-binding peroxisomal integral membrane
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  139191
Seq. ID
                  LIB23-067-Q1-E1-C10
Method
                  BLASTX
                  g1706918
NCBI GI
BLAST score
                  251
E value
                  2.0e-21
Match length
                  95
                  56
% identity
NCBI Description FLAVONOL SULFOTRANSFERASE-LIKE >gi 498647 (U10277)
                  sulfotransferase-like flavonol [Flaveria bidentis]
Seq. No.
                  139192
Seq. ID
                  LIB23-067-Q1-E1-C9
Method
                  BLASTX
NCBI GI
                  q4106395
BLAST score
                  329
E value
                  9.0e-31
Match length
                  116
                  59
% identity
NCBI Description
                  (AF073744) raffinose synthase [Cucumis sativus]
Seq. No.
                  139193
Seq. ID
                  LIB23-067-Q1-E1-E3
Method
                  BLASTN
NCBI GI
                  q3763944
BLAST score
                  237
E value
                  1.0e-131
```

Method

NCBI GI

E value

BLAST score

BLASTN

438

g2760172

0.0e + 00



```
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23
                   (ESSAII project)
Seq. No.
                  139194
Seq. ID
                  LIB23-067-01-E1-E4
Method
                  BLASTX
NCBI GI
                  g4467125
BLAST score
                  195
                  4.0e-15
E value
Match length
                  96
% identity
                  42
NCBI Description
                  (AL035538) putative protein [Arabidopsis thaliana]
Seq. No.
                  139195
                  LIB23-067-Q1-E1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3513739
BLAST score
                  562
E value
                  5.0e-58
Match length
                  125
% identity
                  89
NCBI Description
                  (AF080118) Similar to uridine diphosphate glucose
                  epimerase; F8M12.10 [Arabidopsis thaliana]
                  139196
Seq. No.
Seq. ID
                  LIB23-067-Q1-E1-F4
Method
                  BLASTX
                  g3875004
NCBI GI
BLAST score
                  276
                  2.0e-24
E value
Match length
                  85
% identity
                  35
NCBI Description
                  (Z81484) similar to multidrug resistance protein
                  (p-glycoprotein) (2 domains); cDNA EST yk303b9.5 comes from
                  this gene; cDNA EST yk303b9.3 comes from this gene
                  [Caenorhabditis elegans] >gi_3879215_emb CAB07855 (Z93782)
                  similar to multidrug resistance protein (p-glycoprotein) (2
                  domains); cDNA EST yk303b9.5 comes from this gene; cDNA EST
                  yk303b9.3 comes from this gene [Caenorhabditis elegans]
Seq. No.
                  139197
Seq. ID
                  LIB23-067-Q1-E1-F7
Method
                  BLASTN
NCBI GI
                  g3510347
BLAST score
                  213
E value
                  1.0e-116
Match length
                  445
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139198
Seq. ID
                  LIB23-067-Q1-E1-G6
```



Match length 445 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUB3, complete sequence [Arabidopsis thaliana]

Seq. No. 139199

Seq. ID LIB23-067-Q1-E1-H1

Method BLASTX
NCBI GI g4388834
BLAST score 230
E value 3.0e-19
Match length 101
% identity 50

NCBI Description (AC006528) putative disease resistance protein RPP1, 3'

partial [Arabidopsis thaliana]

Seq. No. 139200

Seq. ID LIB23-068-Q1-E1-A3

Method BLASTN
NCBI GI g3241926
BLAST score 103
E value 4.0e-51
Match length 151
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSG15, complete sequence [Arabidopsis thaliana]

Seq. No. 139201

Seq. ID LIB23-068-Q1-E1-B1

Method BLASTX
NCBI GI g4510373
BLAST score 235
E value 8.0e-20
Match length 60
% identity 68

NCBI Description (AC007017) putative harpin-induced protein [Arabidopsis

thaliana]

Seq. No. 139202

Seq. ID LIB23-068-Q1-E1-C6

Method BLASTX
NCBI GI g2880051
BLAST score 385
E value 3.0e-37
Match length 109
% identity 72

NCBI Description (AC002340) putative protein kinase [Arabidopsis thaliana]

Seq. No. 139203

Seq. ID LIB23-068-Q1-E1-D9

Method BLASTX
NCBI GI g2244766
BLAST score 605
E value 4.0e-63
Match length 116
% identity 98

NCBI Description (Z97335) glucosyltransferase [Arabidopsis thaliana]



```
139204
Seq. No.
Seq. ID
                  LIB23-068-Q1-E1-E12
Method
                  BLASTN
NCBI GI
                  g2924733
BLAST score
                  240
                  1.0e-132
E value
Match length
                  400
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUF9, complete sequence [Arabidopsis thaliana]
                  139205
Seq. No.
Seq. ID
                  LIB23-068-Q1-E1-E8
Method
                  BLASTN
NCBI GI
                  g3510343
BLAST score
                  229
E value
                  1.0e-126
Match length
                  404
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
                  139206
Seq. No.
Seq. ID
                  LIB23-068-Q1-E1-F6
Method
                  BLASTN
NCBI GI
                  g3702722
BLAST score
                  298
E value
                  1.0e-167
Match length
                  301
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K12B20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139207
                  LIB23-068-Q1-E1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4191777
BLAST score
                  392
E value
                  2.0e-38
Match length
                  80
                  90
% identity
NCBI Description
                  (AC005917) putative casein kinase I [Arabidopsis thaliana]
Seq. No.
                  139208
Seq. ID
                  LIB23-068-Q1-E1-H12
Method
                  BLASTN
NCBI GI
                  g2264304
BLAST score
                  320
E value
                  1.0e-180
Match length
                  414
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBG8, complete sequence [Arabidopsis thaliana]
```

Seq. No. 139209

Seq. ID LIB23-069-Q1-E1-A9

BLAST score

E value

141

2.0e-73



```
Method
                  BLASTX
NCBI GI
                  q3158376
BLAST score
                  586
E value
                  7.0e-61
Match length
                  113
% identity
                  97
NCBI Description
                  (AF035385) unknown [Arabidopsis thaliana]
Seq. No.
                  139210
                  LIB23-069-Q1-E1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3256035
BLAST score
                  210
E value
                  1.0e-16
Match length
                  72
                  56
% identity
                  (Y14274) putative serine/threonine protein kinase [Sorghum
NCBI Description
                  bicolor]
                  139211
Seq. No.
                  LIB23-069-Q1-E1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4585952
BLAST score
                  178
E value
                  2.0e-95
Match length
                  421
% identity
                  100
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F26F24,
                  complete sequence
                  139212
Seq. No.
Seq. ID
                  LIB23-069-Q1-E1-B9
Method
                  BLASTX
NCBI GI
                  g2369714
BLAST score
                  512
E value
                  3.0e-52
Match length
                  111
% identity
                  91
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                  139213
Seq. ID
                  LIB23-069-Q1-E1-C4
Method
                  BLASTN
NCBI GI
                  g4159707
BLAST score
                  230
E value
                  1.0e-126
Match length
                  442
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MJK13, complete sequence
Seq. No.
                  139214
Seq. ID
                  LIB23-069-Q1-E1-C5
Method
                  BLASTN
NCBI GI
                  g3869068
```



Match length 291 % identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC16, complete sequence [Arabidopsis thaliana]

Seq. No. 139215

Seq. ID LIB23-069-Q1-E1-E5

Method BLASTN
NCBI GI g457397
BLAST score 264
E value 1.0e-147
Match length 264
% identity 100

NCBI Description Arabidopsis thaliana mRNA for MAP kinase, complete cds

Seq. No. 139216

Seq. ID LIB23-069-Q1-E1-F7

Method BLASTN
NCBI GI g2160155
BLAST score 142
E value 5.0e-74
Match length 360
% identity 100

NCBI Description Sequence of BAC F21M12 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 139217

Seq. ID LIB23-069-Q1-E1-F9

Method BLASTX
NCBI GI g3036807
BLAST score 630
E value 6.0e-66
Match length 136
% identity 91

NCBI Description (AL022373) putative protein [Arabidopsis thaliana]

Seq. No. 139218

Seq. ID LIB23-069-Q1-E1-G3

Method BLASTN
NCBI GI g3980374
BLAST score 336
E value 0.0e+00
Match length 352
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F16P2 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139219

Seq. ID LIB23-069-Q1-E1-G9

Method BLASTN
NCBI GI g4115370
BLAST score 354
E value 0.0e+00
Match length 372
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F27D4 genomic

sequence, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                  139220
Seq. ID
                  LIB23-070-Q1-E1-B1
Method
                  BLASTN
NCBI GI
                  q2827644
BLAST score
                  158
E value
                  1.0e-83
Match length
                  317
% identity
                  99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4
                  (ESSAII project)
Seq. No.
                  139221
Seq. ID
                  LIB23-070-Q1-E1-B11
Method
                  BLASTX
NCBI GI
                  g4538967
BLAST score
                  148
                  2.0e-09
E value
Match length
                  62
% identity
                  60
NCBI Description (AL049488) major intrinsic protein (MIP)-like [Arabidopsis
                  thaliana]
Seq. No.
                  139222
                  LIB23-070-Q1-E1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3688169
BLAST score
                  371
E value
                  0.0e+00
Match length
                  371
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21
                  (ESSAII project)
Seq. No.
                  139223
Seq. ID
                  LIB23-070-Q1-E1-C8
Method
                  BLASTN
                  g4510338
NCBI GI
BLAST score
                  358
                  0.0e+00
E value
Match length
                  358
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC F2H17 genomic
                  sequence, complete sequence
Seq. No.
                  139224
Seq. ID
                  LIB23-070-Q1-E1-D4
Method
                  BLASTX
NCBI GI
                  g3746059
BLAST score
                  483
E value
                  1.0e-48
Match length
                  130
% identity
                  65
NCBI Description
                  (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis
```

thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative

cysteinyl-tRNA synthetase [Arabidopsis thaliana]



```
Seq. No.
                  139225
Seq. ID
                  LIB23-070-Q1-E1-D7
Method
                  BLASTN
NCBI GI
                  q1669656
BLAST score
                  389
                  0.0e+00
E value
Match length
                  389
% identity
                  100
NCBI Description A.thaliana CER3-like gene
                  139226
Seq. No.
Seq. ID
                  LIB23-070-Q1-E1-E5
Method
                  BLASTX
                  g115804
NCBI GI
BLAST score
                  198
E value
                  1.0e-15
Match length
                  37
                  100
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-25) (LHCP) >gi 72730 pir CDPJ25 chlorophyll
                  a/b-binding protein 25 precursor - petunia
                  >gi_20483_emb_CAA26211_ (X02358) cab 25 precursor
                  polypeptide (aa -33 to 233) [Petunia sp.]
Seq. No.
                  139227
Seq. ID
                  LIB23-070-Q1-E1-F10
Method
                  BLASTN
                  g4159702
NCBI GI
BLAST score
                  249
E value
                  1.0e-138
Match length
                  359
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K2N11, complete sequence
Seq. No.
                  139228
Seq. ID
                  LIB23-070-Q1-E1-F12
Method
                  BLASTX
NCBI GI
                  g3249064
BLAST score
                  576
E value
                  1.0e-59
Match length
                  126
% identity
                  89
NCBI Description
                  (AC004473) Strong similarity to trehalose-6-phosphate
                  synthase homolog gb_2245136 from A. thaliana chromosome 4
                  contig gb_Z97344. [Arabidopsis thaliana]
Seq. No.
                  139229
Seq. ID
                  LIB23-070-Q1-E1-H9
Method
                  BLASTN
NCBI GI
                  g4038029
```

NCBI GI 94038029
BLAST score 60
E value 5.0e-25
Match length 218
% identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC F504 genomic sequence, complete sequence [Arabidopsis thaliana]



Seq. No. 139230

Seq. ID LIB23-071-Q1-E1-A1

Method BLASTN NCBI GI q4567259 202 BLAST score E value 1.0e-110 334 Match length % identity 100

Arabidopsis thaliana chromosome II BAC F3K23 genomic NCBI Description

sequence, complete sequence

Seq. No. 139231

Seq. ID LIB23-071-Q1-E1-A3

Method BLASTN NCBI GI q2288979 BLAST score 302 E value 1.0e-169 Match length 306 % identity 100

Arabidopsis thaliana chromosome II BAC T01024 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139232

Seq. ID LIB23-071-Q1-E1-B2

Method BLASTX g136636 NCBI GI BLAST score 380 E value 1.0e-36 Match length 69 % identity 100

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN NCBI Description

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 -

Arabidopsis thaliana >gi_442594 pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi 431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 139233

Seq. ID LIB23-071-Q1-E1-D2

Method BLASTN g2828186 NCBI GI BLAST score 264 E value 1.0e-147 264 Match length % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18I23, complete sequence [Arabidopsis thaliana]

Seq. No. 139234

Seq. ID LIB23-071-Q1-E1-F2

BLASTX Method NCBI GI g2146745

BLAST score 376



E value 3.0e-36 Match length 90 % identity 81 protein kinase (EC 2.7.1.-) - Arabidopsis thaliana NCBI Description >gi_642132_dbj_BAA08215_ (D45354) protein kinase [Arabidopsis thaliana] Seq. No. 139235 LIB23-071-Q1-E1-F6 Seq. ID Method BLASTX g4539009 NCBI GI BLAST score 654 E value 8.0e-69 Match length 120 % identity 100 NCBI Description (AL049481) putative protein [Arabidopsis thaliana] Seq. No. 139236 Seq. ID LIB23-071-Q1-E1-H9 Method BLASTX NCBI GI g3850574 BLAST score 252 E value 1.0e-21 Match length 98 % identity 54 NCBI Description (AC005278) Strong similarity to T08I13.7 gi_2275201 unknown protein from Arabidopsis thaliana BAC gb ACO02337. EST gb Z17450 comes from this gene. [Arabidopsis thaliana] Seq. No. 139237 Seq. ID LIB23-072-Q1-E1-A11 Method BLASTN NCBI GI q1167960 BLAST score 42 E value 3.0e-14 Match length 365 % identity 33 NCBI Description Arabidopsis thaliana extensin (atExt1) gene, complete cds Seq. No. 139238 Seq. ID LIB23-072-01-E1-A12 Method BLASTN NCBI GI g4539402 BLAST score 360 E value 0.0e+00Match length 360 % identity 100 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7L13 (ESSA project) Seq. No. 139239

Seq. ID LIB23-072-Q1-E1-A9

Method BLASTN
NCBI GI g4589415
BLAST score 161
E value 3.0e-85
Match length 353



% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K14A3, complete sequence

Seq. No. 139240

Seq. ID LIB23-072-Q1-E1-B12

Method BLASTN
NCBI GI g1931636
BLAST score 274
E value 1.0e-153
Match length 361
% identity 100

NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No. 139241

Seq. ID LIB23-072-Q1-E1-B4

Method BLASTN
NCBI GI g166657
BLAST score 209
E value 1.0e-114
Match length 233
% identity 97

NCBI Description Arabidopsis thaliana Ccrl mRNA, complete cds

Seq. No. 139242

Seq. ID LIB23-072-Q1-E1-B7

Method BLASTN
NCBI GI 94510338
BLAST score 453
E value 0.0e+00
Match length 453
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F2H17 genomic

sequence, complete sequence

Seq. No. 139243

Seq. ID LIB23-072-Q1-E1-C4

Method BLASTX
NCBI GI g3851711
BLAST score 261
E value 1.0e-22
Match length 139
% identity 42

NCBI Description (AF102265) N-acetylglucosamine-phosphate mutase [Homo

sapiens]

Seq. No. 139244

Seq. ID LIB23-072-Q1-E1-D12

Method BLASTX
NCBI GI g3540196
BLAST score 307
E value 3.0e-28
Match length 103
% identity 61

NCBI Description (AC004260) Putative amp-binding protein [Arabidopsis

thaliana]



```
Seq. No.
                  139245
                  LIB23-072-Q1-E1-D4
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1209241
BLAST score
                   400
                  0.0e + 00
E value
                  424
Match length
                   98
% identity
NCBI Description Arabidopsis thaliana metallothionein mRNA sequence
                  139246
Seq. No.
                  LIB23-072-Q1-E1-D6
Seq. ID
                  BLASTN
                   g4191771
```

Method NCBI GI BLAST score 449 0.0e+00E value 449 Match length

100

139247

Arabidopsis thaliana chromosome II BAC F3P11 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

LIB23-072-Q1-E1-E7 Seq. ID Method BLASTX NCBI GI g4049353 502 BLAST score E value 6.0e-51 Match length 142 % identity 60

% identity

Seq. No.

NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

139248 Seq. No. LIB23-072-Q1-E1-E8 Seq. ID Method BLASTX NCBI GI g2499606 BLAST score 443 E value 5.0e-44 Match length 103

% identity NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 2 (MAP KINASE 2)

(ATMPK2) >gi_533281_dbj_BAA03536_ (D14714) ATMPK2

[Arabidopsis thaliana]

Seq. No. 139249

Seq. ID LIB23-072-Q1-E1-F8

83

Method BLASTX g2245066 NCBI GI BLAST score 789 E value 1.0e-84 146 Match length % identity 100

(Z97342) Beta-Amylase [Arabidopsis thaliana] NCBI Description

Seq. No. 139250

Seq. ID LIB23-072-Q1-E1-G4

Method BLASTN NCBI GI g4335744



BLAST score 130 E value 7.0e-67 Match length 253 % identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139251

Seq. ID LIB23-072-Q1-E1-H12

Method BLASTN
NCBI GI g4757410
BLAST score 367
E value 0.0e+00
Match length 388
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MVE11, complete sequence

Seq. No. 139252

Seq. ID LIB23-072-Q1-E1-H8

Method BLASTX
NCBI GI g4006934
BLAST score 265
E value 2.0e-23
Match length 66
% identity 76

NCBI Description (AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No. 139253

Seq. ID LIB23-073-Q1-E1-A10

Method BLASTX
NCBI GI g2129550
BLAST score 391
E value 6.0e-38
Match length 122
% identity 63

NCBI Description calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -

Arabidopsis thaliana >gi_2129554_pir__S71901

calcium-dependent protein kinase 6 - Arabidopsis thaliana

>gi_836940 (U20623) calcium-dependent protein kinase

[Arabidopsis thaliana] >gi 836944 (U20625)

calcium-dependent protein kinase [Arabidopsis thaliana]
>gi 4454034 emb CAA23031.1 (AL035394) calcium-dependent

protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No. 139254

Seq. ID LIB23-073-Q1-E1-B8

Method BLASTN
NCBI GI g3241939
BLAST score 299
E value 1.0e-168
Match length 299
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T26J13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139255



```
LIB23-073-Q1-E1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4185120
                  365
BLAST score
                  0.0e + 00
E value
Match length
                  390
                  98
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F5F19 sequence,
                  complete sequence [Arabidopsis thaliana]
                  139256
Seq. No.
Seq. ID
                  LIB23-073-Q1-E1-C6
Method
                  BLASTX
NCBI GI
                  g2708752
BLAST score
                  386
E value
                  1.0e-37
Match length
                  94
                  82
% identity
NCBI Description (AC003952) putative histidine kinase [Arabidopsis thaliana]
                  139257
Seq. No.
Seq. ID
                  LIB23-073-Q1-E1-D10
Method
                  BLASTX
NCBI GI
                  g1172599
BLAST score
                  658
E value
                  3.0e-69
Match length
                  127
                  99
% identity
NCBI Description
                  PROTEASOME COMPONENT C5 (MULTICATALYTIC ENDOPEPTIDASE
                  COMPLEX SUBUNIT C5) (TAS-F22/FAFP98)
                  >gi_600387_emb_CAA47753_ (X67338) proteosome subunit
                   [Arabidopsis thaliana]
Seq. No.
                  139258
Seq. ID
                  LIB23-073-Q1-E1-D2
Method
                  BLASTX
NCBI GI
                  q421989
BLAST score
                  243
E value
                  1.0e-20
Match length
                  92
                  52
% identity
NCBI Description
                  serpin - barley >gi_19071_emb_CAA78822_ (Z15116) protein zx
                   [Hordeum vulgare] >gi 444778 prf 1908213A protein Zx
                   [Hordeum vulgare]
Seq. No.
                  139259
Seq. ID
                  LIB23-073-Q1-E1-D8
Method
                  BLASTX
NCBI GI
                  g2244859
BLAST score
                  417
E value
                  5.0e-41
```

Match length 109

% identity 79

(Z97337) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

139260

Seq. ID

LIB23-073-Q1-E1-D9



```
Method
                  BLASTN
NCBI GI
                  q4049332
BLAST score
                  147
E value
                  3.0e-77
Match length
                  155
                  99
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4
                  (ESSAII project)
Seq. No.
                  139261
Seq. ID
                  LIB23-073-Q1-E1-E11
Method
                  BLASTX
NCBI GI
                  g3746071
BLAST score
                  610
E value
                  1.0e-63
Match length
                  120
                  100
% identity
NCBI Description
                  (AC005311) putative GTP-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  139262
Seq. ID
                  LIB23-073-Q1-E1-E12
Method
                  BLASTN
NCBI GI
                  g2351069
BLAST score
                  255
E value
                  1.0e-141
                  372
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSH12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139263
Seq. ID
                  LIB23-073-Q1-E1-E4
Method
                  BLASTN
NCBI GI
                  q4218109
BLAST score
                  161
E value
                  2.0e-85
Match length
                  304
% identity
                  99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16
                  (ESSAII project)
Seq. No.
                  139264
Seq. ID
                  LIB23-073-Q1-E1-E5
Method
                  BLASTX
NCBI GI
                  q4587550
BLAST score
                  287
E value
                  6.0e-26
Match length
                  100
% identity
                  54
                  (AC006577) EST gb R64848 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. No. 139265

Seq. ID LIB23-073-Q1-E1-E7

Method BLASTX NCBI GI g3024526



BLAST score 394
E value 2.0e-38
Match length 78
% identity 100

NCBI Description RAS-RELATED PROTEIN RAB11 >gi_2118459_pir__S59942 small GTP-binding protein Rab11 - Arabidopsis thaliana >gi_451860 (L18883) small GTP-binding protein [Arabidopsis thaliana]

Seq. No. 139266

Seq. ID LIB23-073-Q1-E1-E9

Method BLASTX
NCBI GI g1922937
BLAST score 669
E value 1.0e-70
Match length 129
% identity 99

NCBI Description (AC000106) Similar to Glycine SRC2 (gb_AB000130). ESTs gb H76869,gb T21700,gb ATTS5089 come from this gene.

[Arabidopsis thaliana]

Seq. No. 139267

Seq. ID LIB23-073-Q1-E1-F7

Method BLASTN
NCBI GI g3128136
BLAST score 192
E value 1.0e-104
Match length 373
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K1F13, complete sequence [Arabidopsis thaliana]

Seq. No. 139268

Seq. ID LIB23-073-Q1-E1-G7

Method BLASTX
NCBI GI g3043432
BLAST score 149
E value 6.0e-10
Match length 34

% identity 82

NCBI Description (AJ005348) Ubiquitin conjugating enzyme [Cicer arietinum]

Seq. No. 139269

Seq. ID LIB23-073-Q1-E1-H1

Method BLASTN
NCBI GI g4454022
BLAST score 340
E value 0.0e+00
Match length 374
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16

(ESSAII project)

Seq. No. 139270

Seq. ID LIB23-073-Q1-E1-H9

Method BLASTN
NCBI GI g4467131
BLAST score 389

NCBI Description



```
0.0e + 00
E value
Match length
                  389
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13
NCBI Description
                  (ESSA project)
                  139271
Seq. No.
Seq. ID
                  LIB23-074-Q1-E1-A4
Method
                  BLASTX
NCBI GI
                  g1402912
BLAST score
                  147
E value
                  6.0e-10
Match length
                  28
% identity
                  100
NCBI Description (X98317) peroxidase [Arabidopsis thaliana]
                  139272
Seq. No.
Seq. ID
                  LIB23-074-Q1-E1-B6
Method
                  BLASTX
NCBI GI
                  g2828267
BLAST score
                  432
E value
                  9.0e-43
Match length
                  108
% identity
                  81
NCBI Description (Y14044) geranylgeranyl reductase [Arabidopsis thaliana]
Seq. No.
                  139273
                  LIB23-074-Q1-E1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3983125
BLAST score
                  542
E value
                  1.0e-55
Match length
                  130
                  82
% identity
NCBI Description
                  (AF097648) phosphate/triose-phosphate translocator
                  precursor [Arabidopsis thaliana]
Seq. No.
                  139274
                  LIB23-074-Q1-E1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4220481
BLAST score
                  162
E value
                  4.0e-11
Match length
                  72
% identity
                  47
NCBI Description
                  (AC006069) unknown protein [Arabidopsis thaliana]
                  139275
Seq. No.
Seq. ID
                  LIB23-074-Q1-E1-E10
Method
                  BLASTX
NCBI GI
                  g3123908
BLAST score
                  200
E value
                  8.0e-16
Match length
                  52
% identity
                  63
```

16827

(AF038392) pre-mRNA splicing factor [Homo sapiens]

E value

Match length

NCBI Description

% identity

1.0e-56

110



```
139276
Seq. No.
                  LIB23-074-Q1-E1-E2
Seq. ID
Method
                  BLASTX
                  g3879145
NCBI GI
                  179
BLAST score
                  5.0e-13
E value
                  123
Match length
                  33
% identity
                  (Z93386) predicted using Genefinder; Similarity to Human
NCBI Description
                  placenta (DIFF33) protein (TR:Q13530); cDNA EST yk198a11.5
                  comes from this gene [Caenorhabditis elegans]
                  139277
Seq. No.
Seq. ID
                  LIB23-074-Q1-E1-E5
Method
                  BLASTN
                  g3869075
NCBI GI
BLAST score
                  346
                  0.0e + 00
E value
                  385
Match length
                  90
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXK3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139278
                  LIB23-074-Q1-E1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3688799
BLAST score
                  612
                  7.0e-64
E value
                  123
Match length
% identity
                  99
                  (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  139279
                  LIB23-074-Q1-E1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  590
E value
                  3.0e-61
Match length
                  112
% identity
                  99
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  139280
Seq. No.
Seq. ID
                  LIB23-075-Q1-E1-B9
Method
                  BLASTX
NCBI GI
                  g2244765
BLAST score
                  549
```

(Z97335) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.
                  139281
                  LIB23-075-Q1-E1-C11
Seq. ID
Method
                  BLASTN
                  g3176693
NCBI GI
BLAST score
                  74
E value
                  6.0e-34
Match length
                  134
% identity
                  89
                  Arabidopsis thaliana chromosome I BAC T27I1 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  139282
Seq. No.
Seq. ID
                  LIB23-075-Q1-E1-C9
Method
                  BLASTN
                  g304114
NCBI GI
                  51
BLAST score
                  6.0e-20
E value
                  195
Match length
                  91
% identity
                  Arabidopsis thaliana thioglucosidase mRNA, complete cds
NCBI Description
                  139283
Seq. No.
                  LIB23-075-Q1-E1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3242708
BLAST score
                  292
                   2.0e-26
E value
Match length
                   103
                   55
% identity
                   (AC003040) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   139284
Seq. No.
Seq. ID
                  LIB23-075-Q1-E1-H11
Method
                   BLASTN
NCBI GI
                   g3128136
BLAST score
                   78
                   2.0e-36
E value
Match length
                   110
% identity
                   93
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K1F13, complete sequence [Arabidopsis thaliana]
                   139285
Seq. No.
Seq. ID
                   LIB24-001-Q1-E1-B2
Method
                   BLASTX
NCBI GI
                   q4263777
BLAST score
                   307
E value
                   3.0e-28
Match length
                   89
% identity
                   69
```

NCBI Description

(AC006068) putative serine carboxypeptidase II [Arabidopsis

thaliana] >gi 4510391 gb AAD21479.1 (AC007017) putative

serine carboxypeptidase II [Arabidopsis thaliana]

139286 Seq. No.

LIB24-001-Q1-E1-B4 Seq. ID



Method BLASTX
NCBI GI g2499609
BLAST score 468
E value 6.0e-47
Match length 91
% identity 99
NCBI Description MITOGEN-

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 5 (MAP KINASE 5) (ATMPK5) >gi_629546_pir__S40471 mitogen-activated protein

kinase 5 (EC 2.7.1.-) - Arabidopsis thaliana

>gi_457402_dbj_BAA04868_ (D21841) MAP kinase [Arabidopsis

thaliana]

Seq. No. 139287

Seq. ID LIB24-001-Q1-E1-B5

Method BLASTX
NCBI GI g1351184
BLAST score 311
E value 1.0e-28
Match length 94
% identity 56

NCBI Description TYROSYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR

(TYROSINE--TRNA LIGASE) (TYRRS) >gi_2133198_pir__S59733 tyrosine--tRNA ligase (EC 6.1.1.1), mitochondrial - yeast (Saccharomyces cerevisiae) >gi_825503 (L42333) tyrosyl-tRNA synthetase [Saccharomyces cerevisiae] >gi_1151229 (U43281)

Lpg11p [Saccharomyces cerevisiae]

Seq. No. 139288

Seq. ID LIB24-001-Q1-E1-B9

Method BLASTN
NCBI GI g2828184
BLAST score 297
E value 1.0e-166
Match length 390
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSN9, complete sequence [Arabidopsis thaliana]

Seq. No. 139289

Seq. ID LIB24-001-Q1-E1-D5

Method BLASTX
NCBI GI g2341034
BLAST score 550
E value 1.0e-56
Match length 110
% identity 100

NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No. 139290

Seq. ID LIB24-001-Q1-E1-D6

Method BLASTN
NCBI GI g2062153
BLAST score 402
E value 0.0e+00
Match length 402
% identity 100

NCBI Description Arabidopsis thaliana chromosome III BAC T02004 genomic

NCBI Description





sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  139291
                  LIB24-001-Q1-E1-E5
Seq. ID
Method
                  BLASTX
                  g3337367
NCBI GI
BLAST score
                  237
E value
                  7.0e-20
                  100
Match length
                  41
% identity
NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]
                  139292
Seq. No.
                  LIB24-001-Q1-E1-F12
Seq. ID
Method
                  BLASTX
                  g4455333
NCBI GI
                  269
BLAST score
                  1.0e-23
E value
Match length
                  89
                  56
% identity
NCBI Description (AL035525) hypothetical protein [Arabidopsis thaliana]
                  139293
Seq. No.
                  LIB24-001-Q1-E1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2262155
BLAST score
                  360
                  0.0e+00
E value
Match length
                  363
                  100
% identity
                  DNA sequence of Arabidopsis thaliana BAC F5J6 from
NCBI Description
                  chromosome IV, complete sequence [Arabidopsis thaliana]
                  139294
Seq. No.
Seq. ID
                  LIB24-001-Q1-E1-G6
Method
                  BLASTX
                  g137465
NCBI GI
BLAST score
                  150
                  7.0e-18
E value
Match length
                  70
% identity
                  76
                  VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT)
NCBI Description
                   (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886
                  H+-transporting ATPase (EC 3.6.1.3\overline{5}) 57K chain -
                  Arabidopsis thaliana >gi 166627 (J04185) nucleotide-binding
                  subunit of vacuolar ATPase [Arabidopsis thaliana]
                  139295
Seq. No.
Seq. ID
                  LIB24-001-Q1-E1-H12
Method
                  BLASTN
NCBI GI
                  q3985958
BLAST score
                  215
E value
                  1.0e-117
Match length
                   317
% identity
                   93
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

16831

MZN1, complete sequence [Arabidopsis thaliana]

Match length

% identity

411

99



```
Seq. No.
                   139296
Seq. ID
                  LIB24-002-Q1-E1-A9
Method
                  BLASTX
NCBI GI
                   q3913379
BLAST score
                   518
E value
                  1.0e-66
Match length
                   126
                   99
% identity
                  CRYPTOCHROME 2 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR)
NCBI Description
                   >gi 1857038 (U43397) cryptochrome 2 apoprotein [Arabidopsis
                   thalianal
                   139297
Seq. No.
                  LIB24-002-Q1-E1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2851508
BLAST score
                  166
                   4.0e-12
E value
Match.length
                   33
% identity
                   94
NCBI Description
                  60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to
                   ribosomal protein L21 (gb_L38826). ESTs
                   gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis
                   thaliana] >gi_3482935 (AC003970) Putative ribosomal protein
                  L21 [Arabidopsis thaliana]
Seq. No.
                   139298
Seq. ID
                  LIB24-002-Q1-E1-D1
Method
                  BLASTN
NCBI GI
                   g2351062
BLAST score
                   144
E value
                   3.0e-75
Match length
                   272
                   99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAH20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139299
Seq. ID
                  LIB24-002-Q1-E1-D3
Method
                  BLASTX
NCBI GI
                   g2648032
BLAST score
                   468
E value
                   5.0e-47
Match length
                   113
% identity
                  81
NCBI Description
                  (AJ001374) alpha-glucosidase [Solanum tuberosum]
Seq. No.
                   139300
Seq. ID
                  LIB24-002-Q1-E1-D8
Method
                  BLASTN
NCBI GI
                   g4757388
BLAST score
                   279
E value
                   1.0e-155
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



F15L12, complete sequence

Seq. No. 139301 LIB24-002-Q1-E1-D9 Seq. ID Method BLASTN NCBI GI q4193383 BLAST score 333 0.0e+00 E value Match length 382 67 % identity Arabidopsis thaliana ribosomal protein S27 (ARS27A) gene, NCBI Description complete cds Seq. No. 139302 LIB24-002-Q1-E1-E2 Seq. ID Method BLASTN g2337888 NCBI GI BLAST score 265 E value 1.0e-147 273 Match length 99 % identity

Genomic sequence for Arabidopsis thaliana BAC F14J16, NCBI Description

complete sequence [Arabidopsis thaliana]

Seq. No. 139303

LIB24-002-Q1-E1-E7 Seq. ID

Method BLASTX NCBI GI g4206196 BLAST score 520 E value 4.0e-53 Match length 96 100 % identity

(AF071527) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 139304

Seq. ID LIB24-002-Q1-E1-H1

Method BLASTX NCBI GI g2136141 BLAST score 316 E value 2.0e-29 Match length 94 62 % identity

serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain -NCBI Description

human (fragment)

139305 Seq. No.

LIB24-002-Q1-E1-H11 Seq. ID

Method BLASTX NCBI GI q4539423 BLAST score 392 E value 4.0e-38 Match length 82 % identity 98

(AL049171) pyrophosphate-dependent phosphofructo-1-kinase NCBI Description

[Arabidopsis thaliana]

Seq. No. 139306



```
LIB24-003-Q1-E1-B1
Seq. ID
Method
                  BLASTX
                  g3080434
NCBI GI
                  178
BLAST score
                  4.0e-13
E value
                  50
Match length
                  66
% identity
                  (AL022605) putative gamma-glutamyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  139307
Seq. No.
                  LIB24-003-Q1-E1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2154715
BLAST score
                  145
                  2.0e-09
E value
                  82
Match length
                  44
% identity
                  (Y09418) CDPK-related protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  139308
                  LIB24-003-Q1-E1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2136800
BLAST score
                  219
                  9.0e-18
E value
                  83
Match length
                  54
% identity
                  polyA binding protein II - bovine >gi_1051125_emb_CAA62006_
NCBI Description
                  (X89969) polyA binding protein II [Bos taurus]
                  139309
Seq. No.
                  LIB24-003-Q1-E1-D4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4757396
BLAST score
                  207
E value
                  1.0e-113
Match length
                  249
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K8A10, complete sequence
Seq. No.
                  139310
                  LIB24-003-Q1-E1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4263796
BLAST score
                  345
                  1.0e-32
E value
Match length
                  93
                  71
% identity
NCBI Description
                  (AC006068) hypothetical protein [Arabidopsis thaliana]
```

Seq. No.

139311

Seq. ID LIB24-003-Q1-E1-D6

Method BLASTX NCBI GI g132102 BLAST score 237



E value Match length 100 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No.

139312 Seq. ID LIB24-003-Q1-E1-E8

Method BLASTX g3478700 NCBI GI 304 BLAST score 8.0e-28 E value 75 Match length % identity 81

(AF034387) AFT protein [Arabidopsis thaliana] NCBI Description

Seq. No.

139313

Seq. ID

LIB24-003-Q1-E1-H9

Method BLASTX NCBI GI g2494898 BLAST score 370 1.0e-35 E value Match length 112 % identity 35

NCBI Description PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG >qi 1545982 (U53346)

PWP2H protein [Homo sapiens] >gi_1737066 (U56085) periodic tryptophan protein 2 [Homo sapiens] >gi 1737072 (U56089)

periodic tryptophan protein 2 [Homo sapiens]

Seq. No.

139314

Seq. ID LIB24-004-Q1-E1-A4 Method BLASTN NCBI GI q4725940 BLAST score 171 E value 2.0e-91

Match length 231 % identity 99

Arabidopsis thaliana DNA chromosome 4, BAC clone T1P17 NCBI Description

(ESSA project)

Seq. No. 139315

Seq. ID LIB24-004-Q1-E1-C6

Method BLASTX NCBI GI g480450 BLAST score 391 E value 6.0e-38 Match length 93 87 % identity

ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis NCBI Description

thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid

reductoisomerase [Arabidopsis thaliana]

Seq. No. 139316

Method NCBI GI

BLAST score



```
LIB24-004-Q1-E1-D1
Seq. ID
Method
                  BLASTN
                  q3063438
NCBI GI
                  268
BLAST score
                  1.0e-149
E value
Match length
                  392
                  99
% identity
                  Complete sequence of Arabidopsis F22013, complete sequence
NCBI Description
                   [Arabidopsis thaliana]
                  139317
Seq. No.
Seq. ID
                  LIB24-004-Q1-E1-E4
Method
                  BLASTX
                  g2129727
NCBI GI
BLAST score
                  234
                  9.0e-20
E value
Match length
                  88
                  60
% identity
                  RNA-binding protein 37 - Arabidopsis thaliana >gi_1174153
NCBI Description
                   (U44134) RNA-binding protein [Arabidopsis thaliana]
                  139318
Seq. No.
                  LIB24-004-Q1-E1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129727
BLAST score
                  234
                  1.0e-19
E value
Match length
                  88
                   60
% identity
                  RNA-binding protein 37 - Arabidopsis thaliana >gi 1174153
NCBI Description
                   (U44134) RNA-binding protein [Arabidopsis thaliana]
                   139319
Seq. No.
Seq. ID
                  LIB24-004-Q1-E1-F11
Method
                  BLASTX
                   q2505874
NCBI GI
BLAST score
                   265
E value
                   3.0e-23
Match length
                   125
% identity
                   44
NCBI Description (Y12776) putative kinase [Arabidopsis thaliana]
Seq. No.
                   139320
Seq. ID
                   LIB24-004-Q1-E1-F2
Method
                   BLASTX
NCBI GI
                   q4589488
BLAST score
                   185
E value
                   3.0e-14
Match length
                   68
                   50
% identity
                  (AB023145) KIAA0928 protein [Homo sapiens]
NCBI Description
                   139321
Seq. No.
                  LIB24-004-Q1-E1-G11
Seq. ID
```

16836

BLASTX

206

g2961371

2.0e-16 E value Match length % identity 56 (AL022141) hypothetical protein (fragment) [Arabidopsis NCBI Description thaliana] 139322 Seq. No. LIB24-004-Q1-E1-G7 Seq. ID Method BLASTX g166708 NCBI GI BLAST score 501 E value 8.0e-51 Match length 99 % identity 100 (M64118) glyceraldehyde-3-phosphate dehydrogenase NCBI Description [Arabidopsis thaliana] 139323 Seq. No. Seq. ID LIB24-004-Q1-E1-H5 Method BLASTX g3123264 NCBI GI BLAST score 212 3.0e-17 E value Match length 45 % identity 96 60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279 NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana] 139324 Seq. No. LIB24-005-Q1-E1-A12 Seq. ID Method BLASTN g2494106 156 2.0e-82 355 100 Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, NCBI Description

NCBI GI BLAST score E value Match length % identity

complete sequence [Arabidopsis thaliana]

Seq. No. 139325

LIB24-005-01-E1-A3 Seq. ID

Method BLASTN g3869075 NCBI GI BLAST score 139 E value 3.0e-72 341 Match length 97 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MXK3, complete sequence [Arabidopsis thaliana]

Seq. No. 139326

Seq. ID LIB24-005-Q1-E1-A6

Method BLASTX NCBI GI g3834310 BLAST score 203 2.0e-16 E value Match length 38



```
% identity
                  (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
NCBI Description
                  gb D83004 from Homo sapiens. ESTs gb T88233, gb Z24464,
                  gb N37265, gb H36151, gb Z34711, gb AA040983, and gb T22122
                  come from this gene. [Arabidopsis thaliana]
                  139327
Seq. No.
                  LIB24-005-Q1-E1-B7
Seq. ID
Method
                  BLASTX
                  g4467152
NCBI GI
BLAST score
                  605
E value
                  8.0e-66
Match length
                  128
% identity
                  (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                  139328
Seq. No.
                  LIB24-005-Q1-E1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2828180
BLAST score
                  202
E value
                  1.0e-110
Match length
                  365
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDK4, complete sequence [Arabidopsis thaliana]
                  139329
Seq. No.
                  LIB24-005-Q1-E1-D1
Seq. ID
Method
                  BLASTX
                  g419812
NCBI GI
BLAST score
                  297
                  6.0e-27
E value
Match length
                  129
% identity
                  45
                  crm1+ protein - fission yeast (Schizosaccharomyces pombe)
NCBI Description
                  139330
Seq. No.
                  LIB24-005-Q1-E1-D5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4008005
BLAST score
                  65
E value
                  1.0e-28
Match length
                  125
% identity
                  Arabidopsis thaliana receptor-like protein kinase (RKL1)
NCBI Description
                  gene, complete cds
Seq. No.
                  139331
Seq. ID
                  LIB24-005-Q1-E1-F3
Method
                  BLASTX
NCBI GI
                  g2392895
BLAST score
                  543
                  5.0e-56
E value
Match length
                  102
```

16838

(AF017056) brassinosteroid insensitive 1 [Arabidopsis

100

% identity

NCBI Description

Match length

% identity

404

100



thaliana]

```
139332
 Seq. No.
                   LIB24-005-Q1-E1-G12
 Seq. ID
Method
                   BLASTX
                   g4580519
NCBI GI
BLAST score
                   690
E value
                   5.0e-73
Match length
                   136
                   99
 % identity
                   (AF036303) scarecrow-like 6 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   139333
Seq. ID
                   LIB24-005-Q1-E1-H10
Method
                   BLASTX
NCBI GI
                   g4581207
BLAST score
                   127
                   8.0e-39
E value
Match length
                   108
% identity
                   81
                   (Y17914) cyclic nucleotide and calmodulin-regulated ion
NCBI Description
                   channel [Arabidopsis thaliana]
                   139334
 Seq. No.
                   LIB24-005-Q1-E1-H2
 Seq. ID
Method
                   BLASTX
NCBI GI
                   q4758418
BLAST score
                   163
                   1.0e-11
E value
Match length
                   87
 % identity
                   43
                   guanylate binding protein 2, interferon-inducible
 NCBI Description
                   >qi 1169868 sp P32456 GBP2 HUMAN INTERFERON-INDUCED
                   GUANYLATE-BINDING PROTEIN 2 (GUANINE NUCLEOTIDE-BINDING
                   PROTEIN 2) >gi_2135319_pir__S70524 guanine
                   nucleotide-binding protein 2 - human >gi 829177 (M55543)
                   guanylate binding protein isoform II [Homo sapiens]
 Seq. No.
                   139335
 Seq. ID
                   LIB24-006-Q1-E1-A1
 Method
                   BLASTN
                   g2618599
 NCBI GI
 BLAST score
                   66
E value
                   1.0e-28
Match length
                   185
 % identity
                   84
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MBD2, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   139336
 Seq. ID
                   LIB24-006-Q1-E1-A11
 Method
                   BLASTN
 NCBI GI
                   q2264314
 BLAST score
                   159
 E value
                   4.0e-84
```



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No. 139337

Seq. ID LIB24-006-Q1-E1-A2

Method BLASTX
NCBI GI g282963
BLAST score 366
E value 5.0e-35
Match length 74
% identity 82

NCBI Description transforming protein (myb) homolog (clone myb.Ph2) - garden

petunia >gi 20561 emb CAA78387 (Z13997) protein 2 [Petunia

x hybrida]

Seq. No. 139338

Seq. ID LIB24-006-Q1-E1-A6

Method BLASTX
NCBI GI g3075394
BLAST score 705
E value 9.0e-75
Match length 135
% identity 100

NCBI Description (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana] >gi 3559809 emb CAA09311_ (AJ010713) fiddlehead

protein [Arabidopsis thaliana]

Seq. No. 139339

Seq. ID LIB24-006-Q1-E1-B11

Method BLASTN
NCBI GI g3522932
BLAST score 210
E value 1.0e-114
Match length 389
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F14M4 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139340

Seq. ID LIB24-006-Q1-E1-B5

Method BLASTX
NCBI GI g2956690
BLAST score 413
E value 2.0e-40
Match length 110
% identity 57

NCBI Description (AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928

(AF079800) PsbY precursor [Arabidopsis thaliana]

Seq. No. 139341

Seq. ID LIB24-006-Q1-E1-B8

Method BLASTX
NCBI GI g3776573
BLAST score 269
E value 1.0e-23
Match length 100
% identity 55



NCBI Description (AC005388) Similar to nodulins and lipase homolog F14J9.5

gi_3482914 from Arabidopsis thaliana BAC gb_AC003970. Alternate first exon from 72258 to 72509. [Arabidopsis

thaliana]

Seq. No. 139342

Seq. ID LIB24-006-Q1-E1-C7

Method BLASTX
NCBI GI g544424
BLAST score 441
E value 8.0e-44
Match length 85
% identity 100

NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147

glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding

protein [Arabidopsis thaliana]

>gi_4567224_gb_AAD23639.1 AC007119_5 (AC007119)

glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No. 139343

Seq. ID LIB24-006-Q1-E1-D11

Method BLASTN
NCBI GI g4249393
BLAST score 260
E value 1.0e-144
Match length 384
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T9J23 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139344

Seq. ID LIB24-006-Q1-E1-D2

Method BLASTN
NCBI GI g4325336
BLAST score 400
E value 0.0e+00
Match length 408
% identity 100

NCBI Description Arabidopsis thaliana BAC F15P23

Seq. No. 139345

Seq. ID LIB24-006-Q1-E1-D6

Method BLASTX
NCBI GI g4539343
BLAST score 453
E value 3.0e-45
Match length 137
% identity 74

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 139346

Seq. ID LIB24-006-Q1-E1-D7

Method BLASTX NCBI GI g2651316 BLAST score 473



```
E value
                  1.0e-47
Match length
                  95
% identity
                  100
                  (AC002336) unknown protein [Arabidopsis thaliana]
NCBI Description
                  139347
Seq. No.
                  LIB24-006-Q1-E1-D8
Seq. ID
Method
                  BLASTX
                  g4056502
NCBI GI
BLAST score
                  442
                  6.0e-44
E value
                  91
Match length
                  100
% identity
                  (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  139348
                  LIB24-006-Q1-E1-E1
Seq. ID
                  BLASTN
Method
                  q4680765
NCBI GI
BLAST score
                  141
                  2.0e-73
E value
Match length
                  407
                  99
% identity
                  Arabidopsis thaliana BAC F14I23 from chromosome V near 69
NCBI Description
                  cM, complete sequence
Seq. No.
                  139349
                  LIB24-006-Q1-E1-E10
Seq. ID
Method
                  BLASTN
                  g4757392
NCBI GI
BLAST score
                  163
                  7.0e-87
E value
                  163
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                  K14A17, complete sequence
Seq. No.
                  139350
                  LIB24-006-Q1-E1-E12
Seq. ID
Method
                  BLASTN
                  q4587641
NCBI GI
                  205
BLAST score
                  1.0e-111
E value
                  424
Match length
% identity
                  Arabidopsis thaliana chromosome I BAC F20D21 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  139351
Seq. ID
                  LIB24-006-Q1-E1-E5
Method
                  BLASTN
NCBI GI
                  q4220632
BLAST score
                   327
E value
                  0.0e+00
Match length
                   385
% identity
                   99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
```





K6M13, complete sequence [Arabidopsis thaliana]

```
139352
Seq. No.
                  LIB24-006-Q1-E1-E8
Seq. ID
                  BLASTX
Method
                  g4510345
NCBI GI
                  386
BLAST score
                  2.0e-37
E value
Match length
                  72
                  100
% identity
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
                  139353
Seq. No.
                  LIB24-006-Q1-E1-F1
Seq. ID
Method
                  BLASTX
                  g2275216
NCBI GI
                  250
BLAST score
                  2.0e-21
E value
Match length
                  64
                  75
% identity
                  (AC002337) cytochrome c oxidase Vc subunit isolog
NCBI Description
                  [Arabidopsis thaliana]
                  139354
Seq. No.
                  LIB24-006-Q1-E1-F10
Seq. ID
Method
                  BLASTX
                  g267077
NCBI GI
BLAST score
                  709
                  3.0e-75
E value
                  131
Match length
                  100
% identity
                  TUBULIN BETA-5 CHAIN >gi 320186_pir__JQ1589 tubulin beta-5
NCBI Description
                  chain - Arabidopsis thaliana >gi_166902 (M84702) beta-5
                  tubulin [Arabidopsis thaliana]
                  139355
Seq. No.
                  LIB24-006-Q1-E1-F7
Seq. ID
Method
                  BLASTN
                  g4567237
NCBI GI
BLAST score
                  206
                  1.0e-112
E value
                  354
Match length
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC T22F11 genomic
NCBI Description
                  sequence, complete sequence
                  139356
Seq. No.
                  LIB24-006-Q1-E1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1652745
BLAST score
                  262
E value
                  8.0e-23
Match length
                  98
                   50
% identity
                  (D90908) hypothetical protein [Synechocystis sp.]
NCBI Description
```

16843

139357

Seq. No.



```
LIB24-006-Q1-E1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4531443
                  395
BLAST score
                  2.0e-38
E value
Match length
                  117
% identity
                   (AC006224) putative 50s ribosomal protein L3 [Arabidopsis
NCBI Description
                  thaliana]
                  139358
Seq. No.
Seq. ID
                  LIB24-006-Q1-E1-G10
Method
                  BLASTN
NCBI GI
                  q2760164
                   374
BLAST score
                  0.0e+00
E value
Match length
                  395
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K18P6, complete sequence [Arabidopsis thaliana]
                  139359
Seq. No.
                  LIB24-006-Q1-E1-G2
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4220643
BLAST score
                   359
E value
                   0.0e + 00
Match length
                   359
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MWD22, complete sequence [Arabidopsis thaliana]
                   139360
Seq. No.
Seq. ID
                   LIB24-006-Q1-E1-G5
Method
                   BLASTN
NCBI GI
                   q4056476
BLAST score
                   414
E value
                   0.0e+00
                   414
Match length
% identity
                   100
                  Arabidopsis thaliana chromosome II BAC F3G5 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139361
Seq. ID
                   LIB24-006-Q1-E1-G7
Method
                   BLASTN
NCBI GI
                   q2337888
BLAST score
                   361
E value
                   0.0e + 00
Match length
                   419
% identity
                   100
```

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14J16,

complete sequence [Arabidopsis thaliana]

Seq. No. 139362

Seq. ID LIB24-006-Q1-E1-H11

Method BLASTX



```
q421826
NCBI GI
BLAST score
                  328
E value
                  8.0e-31
Match length
                  65
                  100
% identity
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                  >gi 298036 emb_CAA50712_ (X71878) CP29 [Arabidopsis
                  thaliana]
                  139363
Seq. No.
                  LIB24-006-Q1-E1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3176693
BLAST score
                  274
                  1.0e-152
E value
Match length
                  414
                  100
% identity
                  Arabidopsis thaliana chromosome I BAC T27I1 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  139364
Seq. No.
                  LIB24-007-Q1-E1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4678371
BLAST score
                  361
E value
                  0.0e+00
Match length
                  382
                  98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15
NCBI Description
                  (ESSA project)
                  139365
Seq. No.
                  LIB24-007-Q1-E1-B5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4455262
BLAST score
                  84
                  5.0e-40
E value
Match length
                  88
% identity
                  99
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
NCBI Description
                  (ESSAII project)
                  139366
Seq. No.
                  LIB24-007-Q1-E1-C3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2760316
BLAST score
                  117
                  4.0e-59
E value
Match length
                  358
% identity
                  98
NCBI Description
                  The sequence of BAC F1N21 from Arabidopsis thaliana
                  chromosome 1, complete sequence [Arabidopsis thaliana]
```

Seq. No. 139367

Seq. ID LIB24-007-Q1-E1-F5

Method BLASTX NCBI GI g99660



```
BLAST score
E value
                  1.0e-35
                  91
Match length
% identity
                  78
                  S-locus-specific glycoprotein SLR1 precursor - Arabidopsis
NCBI Description
                  thaliana >gi_246209_bbs_84925 (S84921) S-locus related
                  protein SLR1 homolog=AtS1 [Arabidopsis thaliana, Peptide,
                  439 aa] [Arabidopsis thaliana]
                  139368
Seq. No.
Seq. ID
                  LIB24-007-Q1-E1-F8
Method
                  BLASTX
NCBI GI
                  q4371280
BLAST score
                  275
                  2.0e-24
E value
                  103
Match length
                  57
% identity
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  139369
                  LIB24-007-Q1-E1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4454447
BLAST score
                  100
E value
                  7.0e-49
Match length
                  415
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F5H14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  139370
Seq. No.
                  LIB24-007-Q1-E1-G5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3461810
BLAST score
                  110
E value
                  5.0e-55
Match length
                  274
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T17M13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  139371
Seq. No.
Seq. ID
                  LIB24-008-Q1-E1-C3
Method
                  BLASTX
NCBI GI
                  q3551954
BLAST score
                  176
                  6.0e-13
E value
Match length
                  73
% identity
                  45
NCBI Description
                  (AF082030) senescence-associated protein 5 [Hemerocallis
                  hybrid cultivar]
```

Seq. No. 139372 Seq. ID LIB24-008-Q1-E1-D10

MethodBLASTNNCBI GIg4691223BLAST score199



E value 1.0e-108 Match length 207

% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15

(ESSA project)

Seq. No. 139373

Seq. ID LIB24-008-Q1-E1-D11

Method BLASTN
NCBI GI g3702315
BLAST score 268
E value 1.0e-149
Match length 363
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139374

Seq. ID LIB24-008-Q1-E1-F1

Method BLASTX
NCBI GI g2129578
BLAST score 608
E value 2.0e-63
Match length 119
% identity 98

NCBI Description dTDP-glucose 4-6-dehydratases homolog - Arabidopsis

thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435 prf_2124427B diamide resistance gene

[Arabidopsis thaliana]

Seq. No. 139375

Seq. ID LIB24-008-Q1-E1-F6

Method BLASTN
NCBI GI g3548797
BLAST score 370
E value 0.0e+00
Match length 370
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T18E12 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139376

Seq. ID LIB24-008-Q1-E1-F8

Method BLASTX
NCBI GI g4218120
BLAST score 376
E value 3.0e-36
Match length 118
% identity 61

NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis

thaliana]

Seq. No. 139377

Seq. ID LIB24-008-Q1-E1-G1

Method BLASTX NCBI GI g1730512



BLAST score 365 E value 5.0e-35 Match length 112 % identity 71

NCBI Description PHOSPHOGLYCERATE KINASE, CHLOROPLAST

>gi_2129669_pir__S71368 phosphoglycerate kinase Arabidopsis thaliana (fragment) >gi_1022805 (U37701)

phosphoglycerate kinase [Arabidopsis thaliana]

Seq. No. 139378

Seq. ID LIB24-008-Q1-E1-G9

Method BLASTN
NCBI GI g4699904
BLAST score 368
E value 0.0e+00
Match length 368
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F1E22,

complete sequence

Seq. No. 139379

Seq. ID LIB24-008-Q1-E1-H10

Method BLASTN
NCBI GI g2760164
BLAST score 172
E value 3.0e-92
Match length 172
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18P6, complete sequence [Arabidopsis thaliana]

Seq. No. 139380

Seq. ID LIB24-008-Q1-E1-H2

Method BLASTX
NCBI GI g3193287
BLAST score 75
E value 4.0e-21
Match length 85
% identity 67

NCBI Description (AF069298) Arabidopsis predicted protein of unknown

function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No. 139381

Seq. ID LIB24-008-Q1-E1-H5

Method BLASTN
NCBI GI g4455168
BLAST score 364
E value 0.0e+00
Match length 395
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10

(ESSAII project)

Seq. No. 139382

Seq. ID LIB24-008-Q1-E1-H9

Method BLASTN NCBI GI g2435510

% identity

60

NCBI Description Xenopus laevis cDNA clone 27A6-1



```
BLAST score
                  1.0e-155
E value
Match length
                  401
                  100
% identity
NCBI Description Arabidopsis thaliana BAC TM017A05
                  139383
Seq. No.
                  LIB24-009-Q1-E1-A1
Seq. ID
Method
                  BLASTN
                  g4468801
NCBI GI
BLAST score
                  160
                  7.0e-85
E value
                  195
Match length
% identity
                  99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17
                  (ESSA project)
                  139384
Seq. No.
                  LIB24-009-Q1-E1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2262097
                  200
BLAST score
                  1.0e-109
E value
                  200
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome IV BAC T19F6 genomic
                  sequence, complete sequence
                  139385
Seq. No.
                  LIB24-009-Q1-E1-A12
Seq. ID
Method
                  BLASTX
                  g2829881
NCBI GI
BLAST score
                  160
                  7.0e-11
E value
Match length
                  77
                  48
% identity
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]
                  139386
Seq. No.
                  LIB24-009-Q1-E1-A8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2191126
BLAST score
                  160
                   5.0e-85
E value
Match length
                  188
% identity
                   96
NCBI Description Arabidopsis thaliana BAC IG002N01
Seq. No.
                   139387
                  LIB24-009-Q1-E1-D6
Seq. ID
Method
                  BLASTN
                   q3821780
NCBI GI
BLAST score
                   35
                   7.0e-11
E value
Match length
                   36
```



```
Seq. No.
                  139388
                                                                           ، المعاولية م
Seq. ID
                  LIB24-009-Q1-E1-E11
Method
                  BLASTX
                  q4263722
NCBI GI
                  347
BLAST score
E value
                   6.0e-33
                  78
Match length
                  78
% identity
                  (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  139389
Seq. ID
                  LIB24-009-Q1-E1-F4
Method
                  BLASTX
                  q2244946
NCBI GI
                   396
BLAST score
                   6.0e-39
E value
Match length
                   80
                   96
% identity
                   (Z97339) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                   >gi 2326344 emb_CAA72072_ (Y11187) G14587-6 [Arabidopsis
                   thaliana]
Seq. No.
                   139390
                  LIB24-009-Q1-E1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4581116
BLAST score
                   541
E value
                   9.0e-56
Match length
                   102
                   100
% identity
                   (AC005825) putative beta-galactosidase [Arabidopsis
NCBI Description
                   thaliana]
                   139391
Seq. No.
                   LIB24-010-Q1-E1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2213583
BLAST score
                   350
E value
                   3.0e-33
Match length
                   105
                   76
% identity
NCBI Description (AC000348) T7N9.3 [Arabidopsis thaliana]
Seq. No.
                   139392
Seq. ID
                   LIB24-010-Q1-E1-F1
Method
                   BLASTN
NCBI GI
                   g3426033
BLAST score
                   305
E value
                   1.0e-171
Match length
                   419
% identity
                   100
                   Arabidopsis thaliana chromosome II BAC F12C20 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```

16850

139393

LIB24-010-Q1-E1-F10

Seq. No.

Seq. ID



```
BLASTX
Method
                  q3402672
NCBI GI
                  288
BLAST score
                  3.0e-26
E value
Match length
                  80
                  65
% identity
                  (AC004697) putative white protein [Arabidopsis thaliana]
NCBI Description
                  139394
Seq. No.
                  LIB24-010-Q1-E1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132677
BLAST score
                  254
E value
                  2.0e-22
Match length
                  55
                  93
% identity
                  50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15)
NCBI Description
                  >gi_71241_pir__R5MUL5 ribosomal protein L15 precursor,
                  chloroplast - Arabidopsis thaliana >gi 16497 emb CAA77593
                  (Z11508) Plastid ribosomal protein CL15 [Arabidopsis
                  thaliana]
                  139395
Seq. No.
Seq. ID
                  LIB24-010-Q1-E1-G12
Method
                  BLASTX
NCBI GI
                  g3738310
BLAST score
                  434
                  4.0e-43
E value
                  104
Match length
                  82
% identity
                  (AC005309) putative nuclear protein [Arabidopsis thaliana]
NCBI Description
                  139396
Seq. No.
                  LIB24-011-Q1-E1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1710581
BLAST score
                  616
                  3.0e-64
E value
Match length
                  125
                  96
% identity
                  60S RIBOSOMAL PROTEIN L9 >gi 2129720 pir S71255 ribosomal
NCBI Description
                  protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_
                  (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]
Seq. No.
                  139397
                  LIB24-011-Q1-E1-B2
Seq. ID
Method
                  BLASTN
                  q4432811
NCBI GI
BLAST score
                  314
                  1.0e-176
E value
Match length
                  318
```

100 % identity

Arabidopsis thaliana chromosome II BAC F16D14 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139398

LIB24-011-Q1-E1-B7 Seq. ID



```
Method
                  BLASTN
                  g3600045
NCBI GI
BLAST score
                  167
                  7.0e-89
E value
                  338
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana BAC F2P3
                  139399
Seq. No.
                  LIB24-011-Q1-E1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3273743
BLAST score
                  620
E value
                  9.0e-65
Match length
                  118
% identity
                  100
                  (AF057357) lipid transfer protein 2 precursor [Arabidopsis
NCBI Description
                  thaliana] >gi_3786019 (AC005499) unknown protein
                   [Arabidopsis thaliana]
Seq. No.
                  139400
                  LIB24-011-Q1-E1-D10
Seq. ID
                  BLASTN
Method
                  g4510323
NCBI GI
BLAST score
                  51
                  4.0e-20
E value
                  87
Match length
% identity
                  90
                  Arabidopsis thaliana BAC T7B11 from chromosome IV near 10
NCBI Description
                  cM, complete sequence
                  139401
Seq. No.
                  LIB24-011-Q1-E1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351272
                  157
BLAST score
                   4.0e-11
E value
Match length
                  29
                   100
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550
NCBI Description
                   (U02949) cytosolic triose phosphate isomerase [Arabidopsis
                   thaliana] >gi 742408 prf 2009415A triose phosphate
                   isomerase [Arabidopsis thaliana]
                   139402
Seq. No.
Seq. ID
                  LIB24-011-Q1-E1-D4
Method
                  BLASTN
NCBI GI
                   q4589419
                   159
```

BLAST score 3.0e-84 E value Match length 381 74 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K2I5, complete sequence

Seq. No. 139403

Seq. ID LIB24-011-Q1-E1-E1



97

[Gossypium hirsutum]

% identity

NCBI Description

```
Method
NCBI GI
                  q3063438
                  151
BLAST score
                  2.0e-79
E value
Match length
                  381
% identity
                  99
NCBI Description
                  Complete sequence of Arabidopsis F22013, complete sequence
                  [Arabidopsis thaliana]
                  139404
Seq. No.
Seq. ID
                  LIB24-011-Q1-E1-E7
Method
                  BLASTN
NCBI GI
                  g1905875
BLAST score
                  287
                  1.0e-160
E value
                  291
Match length
                  100
% identity
                  Arabidopsis thaliana biotin carboxylase subunit (CAC2)
NCBI Description
                  mRNA, complete cds
                  139405
Seq. No.
                  LIB24-011-Q1-E1-F6
Seq. ID
Method
                  BLASTX
                  g399091
NCBI GI
BLAST score
                  459
E value
                  7.0e-46
Match length
                  109
% identity
                  8.5
                  PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP
NCBI Description
                   (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)
                   (H+-PPASE) >gi 282878 pir A38230 inorganic pyrophosphatase
                   (EC 3.6.1.1), H+-translocating pyrophosphate-energized -
                  Arabidopsis thaliana >gi_166634 (M81892) vacuolar
                  H+-phosphatase [Arabidopsis thaliana]
Seq. No.
                  139406
Seq. ID
                  LIB24-011-Q1-E1-F7
Method
                  BLASTX
                  q1706476
NCBI GI
BLAST score
                  196
                  4.0e-15
E value
                  63
Match length
% identity
                  62
                  DNAJ-LIKE PROTEIN SLR0093 >gi 1001729_dbj_BAA10566_
NCBI Description
                   (D64004) DnaJ [Synechocystis sp.]
Seq. No.
                  139407
Seq. ID
                  LIB24-011-Q1-E1-F8
Method
                  BLASTX
NCBI GI
                  q4588012
BLAST score
                   358
E value
                   9.0e-41
Match length
                  89
```

16853

(AF085717) putative callose synthase catalytic subunit

% identity



```
139408
Seq. No.
                  LIB24-011-Q1-E1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1806140
BLAST score
                  365
                  6.0e-35
E value
                  119
Match length
% identity
                  64
                  (X97314) cdc2MsC [Medicago sativa]
NCBI Description
                  139409
Seq. No.
                  LIB24-011-Q1-E1-G7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3548797
BLAST score
                  153
E value
                  2.0e-80
                  394
Match length
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC T18E12 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  139410
Seq. No.
                  LIB24-011-Q1-E1-H4
Seq. ID
Method
                  BLASTX
                  g544424
NCBI GI
BLAST score
                  204
                  4.0e-16
E value
Match length
                  39
% identity
                  97
                  GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir S30147
NCBI Description
                  glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                  >gi 16301 emb CAA78711 (Z14987) glycine rich protein
                  [Arabidopsis thaliana] >gi 166837 (L00648) RNA-binding
                  protein [Arabidopsis thaliana]
                  >gi 4567224 gb AAD23639.1 AC007119 5 (AC007119)
                  glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
Seq. No.
                  139411
                  LIB24-011-Q1-E1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4512690
BLAST score
                  327
E value
                  0.0e+00
Match length
                  360
                  97
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F11A3 genomic
                  sequence, complete sequence
                  139412
Seq. No.
Seq. ID
                  LIB24-012-Q1-E1-A1
Method
                  BLASTN
                  q4490734
NCBI GI
BLAST score
                  299
                  1.0e-167
E value
Match length
                  411
```

16854

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone



project)

139413 Seq. No. LIB24-012-Q1-E1-A4 Seq. ID Method BLASTN q3063438 NCBI GI 240 BLAST score 1.0e-132 E value 240 Match length

% identity Complete sequence of Arabidopsis F22013, complete sequence NCBI Description

[Arabidopsis thaliana]

Seq. No. 139414

Seq. ID LIB24-012-Q1-E1-A8

80

Method BLASTN g2264310 NCBI GI 252 BLAST score 1.0e-139 E value Match length 394 % identity 100

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MKP11, complete sequence [Arabidopsis thaliana]

139415 Seq. No.

Seq. ID LIB24-012-Q1-E1-B1

BLASTN Method NCBI GI g3687221 BLAST score 163 7.0e-87 E value 189 Match length 96 % identity

Arabidopsis thaliana chromosome II BAC F6F22 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

139416 Seq. No.

LIB24-012-Q1-E1-B10 Seq. ID

Method BLASTX g2529665 NCBI GI 653 BLAST score E value 1.0e-68 133 Match length % identity 95

(AC002535) putative ribosomal protein L7A [Arabidopsis NCBI Description

thaliana]

139417 Seq. No.

LIB24-012-Q1-E1-C1 Seq. ID

Method BLASTX NCBI GI g1931637 BLAST score 721 1.0e-76 E value Match length 137 100 % identity

(U95973) receptor-associated kinase isolog [Arabidopsis NCBI Description



```
139418
Seq. No.
                  LIB24-012-Q1-E1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3341671
BLAST score
                  415
                  0.0e + 00
E value
                  415
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F16B22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  139419
Seq. No.
                  LIB24-012-Q1-E1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4580476
                  291
BLAST score
                  4.0e-26
E value
                  97
Match length
                  59
% identity
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                  139420
Seq. No.
                  LIB24-012-Q1-E1-E1
Seq. ID
                  BLASTN
Method
                  g2660661
NCBI GI
BLAST score
                  128
                  1.0e-65
E value
Match length
                  222
% identity
                  100
                  Arabidopsis thaliana chromosome V BAC T19K24 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   139421
Seq. No.
                  LIB24-012-Q1-E1-F4
Seq. ID
Method
                   BLASTN
                   g2285791
NCBI GI
BLAST score
                   208
E value
                   1.0e-113
                   212
Match length
                   100
% identity
NCBI Description Arabidopsis thaliana mRNA for cyanase, complete cds
                   139422
Seq. No.
                   LIB24-012-Q1-E1-G7
Seq. ID
                   BLASTN
Method
                   g4589440
NCBI GI
BLAST score
                   224
E value
                   1.0e-123
Match length
                   354
% identity
                   100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
```

MSD21, complete sequence

Seq. No. 139423

Seq. ID LIB24-012-Q1-E1-H2

Method BLASTN NCBI GI g2477521



```
BLAST score
                    0.0e + 00
 E value
 Match length
                    393
 % identity
                    100
                   Arabidopsis thaliana chromosome I BAC F22K20 genomic
 NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
                    139424
 Seq. No.
                    LIB24-013-Q1-E1-B11
- Seq. ID
 Method
                    BLASTX
                    g1592545
 NCBI GI
 BLAST score
                    173
 E value
                    2.0e-12
 Match length
                    111
 % identity
                    38
                    (U37486) peroxisomal multifunctional enzyme type II [Rattus
 NCBI Description
                    norvegicus]
                    139425
 Seq. No.
                    LIB24-013-Q1-E1-B3
 Seq. ID
 Method
                    BLASTN
                    g2245073
 NCBI GI
 BLAST score
                    252
 E value
                    1.0e-139
 Match length
                    369
 % identity
                    99
                    Arabidopsis thaliana DNA chromosome 4, ESSA I contig
 NCBI Description
                    fragment No
                    139426
 Seq. No.
                    LIB24-013-Q1-E1-E4
 Seq. ID
 Method
                    BLASTN
                    q2584827
 NCBI GI
                    175
 BLAST score
                    9.0e-94
 E value
                    333
 Match length
 % identity
                    95
                    Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
 NCBI Description
                    complete sequence [Arabidopsis thaliana]
                    139427
 Seq. No.
                    LIB24-013-Q1-E1-F8
 Seq. ID
                    BLASTN
 Method
                    g431257
 NCBI GI
 BLAST score
                    435
                    0.0e+00
 E value
                    435
 Match length
                    100
 % identity
 NCBI Description Arabidopsis thaliana lipoxygenase (Lox2) mRNA, complete cds
                    139428
 Seq. No.
```

Seq. ID LIB24-013-Q1-E1-G11

Method BLASTX NCBI GI g2829910 BLAST score 147 E value 7.0e-10 Match length 37



```
% identity
                   (AC002291) Unknown protein, contains regulator of
NCBI Description
                   chromosome condensation motifs [Arabidopsis thaliana]
                   139429
Seq. No.
                   LIB24-013-Q1-E1-H8
Seq. ID
Method
                   BLASTN
                   g3395421
NCBI GI
BLAST score
                   270
                   1.0e-150
E value
Match length
                   270
                   100
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T19C21 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   139430
Seq. No.
                   LIB24-014-Q1-E1-C2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2262155
                   109
BLAST score
                   1.0e-54
E value
                   214
Match length
                   96
% identity
                   DNA sequence of Arabidopsis thaliana BAC F5J6 from
NCBI Description
                   chromosome IV, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139431
                   LIB24-014-Q1-E1-C3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q544424
BLAST score
                   204
E value
                   4.0e-16
Match length
                   39
                   97
% identity
                   GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147
NCBI Description
                   glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                   >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding
                   protein [Arabidopsis thaliana]
                   >gi 4567224 gb AAD23639.1_AC007119_5 (AC007119)
                   glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
Seq. No.
                   139432
                   LIB24-014-Q1-E1-H3
Seq. ID
Method
                   BLASTN
                   g2511575
NCBI GI
                   159
BLAST score
                   1.0e-84
E value
Match length
                   159
% identity
                   100
NCBI Description Arabidopsis thaliana mRNA for proteasome subunit prcfc
```

139433 Seq. No.

LIB24-015-Q1-E1-A11 Seq. ID

Method BLASTX NCBI GI g3914212 BLAST score 264



E value 4.0e-23 Match length 127 % identity 46

NCBI Description 5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE)

(5-OPASE) >gi_1732065 (U70825) 5-oxo-L-prolinase [Rattus

norvegicus]

Seq. No. 139434

Seq. ID LIB24-015-Q1-E1-A2

Method BLASTN
NCBI GI g2494106
BLAST score 142
E value 4.0e-74
Match length 142
% identity 100

NCBI Description Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 139435

Seq. ID LIB24-015-Q1-E1-A8

Method BLASTX
NCBI GI g3643611
BLAST score 535
E value 7.0e-55
Match length 124
% identity 73

NCBI Description (AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No. 139436

Seq. ID LIB24-015-Q1-E1-B4

Method BLASTX
NCBI GI g131398
BLAST score 343
E value 2.0e-32
Match length 70
% identity 100

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 139437

Seq. ID LIB24-015-Q1-E1-D11

Method BLASTX
NCBI GI g3688195
BLAST score 395
E value 7.0e-39
Match length 78
% identity 95

NCBI Description (AJ010092) MAP3K beta 3 protein kinase [Arabidopsis

thaliana]

Seq. ID

Method



```
Seq. No.
                  139438
Seq. ID
                  LIB24-015-Q1-E1-E5
Method
                  BLASTX
NCBI GI
                  g3004555
BLAST score
                  613
E value
                  5.0e-64
Match length
                  122
                  20
% identity
NCBI Description
                  (AC003673) similar to salt inducible protein [Arabidopsis
                  thaliana]
Seq. No.
                  139439
Seq. ID
                  LIB24-015-Q1-E1-F3
Method
                  BLASTN
NCBI GI
                  q3236234
BLAST score
                  263
E value
                  1.0e-146
Match length
                  376
% identity
                  Arabidopsis thaliana chromosome II BAC F13M22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139440
Seq. ID
                  LIB24-015-Q1-E1-H10
Method
                  BLASTX
                  q4539419
NCBI GI
                  415
BLAST score
E value
                  8.0e-41
Match length
                  105
                  80
% identity
                  (AL049171) putative ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  139441
Seq. ID
                  LIB24-015-Q1-E1-H9
Method
                  BLASTX
NCBI GI
                  q2961085
BLAST score
                  388
E value
                  9.0e-38
Match length
                  103
% identity
                  (AF037228) transcription factor [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  139442
Seq. ID
                  LIB24-016-Q1-E1-A9
Method
                  BLASTN
NCBI GI
                  g3335331
BLAST score
                  163
                  1.0e-86
E value
Match length
                  299
                  90
% identity
                  Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  139443
Seq. No.
```

16860

LIB24-016-Q1-E1-D12

BLASTN



NCBI GI g4263694 BLAST score 166 E value 1.0e-88 Match length 166 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139444

Seq. ID LIB24-016-Q1-E1-D3

Method BLASTN
NCBI GI g2696018
BLAST score 132
E value 3.0e-68
Match length 238
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXC9, complete sequence [Arabidopsis thaliana]

Seq. No. 139445

Seq. ID LIB24-016-Q1-E1-D9

Method BLASTX
NCBI GI g141435
BLAST score 190
E value 2.0e-14
Match length 83
% identity 42

NCBI Description DIHYDRONEOPTERIN ALDOLASE (DHNA) >gi_98360_pir_E37854 folate biosynthesis protein 1 (sul 3' region) - Bacillus

folate biosynthesis protein 1 (sul 3' region) - Bacillus subtilis >gi_143411 (M34053) ORF1 [Bacillus subtilis] >gi_467467_dbj_BAA05313_ (D26185) unknown [Bacillus

subtilis] >gi 2632345 emb CAB11854 (Z99104) dihydroneopterin aldolase [Bacillus subtilis]

Seq. No. 139446

Seq. ID LIB24-016-Q1-E1-E1

Method BLASTN
NCBI GI g4757678
BLAST score 136
E value 2.0e-70
Match length 136
% identity 86

NCBI Description Arabidopsis thaliana chromosome I BAC F9H16 genomic

sequence, complete sequence

Seq. No. 139447

Seq. ID LIB24-016-Q1-E1-E2

Method BLASTX
NCBI GI g1076389
BLAST score 478
E value 3.0e-48
Match length 96
% identity 100

NCBI Description protein phosphatase 2A pDF1 - Arabidopsis thaliana

>gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65

kDa regulatory subunit [Arabidopsis thaliana]



```
Seq. No.
                   139448
                   LIB24-016-Q1-E1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4432846
BLAST score
                   200
                   1.0e-15
E value
                   115
Match length
                   41
% identity
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                   139449
Seq. No.
                   LIB24-016-Q1-E1-G2
Seq. ID
Method
                   BLASTX
                   g2498977
NCBI GI
                   204
BLAST score
                   5.0e-16
E value
                   114
Match length
                   39
% identity
                   SURFEIT LOCUS PROTEIN 5 >gi_1150512_emb_CAA59453_ (X85169)
NCBI Description
                   SURF-5 protein [Mus musculus]
                   139450
Seq. No.
                   LIB24-016-Q1-E1-G7
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2760169
                   230
BLAST score
                   1.0e-126
E value
                   242
Match length
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MFB13, complete sequence [Arabidopsis thaliana]
                   139451
Seq. No.
                   LIB24-016-Q1-E1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3334404
BLAST score
                   175
                   7.0e-13
E value
Match length
                   77
                   96
% identity
                   VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                   SUBUNIT) >gi_2266990 (U65638) vacuolar type ATPase subunit A [Arabidopsis thaliana] >gi_3834305 (AC005679) Identical
                   to gb U65638 Arabidopsis thaliana vacuolar type ATPase
                   subunīt A mRNA. ESTs gb_N96435, gb_N96106, gb_N96189,
                   gb_N96091, gb_AA042286, gb_F14324, gb_W43643, gb_N96027,
                   gb N96299, gb R29943, gb T43460, gb T43544, gb T22472
Seq. No.
                   139452
                   LIB24-017-Q1-E1-A9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3080406
BLAST score
                   370
E value
                   0.0e+00
Match length
                   370
% identity
                   100
```

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12



(ESSA project)

```
Seq. No.
                  139453
                  LIB24-017-Q1-E1-B12
Seq. ID
Method
                  BLASTN
                  g2281081
NCBI GI
BLAST score
                  195
                  1.0e-105
E value
Match length
                  195
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F18019 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139454
                  LIB24-017-Q1-E1-B7
Seq. ID
                  BLASTX
Method
                  g2651313
NCBI GI
                  571
BLAST score
                  4.0e-59
E value
Match length
                  126
% identity
                  64
                  (AC002336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  139455
Seq. No.
Seq. ID
                  LIB24-017-Q1-E1-B9
Method
                  BLASTX
                  g3426051
NCBI GI
BLAST score
                  626
                  1.0e-65
E value
Match length
                  125
% identity
                  100
                  (AC005168) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  139456
Seq. No.
                  LIB24-017-Q1-E1-C3
Seq. ID
Method
                  BLASTN
                  g3687221
NCBI GI
BLAST score
                  71
                  3.0e - 32
E value
Match length
                  101
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC F6F22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139457
Seq. ID
                  LIB24-017-Q1-E1-C8
Method
                  BLASTN
NCBI GI
                  q3047074
BLAST score
                  160
E value
                  7.0e-85
Match length
                  301
                  100
% identity
```

NCBI Description Arabidopsis thaliana BAC F21E10

Seq. No. 139458

Seq. ID LIB24-018-Q1-E1-B4

Method BLASTN



```
q4217996
NCBI GI
BLAST score
                  166
E value
                  2.0e-88
Match length
                  203
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC F24H14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  139459
Seq. No.
                  LIB24-018-Q1-E1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499708
BLAST score
                  217
E value
                  8.0e-18
                  95
Match length
                  48
% identity
                  PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
NCBI Description
                  (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                  >gi 1020409 dbj BAA11135 (D73410) phospholipase D [Zea
                  mays]
                  139460
Seq. No.
                  LIB24-018-Q1-E1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4325369
BLAST score
                  451
                  4.0e-45
E value
                  112
Match length
% identity
                  83
                  (AF128396) T3H13.3 gene product [Arabidopsis thaliana]
NCBI Description
                  139461
Seq. No.
                  LIB24-018-Q1-E1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g99681
BLAST score
                  510
E value
                  6.0e-52
                  130
Match length
% identity
NCBI Description
                  cold-regulated protein cor47 - Arabidopsis thaliana
                  (fragment) >gi_388259_emb_CAA42483_ (X59814) Cold and ABA
                  regulated gene [Arabidopsis thaliana]
Seq. No.
                  139462
Seq. ID
                  LIB24-019-Q1-E1-A5
Method
                  BLASTX
NCBI GI
                  g2576361
BLAST score
                  262
E value
                  8.0e-23
```

Match length 118 % identity

(U39782) lysine and histidine specific transporter NCBI Description

[Arabidopsis thaliana]

Seq. No. 139463

Seq. ID LIB24-019-Q1-E1-B2

BLASTX Method



```
q68510
NCBI GI
BLAST score
                  212
                  2.0e-17
E value
Match length
                   63
                  62
% identity
                  translation releasing factor eRF - rabbit
NCBI Description
                  139464
Seg. No.
                  LIB24-019-Q1-E1-B3
Seq. ID
                  BLASTN
Method
                  g4204848
NCBI GI
                   174
BLAST score
                   4.0e-93
E value
Match length
                   174
% identity
                   100
                  Arabidopsis thaliana protein kinase (RPK1) mRNA, complete
NCBI Description
                   cds
Seq. No.
                   139465
                  LIB24-019-Q1-E1-H9
Seq. ID
Method
                   BLASTX
                   g730465
NCBI GI
BLAST score
                   155
                   2.0e-10
E value
                   105
Match length
% identity
                   32
                   DNA REPAIR AND RECOMBINATION PROTEIN RAD26
NCBI Description
                   >gi_626090_pir__JC2227 probable helicase RAD26 - yeast
                   (Saccharomyces cerevisiae) >gi_506419 (L26910) gtA1085
                   [Saccharomyces cerevisiae] >gi_1015683_emb_CAA89562_
                   (Z49535) ORF YJR035w [Saccharomyces cerevisiae]
                   139466
Seq. No.
                   LIB24-020-Q1-E1-A6
Seq. ID
Method
                   BLASTN
                   g2351063
NCBI GI
BLAST score
                   212
E value
                   1.0e-116
                   410
Match length
                   100
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCL19, complete sequence [Arabidopsis thaliana]
                   139467
Seq. No.
                   LIB24-020-Q1-E1-B9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3292807
BLAST score
                   185
E value
                   1.0e-100
Match length
                   230
% identity
                   100
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19
NCBI Description
                   (ESSAII project)
```

Seq. No. 139468

Seq. ID LIB24-020-Q1-E1-D4

Method BLASTX

Seq. ID

BLASTX

g2245009

Method

NCBI GI

```
q549848
NCBI GI
BLAST score
                  284
E value
                  2.0e-25
                  131
Match length
% identity
                  44
NCBI Description (M86958) putative [Caenorhabditis elegans]
                  139469
Seq. No.
                  LIB24-020-Q1-E1-D8
Seq. ID
Method
                  BLASTX
                  g544285
NCBI GI
BLAST score
                  206
E value
                  3.0e-16
Match length
                  44
% identity
                  86
                  FIBRILLARIN >gi 422056_pir__S33690 fibrillarin - fission
NCBI Description
                  yeast (Schizosaccharomyces pombe) >gi_296704_emb_CAA49550_
                  (X69930) fibrillarin [Schizosaccharomyces pombe]
                  >gi 3687500 emb CAA21168 (AL031788) fibrillarin
                  [Schizosaccharomyces pombe]
Seq. No.
                  139470
                  LIB24-020-Q1-E1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454036
BLAST score
                  226
                  1.0e-18
E value
                  56
Match length
                  70
% identity
                  (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                  thaliana]
                  139471
Seq. No.
                  LIB24-020-Q1-E1-E3
Seq. ID
Method
                  BLASTN
                  g4585896
NCBI GI
BLAST score
                  287
E value
                  1.0e-160
Match length
                  347
                  75
% identity
                  Arabidopsis thaliana chromosome II BAC F13I13 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  139472
Seq. ID
                  LIB24-020-Q1-E1-E5
Method
                  BLASTX
                  g3935148
NCBI GI
BLAST score
                  223
                  3.0e-18
E value
Match length
                  111
% identity
                  42
NCBI Description
                  (AC005106) T25N20.12 [Arabidopsis thaliana]
Seq. No.
                  139473
                  LIB24-020-Q1-E1-F8
```



```
BLAST score
E value
                   2.0e-53
                   122
Match length
                   86
% identity
                  (297341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   139474
Seq. No.
                  LIB24-021-Q1-E1-A3
Seq. ID
Method
                   BLASTX
                   g4406814
NCBI GI
BLAST score
                   384
                   4.0e-37
E value
Match length
                   77
% identity
                   100
                   (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis
NCBI Description
                   thaliana]
                   139475
Seq. No.
                   LIB24-021-Q1-E1-A8
Seq. ID
                   BLASTX
Method
                   g2583123
NCBI GI
                   166
BLAST score
                   1.0e-11
E value
Match length
                   38
% identity
                   74
                   (AC002387) putative nucleotide sugar epimerase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   139476
                   LIB24-021-Q1-E1-B1
Seq. ID
Method
                   BLASTX
                   g1805654
NCBI GI
BLAST score
                   611
E value
                   9.0e-64
                   131
Match length
% identity
                   90
                   (X99972) calmodulin-stimulated calcium-ATPase [Brassica
NCBI Description
                   oleracea]
Seq. No.
                   139477
                   LIB24-021-Q1-E1-B4
Seq. ID
                   BLASTX
Method
                                                                         50-
NCBI GI
                   g4263722
BLAST score
                   582
E value
                   2.0e-60
Match length
                   129
% identity
                   (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   139478
                   LIB24-021-Q1-E1-B8
Seq. ID
                   BLASTX
Method
                   g4490714
NCBI GI
BLAST score
                   208
                   5.0e-17
E value
```

16867

51

80

Match length

% identity

```
(AL035680) kinesin-related protein katB [Arabidopsis
NCBI Description
                  thaliana]
                  139479
Seq. No.
                  LIB24-021-Q1-E1-B9
Seq. ID
                  BLASTX
Method
                  g4325375
NCBI GI
BLAST score
                  685
                  2.0e-72
E value
                  134
Match length
                  100
% identity
                  (AF128396) similar to arginases (Pfam: PF00491,
NCBI Description
                  Score=353.2, E=1.4e-119, N=1) [Arabidopsis thaliana]
Seq. No.
                  139480
                  LIB24-021-Q1-E1-C12
Seq. ID
Method
                  BLASTN
                  q4220633
NCBI GI
                  326
BLAST score
                  0.0e+00
E value
Match length
                  398
                  100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K7J8, complete sequence [Arabidopsis thaliana]
                  139481
Seq. No.
                  LIB24-021-Q1-E1-C5
Seq. ID
                  BLASTN
Method
                  g3241916
NCBI GI
                  139
BLAST score
                  3.0e-72
E value
                   400
Match length
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K15N18, complete sequence [Arabidopsis thaliana]
                  139482
Seq. No.
                  LIB24-021-Q1-E1-C7
Seq. ID
                  BLASTX
Method
                   q4263704
NCBI GI
BLAST score
                   460
                   4.0e-46
E value
                   124
Match length
                   77
% identity
                   (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
```

139483 Seq. No.

LIB24-021-Q1-E1-D6 Seq. ID

BLASTX Method NCBI GI q99752 654 BLAST score 9.0e-69 E value 134 Match length 99 % identity

protochlorophyllide reductase (EC 1.3.1.33) precursor -NCBI Description

Arabidopsis thaliana



```
139484
Seq. No.
Seq. ID
                  LIB24-021-Q1-E1-E1
Method
                  BLASTN
NCBI GI
                  q4725940
BLAST score
                  398
E value
                  0.0e + 00
Match length
                  398
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T1P17
NCBI Description
                   (ESSA project)
Seq. No.
                  139485
                  LIB24-021-Q1-E1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4049353
BLAST score
                  458
E value
                  8.0e-46
Match length
                  133
% identity
                   68
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  139486
                  LIB24-021-Q1-E1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2696018
BLAST score
                   126
E value
                   2.0e-64
Match length
                   126
% identity
                   100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC9, complete sequence [Arabidopsis thaliana]
                   139487
Seq. No.
                   LIB24-021-Q1-E1-G6
Seq. ID
                  BLASTX
Method
                   g1710394
NCBI GI
                   664
BLAST score
E value
                   6.0e-70
Match length
                   132
% identity
                   99
                  RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN
NCBI Description
                   (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)
                   >gi 840719 emb CAA54549 (X77336) ribonucleotide reductase
                   R2 [Arabidopsis thaliana]
Seq. No.
                   139488
                   LIB24-022-Q1-E1-B4
Seq. ID
Method
                   BLASTN
                   g3193282
NCBI GI
BLAST score
                   202
E value
                   1.0e-110
Match length
                   383
```

Seq. No. 139489

% identity

100

NCBI Description Arabidopsis thaliana BAC T14P8



LIB24-022-Q1-E1-D10 Seq. ID Method BLASTN NCBI GI g4519193 BLAST score 244 E value 1.0e-135 Match length 388 % identity 98 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MDC11, complete sequence Seq. No. 139490 LIB24-022-Q1-E1-D12 Seq. ID Method BLASTN NCBI GI g2914688 BLAST score 32 E value 9.0e-09 Match length 32 % identity 100 Arabidopsis thaliana chromosome II BAC F24L7 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 139491 LIB24-022-Q1-E1-E3 Seq. ID Method BLASTN NCBI GI q4567237 BLAST score 210 E value 1.0e-115 Match length 210 100 % identity Arabidopsis thaliana chromosome II BAC T22F11 genomic NCBI Description sequence, complete sequence 139492 Seq. No. LIB24-022-Q1-E1-E8 Seq. ID Method BLASTX g2245131 NCBI GI BLAST score 303 1.0e-27 E value Match length 98 % identity 69 (Z97344) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 139493 LIB24-022-Q1-E1-F7 Seq. ID BLASTN Method g3386593 NCBI GI BLAST score 58

7.0e-24 E value 94 Match length 90 % identity

Arabidopsis thaliana chromosome II BAC F4I18 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

139494 Seq. No.

LIB24-022-Q1-E1-G7 Seq. ID

Method BLASTX NCBI GI g2459417



```
BLAST score
                  2.0e-44
E value
Match length
                  85
                  100
% identity
                  (AC002332) putative pre-mRNA splicing factor PRP19
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  139495
                  LIB24-022-Q1-E1-H11
Seq. ID
Method
                  BLASTX
                  g4220514
NCBI GI
                  260
BLAST score
                  1.0e-22
E value
Match length
                  81
% identity
                  63
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                  139496
Seq. No.
                  LIB24-022-Q1-E1-H5
Seq. ID
Method
                  BLASTX
                  g3915847
NCBI GI
BLAST score
                  403
                  2.0e-39
E value
                  88
Match length
                  90
% identity
                  40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
NCBI Description
                  40S ribosomal protein S2 [Arabidopsis thaliana]
                  139497
Seq. No.
                  LIB24-023-Q1-E1-A11
Seq. ID
                  BLASTX
Method
                  g115783
NCBI GI
                  508
BLAST score
                   1.0e-51
E value
                   98
Match length
                   98
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_
                                                            (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
                   139498
Seq. No.
                   LIB24-023-Q1-E1-A9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3449322
                   307
BLAST score
                   1.0e-172
E value
                   315
Match length
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXC17, complete sequence [Arabidopsis thaliana]
```

Seq. No. 139499

Seq. ID LIB24-023-Q1-E1-B2

Method BLASTX
NCBI GI g2244760
BLAST score 286



99

93

Match length

% identity

```
3.0e-26
E value
Match length
                   71
% identity
                   75
                  (Z97335) selenium-binding protein [Arabidopsis thaliana]
NCBI Description
                  139500
Seq. No.
                  LIB24-023-Q1-E1-C9
Seq. ID
Method
                  BLASTX
                  g3367516
NCBI GI
                   485
BLAST score
                   5.0e-49
E value
                   93
Match length
                   100
% identity
                   (AC004392) Similar to beta-glucosidase BGQ60 precursor
NCBI Description
                   gb_L41869 from Hordeum vulgare. [Arabidopsis thaliana]
                   139501
Seq. No.
                   LIB24-023-Q1-E1-D8
Seq. ID
                   BLASTN
Method
                   g3869069
NCBI GI
                   123
BLAST score
                   8.0e-63
E value
                   223
Match length
                   89
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MEB5, complete sequence [Arabidopsis thaliana]
                   139502
Seq. No.
                   LIB24-023-Q1-E1-E9
Seq. ID
Method
                   BLASTN
                   g2827513
NCBI GI
                   342
BLAST score
                   0.0e + 00
E value
                   366
Match length
                   99
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16
NCBI Description
                   (ESSAII project)
                   139503
Seq. No.
Seq. ID
                   LIB24-023-Q1-E1-G3
Method
                   BLASTN
NCBI GI
                   g2947056
BLAST score
                   141
                   1.0e-73
E value
Match length
                   197
                   93
% identity
                   Arabidopsis thaliana chromosome II BAC T20F6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   139504
Seq. No.
                   LIB24-023-Q1-E1-H7
Seq. ID
Method
                   BLASTN
                   q4490734
NCBI GI
BLAST score
                   46
E value
                   3.0e-17
```

% identity

NCBI Description

94



```
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone
                  project)
                  139505
Seq. No.
                  LIB24-024-Q1-E1-D2
Seq. ID
                  BLASTN
Method
                  q4454447
NCBI GI
BLAST score
                  202
                  1.0e-110
E value
                  210
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC F5H14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139506
                  LIB24-024-Q1-E1-E2
Seq. ID
                  BLASTN
Method
                  q3985934
NCBI GI
                  82
BLAST score
                  1.0e-38
E value
Match length
                  146
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJE7, complete sequence [Arabidopsis thaliana]
                  139507
Seq. No.
                  LIB24-024-Q1-E1-F3
Seq. ID
                  BLASTN
Method
                  q3927822
NCBI GI
                  31
BLAST score
                  3.0e-08
E value
                  148
Match length
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC F8N16 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  139508
Seq. No.
                  LIB24-025-Q1-E1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1239959
                  205
BLAST score
                  4.0e-16
E value
Match length
                   41
                  100
% identity
NCBI Description
                  (X95469) MADS-box gene [Antirrhinum majus]
                  139509
Seq. No.
                  LIB24-025-Q1-E1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2924653
BLAST score
                   71
E value
                   3.0e-32
Match length
                   95
```

MDA7, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



```
Seq. No. 139510
Seq. ID LIB24-
```

LIB24-025-Q1-E1-D10

Method BLASTN
NCBI GI 94584339
BLAST score 253
E value 1.0e-140
Match length 253
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T23A1 genomic

sequence, complete sequence

Seq. No. 139511

Seq. ID LIB24-025-Q1-E1-E10

Method BLASTX
NCBI GI g585536
BLAST score 250
E value 5.0e-22
Match length 62
% identity 74

NCBI Description MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)

>gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase
[Arabidopsis thaliana] >gi 871990 emb CAA55786 (X79194)

thioglucosidase [Arabidopsis thaliana]

Seq. No. 139512

Seq. ID LIB24-025-Q1-E1-E3

Method BLASTX
NCBI GI g2924512
BLAST score 585
E value 8.0e-61
Match length 115
% identity 98

NCBI Description (AL022023) beta-galactosidase-like protein [Arabidopsis

thaliana]

Seq. No. 139513

Seq. ID LIB24-025-Q1-E1-E4

Method BLASTN
NCBI GI g4567300
BLAST score 286
E value 1.0e-160
Match length 315
% identity 97

NCBI Description Arabidopsis thaliana chromosome II P1 MHK10 genomic

sequence, complete sequence

Seq. No. 139514

Seq. ID LIB24-025-Q1-E1-F6

Method BLASTN
NCBI GI g3738275
BLAST score 175
E value 5.0e-94
Match length 191
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F17A22 genomic

sequence, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                  139515
                LIB24-025-Q1-E1-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220645
BLAST score
                  188
                  1.0e-102
E value
Match length
                  204
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MYA6, complete sequence [Arabidopsis thaliana]
                  139516
Seq. No.
Seq. ID
                  LIB24-025-Q1-E1-G5
                  BLASTN
Method
                  g3702728
NCBI GI
                  173
BLAST score
                  2.0e-92
E value
                  360
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19M13, complete sequence [Arabidopsis thaliana]
                  139517
Seq. No.
Seq. ID
                  LIB24-026-Q1-E1-C4
                  BLASTX
Method
NCBI GI
                  g1353352
BLAST score
                  224
                  6.0e-19
E value
Match length
                  62
                  68
% identity
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
Seq. No.
                  139518
Seq. ID
                  LIB24-026-Q1-E1-C8
Method
                  BLASTX
NCBI GI
                  g2507281
                  556
BLAST score
E value
                  2.0e-57
Match length
                  101
                  100
% identity
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi 1668706_emb_CAA66048_
                   (X97380) atran2 [Arabidopsis thaliana]
                  139519
Seq. No.
Seq. ID
                  LIB24-026-Q1-E1-D4
Method
                  BLASTX
NCBI GI
                  q629511
BLAST score
                  331
E value
                  5.0e-31
Match length
                  111
% identity
                  72
                  cold-regulated protein cor15b precursor - Arabidopsis
NCBI Description
                  thaliana >gi_4559338_gb AAD23000.1_AC007087 19 (AC007087)
```

16875

thaliana]

cold-regulated protein cor15b precursor [Arabidopsis

NCBI Description

139525

LIB24-027-Q1-E1-B2

Seq. No.

Seq. ID



```
139520
Seq. No.
                  LIB24-026-Q1-E1-E1
Seq. ID
Method
                  BLASTN
                  g3738313
NCBI GI
                  385
BLAST score
                  0.0e+00
E value
                  385
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T29E15 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                  139521
Seq. No.
                  LIB24-027-Q1-E1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                   q4165340
BLAST score
                   102
                   1.0e-50
E value
                   155
Match length
                   100
% identity
                  Arabidopsis thaliana chromosome I BAC F11M15 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   139522
Seq. No.
                   LIB24-027-Q1-E1-A6
Seq. ID
Method
                   BLASTN
                   g3702315
NCBI GI
BLAST score
                   98
                   5.0e-48
E value
                   186
Match length
                   88
% identity
                  Arabidopsis thaliana chromosome II BAC T3F17 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   139523
Seq. No.
                   LIB24-027-Q1-E1-A8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4733953
BLAST score
                   21
                   9.0e-02
E value
Match length
                   410
                   93
% identity
                   Arabidopsis thaliana chromosome I BAC F13011 genomic
NCBI Description
                   sequence, complete sequence
                   139524
Seq. No.
                   LIB24-027-Q1-E1-B1
Seq. ID
                   BLASTX
Method
                   g2739010
NCBI GI
                   281
BLAST score
E value
                   4.0e-25
                   109
Match length
% identity
                   54
```

16876

(AF022464) CYP77A3p [Glycine max]



```
Method
                    BLASTX
 NCBI GI
                    q1749412
 BLAST score
                    481
 E value
                    2.0e-48
Match length
                    135
 % identity
                    64
NCBI Description
                    (D89102) similar to Saccharomyces cerevisiae ADP, ATP
                    carrier protein (ADP/ATP translocase), SWISS-PROT Accession
                    Number P18239 [Schizosaccharomyces pombe]
Seq. No.
                    139526
Seq. ID
                    LIB24-027-Q1-E1-D10
Method
                   BLASTX
NCBI GI
                    g2280528
BLAST score
                    178
E value
                    6.0e-13
Match length
                    33
% identity
                   100
NCBI Description (AB005888) ATMYB3 [Arabidopsis thaliana]
Seq. No.
                   139527
Seq. ID
                   LIB24-027-Q1-E1-D8
Method
                   BLASTX
NCBI GI
                   g115783
BLAST score
                   549
E value
                   2.0e-56
Match length
                   107
% identity
                   97
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                    (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                   chlorophyll a/b bind\overline{\text{ing}} protein (LHCP \overline{\text{AB}} 140) [Arabidopsis
                   thaliana]
Seq. No.
                   139528
Seq. ID
                   LIB24-027-Q1-E1-E11
Method
                   BLASTN
NCBI GI
                   g4589430
BLAST score
                   89
                   1.0e-42
E value
Match length
                   156
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MLD14, complete sequence
Seq. No.
                   139529
Seq. ID
                   LIB24-027-Q1-E1-F10
Method
                   BLASTX
                   g2262163
                   207
                   2.0e-16
                   38
```

NCBI GI BLAST score E value Match length % identity 100

NCBI Description (AC002329) hypothetical protein similar to F5J6.10

[Arabidopsis thaliana]

Seq. No. 139530

Seq. ID LIB24-027-Q1-E1-G12



```
BLASTN
Method
                  g1488526
NCBI GI
BLAST score
                  193
                  1.0e-104
E value
                  205
Match length
                  99
% identity
NCBI Description B.juncea ribosomal intergenic spacer
Seq. No.
                  139531
                  LIB24-027-Q1-E1-G5
Seq. ID
                  BLASTX
Method
                  g3461813
NCBI GI
BLAST score
                  240
E value
                  8.0e-21
Match length
                  63
% identity
                  78
                  (AC004138) putative sucrose/H+ symporter [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  139532
                  LIB24-027-Q1-E1-G8
Seq. ID
                  BLASTX
Method
                  g2493289
NCBI GI
BLAST score
                  169
                  6.0e-12
E value
Match length
                  112
% identity
                  39
NCBI Description RIBONUCLEASE
                  139533
Seq. No.
                  LIB24-027-Q1-E1-H2
Seq. ID
Method
                  BLASTN
                  q4490701
NCBI GI
                  224
BLAST score
E value
                  1.0e-123
Match length
                  392
                  99
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18
                  (ESSA project)
                  139534
Seq. No.
                  LIB24-027-Q1-E1-H5
Seq. ID
                  BLASTN
Method
                  g3449334
NCBI GI
BLAST score
                  268
E value
                  1.0e-149
Match length
                  300
                  97
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MYH9, complete sequence [Arabidopsis thaliana]
                  139535
Seq. No.
Seq. ID
                  LIB24-027-Q1-E1-H6
```

Method BLASTX
NCBI GI g3885341
BLAST score 197
E value 3.0e-15

```
Match length
% identity
                  53
                  (AC005623) unknown protein [Arabidopsis thaliana]
NCBI Description
                  139536
Seq. No.
                  LIB24-028-Q1-E1-B10
Seq. ID
                  BLASTX
Method
                  g4262149
NCBI GI
BLAST score
                  418
                  3.0e-41
E value
Match length
                  72
                  100
% identity
                  (AC005275) putative xyloglucan endotransglycosylase
NCBI Description
                  [Arabidopsis thaliana]
                  139537
Seq. No.
                  LIB24-028-Q1-E1-C12
Seq. ID
                  BLASTX
Method
                  q1184953
NCBI GI
                  317
BLAST score
                  3.0e-29
E value
                  60
Match length
                  100
% identity
                  (U46574) protein farnesyl transferase beta subunit
NCBI Description
                  [Arabidopsis thaliana]
                  139538
Seq. No.
                  LIB24-028-Q1-E1-C9
Seq. ID
                  BLASTN
Method
                  g4519188
NCBI GI
                  125
BLAST score
                  6.0e-64
E value
                  313
Match length
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21L19, complete sequence
                  139539
Seq. No.
                  LIB24-028-Q1-E1-E11
Seq. ID
                  BLASTX
Method
                  q4510398
NCBI GI
BLAST score
                   300
                   3.0e-27
E value
Match length
                   95
                   67
% identity
                  (AC006587) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   139540
Seq. No.
                   LIB24-028-Q1-E1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2341034
                   325
BLAST score
E value
                   2.0e-30
Match length
                   62
```

(AC000104) F19P19.13 [Arabidopsis thaliana]

100

% identity

NCBI Description



```
Seq. No.
                  139541
                  LIB24-028-Q1-E1-G1
Seq. ID
Method
                  BLASTX
                  q3805846
NCBI GI
BLAST score
                  280
                  4.0e-25
E value
                  94
Match length
                  98
% identity
                  (ALO31986) DNA-directed RNA polymerase (EC 2.7.7.6) II
NCBI Description
                  largest chain [Arabidopsis thaliana]
                  139542
Seq. No.
                  LIB24-028-Q1-E1-G3
Seq. ID
Method
                  BLASTX
                  g4006827
NCBI GI
                  329
BLAST score
                  1.0e-30
E value
                  124
Match length
                  54
% identity
                  (AC005970) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
                  139543
Seq. No.
                  LIB24-028-Q1-E1-H2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4468801
                  330
BLAST score
                  0.0e+00
E value
Match length
                  330
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17
NCBI Description
                   (ESSA project)
                  139544
Seq. No.
                  LIB24-028-Q1-E1-H4
Seq. ID
Method
                  BLASTN
                   g3128141
NCBI GI
BLAST score
                  130
E value
                   6.0e-67
Match length
                   316
% identity
                   99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQD22, complete sequence [Arabidopsis thaliana]
                  139545
Seq. No.
                  LIB24-029-Q1-E1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3212846
BLAST score
                  111
E value
                   6.0e-56
Match length
                  135
% identity
                   94
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
```

139546 Seq. No.

Seq. ID LIB24-029-Q1-E1-A10

Method BLASTX

16880

sequence, complete sequence [Arabidopsis thaliana]



NCBI GI g4056433 BLAST score 306 E value 5.0e-28 Match length 115 % identity 57

NCBI Description (AC005990) Similar to anter-specific proline-rich **p**rotein (CEX) gb_X60376 from Brassica napus. [Arabidopsis thaliana]

Seq. No. 139547

Seq. ID LIB24-029-Q1-E1-B5

Method BLASTX
NCBI GI g2129608
BLAST score 382
E value 1.0e-44
Match length 98
% identity 100

NCBI Description GTP-binding protein, 68K - Arabidopsis thaliana >gi_807577

(L38614) GTP-binding protein [Arabidopsis thaliana]

Seq. No. 139548

Seq. ID ' LIB24-029-Q1-E1-C2

Method BLASTN
NCBI GI g4567300
BLAST score 366
E value 0.0e+00
Match length 395
% identity 98

NCBI Description Arabidopsis thaliana chromosome II P1 MHK10 genomic

sequence, complete sequence

Seq. No. 139549

Seq. ID LIB24-029-Q1-E1-D11

Method BLASTX
NCBI GI 94678226
BLAST score 511
E value 5.0e-52
Match length 119
% identity 88

NCBI Description (AC007135) putative 40S ribosomal protein S14 [Arabidopsis

thaliana]

Seq. No. 139550

Seq. ID LIB24-029-Q1-E1-F9

Method BLASTN
NCBI GI g3341671
BLAST score 142
E value 3.0e-74
Match length 211
% identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC F16B22 genomaic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139551

Seq. ID LIB24-029-Q1-E1-G1

Method BLASTN NCBI GI g4589445

BLAST score 43

```
E value
Match length
                  159
                  82
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MWL2, complete sequence
Seq. No.
                  139552
Seq. ID
                  LIB24-030-Q1-E1-A10
Method
                  BLASTX
NCBI GI
                  q2275201
BLAST score
                  352
E value
                  6.0e - 34
Match length
                  72
                  93
% identity
NCBI Description (AC002337) unknown protein [Arabidopsis thaliana]
Seq. No.
                  139553
Seq. ID
                  LIB24-030-Q1-E1-B2
Method
                  BLASTX
                  g2961357
NCBI GI
BLAST score
                  612
                  7.0e-64
E value
Match length
                  132
% identity
                  (AL022140) putative protein [Arabidopsis thaliana]
NCBI Description
                  139554
Seq. No.
                  LIB24-030-Q1-E1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3135250
BLAST score
                  248
                  1.0e-137
E value
Match length
                  277
% identity
                  Arabidopsis thaliana chromosome II BAC F27F23 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  139555
Seq. No.
Seq. ID
                  LIB24-030-Q1-E1-B9
Method
                  BLASTN
NCBI GI
                  g2245073
BLAST score
                  350
                  0.0e+00
E value
Match length
                  350
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  139556
Seq. No.
Seq. ID
                  LIB24-030-Q1-E1-D9
                  BLASTN
Method
                  q4757392
NCBI GI
                  96
BLAST score
E value
                  7.0e-47
                  179
Match length
```

16882

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

99

% identity

Seq. No.

139562



K14A17, complete sequence

```
Seq. No.
                  139557
Seq. ID
                  LIB24-030-Q1-E1-E11
                  BLASTN
Method
NCBI GI
                  g4580744
BLAST score
                  165
E value
                  7.0e-88
Match length
                  250
                  97
% identity
                  Sequence of BAC F15I1 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence
Seq. No.
                  139558
Seq. ID
                  LIB24-030-Q1-E1-E7
Method
                  BLASTN
NCBI GI
                  g2494106
BLAST score
                  109
                  1.0e-54
E value
Match length
                  230
% identity
                  100
                  Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  139559
Seq. ID
                  LIB24-030-Q1-E1-E9
                  BLASTX
Method
NCBI GI
                   g3176726
BLAST score
                  205
                  1.0e-16
E value
Match length
                  50
                   78
% identity
                   (AC002392) putative serine proteinase [Arabidopsis
NCBI Description
                  thaliana]
                   139560
Seq. No.
                  LIB24-030-Q1-E1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g349470
BLAST score
                   454
E value
                   1.0e-45
Match length
                   85
% identity
                   94
NCBI Description
                  (L23114) binding protein [Homo sapiens]
Seq. No.
                   139561
                  LIB24-030-Q1-E1-F2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2264306
                   375
BLAST score
E value
                   0.0e+00
Match length
                   375
% identity
                   42
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBK5, complete sequence [Arabidopsis thaliana]
```

NCBI Description



```
Seq. ID
                  LIB24-030-Q1-E1-F3
Method
                  BLASTX
NCBI GI
                  g131381
BLAST score
                  194
                  2.0e-15
E value
Match length
                  46
% identity
                  91
NCBI Description
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi_99745_pir__S11852
                  photosystem II oxygen-evolving complex protein 1 precursor
                   - Arabidopsis thaliana >gi_22571_emb_CAA36675_ (X52428) 33
                  kDa oxygen-evolving protein [Arabidopsis thaliana]
Seq. No.
                  139563
                  LIB24-030-Q1-E1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4754062
BLAST score
                  360
E value
                  2.0e-34
Match length
                  75
                  91
% identity
                  (AF072881) SOCS box-containing WD protein SWiP-2 [Mus
NCBI Description
                  musculus]
                  139564
Seq. No.
Seq. ID
                  LIB24-030-Q1-E1-H3
Method
                  BLASTN
NCBI GI
                  g2749918
BLAST score
                  134
                  1.0e-69
E value
Match length
                  166
% identity
                  94
                  Arabidopsis thaliana chromosome I BAC F316 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139565
Seq. ID
                  LIB24-031-Q1-E1-C7
Method
                  BLASTN
NCBI GI
                  g4063737
BLAST score
                  184
                  3.0e-99
E value
Match length
                  208
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F24D13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  139566
Seq. No.
Seq. ID
                  LIB24-031-Q1-E1-D7
Method
                  BLASTN
NCBI GI
                  q3241922
BLAST score
                  166
E value
                  2.0e-88
Match length
                  256
% identity
                  100
```

MLM24, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:



```
139567
Seq. No.
                  LIB24-031-Q1-E1-D9
Seq. ID
                  BLASTX
Method
                  g4585998
NCBI GI
                  592
BLAST score
                  2.0e-61
E value
                  137
Match length
% identity
                  86
                  (AC005287) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  139568
Seq. No.
                  LIB24-031-Q1-E1-E8
Seq. ID
Method
                  BLASTX
                  g3377814
NCBI GI
                  520
BLAST score
                  3.0e-53
E value
                  103
Match length
                  95
% identity
                  (AF076275) similar to protein kinases (Pfam: pkinase.hmm,
NCBI Description
                  score: 228.02) [Arabidopsis thaliana]
                  139569
Seq. No.
                  LIB24-031-Q1-E1-F2
Seq. ID
                  BLASTN
Method
                  g3869075
NCBI GI
BLAST score
                  61
                  3.0e-26
E value
                  85
Match length
% identity
                  93
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXK3, complete sequence [Arabidopsis thaliana]
                  139570
Seq. No.
                  LIB24-031-Q1-E1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2443878
                   228
BLAST score
                   4.0e-19
E value
                   58
Match length
% identity
                   74
                  (AC002294) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   139571
Seq. No.
                  LIB24-031-Q1-E1-G11
Seq. ID
                  BLASTX
Method
                   q2244865
NCBI GI
                   524
BLAST score
E value
                   8.0e-54
                   93
Match length
% identity
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

16885

139572

BLASTN

g4455168

LIB24-031-Q1-E1-H4

Seq. No. Seq. ID

Method

NCBI GI



```
BLAST score
E value
                  1.0e-158
                  324
Match length
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10
NCBI Description
                  (ESSAII project)
Seq. No.
                  139573
                  LIB24-032-Q1-E1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2459418
                  244
BLAST score
                  6.0e-21
E value
Match length
                  56
% identity
                  86
                  (AC002332) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  139574
Seq. No.
                  LIB24-032-Q1-E1-B10
Seq. ID
Method
                  BLASTN
                  g3985931
NCBI GI
BLAST score
                  150
                  6.0e-79
E value
                  286
Match length
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21H1, complete sequence [Arabidopsis thaliana]
                  139575
Seq. No.
Seq. ID
                  LIB24-032-Q1-E1-B6
Method
                  BLASTX
                  g3169173
NCBI GI
BLAST score
                  290
                  2.0e-26
E value
Match length
                  63
                  89
% identity
                  (AC004401) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                  thaliana] >gi_3445215 (AC004786) putative serine
                  carboxypeptidase I [Arabidopsis thaliana]
Seq. No.
                  139576
                  LIB24-032-Q1-E1-E12
Seq. ID
Method
                  BLASTN
                  g4587641
NCBI GI
BLAST score
                  109
                  9.0e-55
E value
Match length
                  137
                  95
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F20D21 genomic
                  sequence, complete sequence
                  139577
Seq. No.
```

Seq. ID LIB24-032-Q1-E1-E9

Method BLASTN
NCBI GI g4589418
BLAST score 208
E value 1.0e-113



Match length 228 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21G20, complete sequence

Seq. No. 139578

Seq. ID LIB24-032-Q1-E1-F10

Method BLASTX
NCBI GI g267073
BLAST score 630
E value 6.0e-66
Match length 115
% identity 100

NCBI Description TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin

beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)

beta-3 tubulin [Arabidopsis thaliana]

Seq. No. 139579

Seq. ID LIB24-032-Q1-E1-H1

Method BLASTN
NCBI GI g3046854
BLAST score 48
E value 6.0e-18
Match length 174
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRG7, complete sequence [Arabidopsis thaliana]

Seq. No. 139580

Seq. ID LIB24-033-Q1-E1-A4

Method BLASTN
NCBI GI 94753195
BLAST score 123
E value 5.0e-63
Match length 192
% identity 99

NCBI Description Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5

cM, complete sequence

Seq. No. 139581

Seq. ID LIB24-033-Q1-E1-A7

Method BLASTN
NCBI GI g3128139
BLAST score 244
E value 1.0e-135
Match length 381
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MIK19, complete sequence [Arabidopsis thaliana]

Seq. No. 139582

Seq. ID LIB24-033-Q1-E1-B8

Method BLASTN
NCBI GI g3859590
BLAST score 213
E value 1.0e-116



Match length 381 % identity 100

NCBI Description Arabidopsis thaliana BAC T15B16

Seq. No. 139583

Seq. ID LIB24-033-Q1-E1-B9

Method BLASTN
NCBI GI g3510344
BLAST score 53
E value 7.0e-21
Match length 130
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJG14, complete sequence [Arabidopsis thaliana]

Seq. No. 139584

Seq. ID LIB24-033-Q1-E1-C11

Method BLASTN
NCBI GI g2642152
BLAST score 225
E value 1.0e-123
Match length 388
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T517 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139585

Seq. ID LIB24-033-Q1-E1-C3

Method BLASTN
NCBI GI g2827698
BLAST score 206
E value 1.0e-112
Match length 365
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 5, BAC clone F6H11

(ESSAII project)

Seq. No. 139586

Seq. ID LIB24-033-Q1-E1-C9

Method BLASTX
NCBI GI g3915023
BLAST score 474
E value 1.0e-47
Match length 105
% identity 87

NCBI Description SUCROSE-PHOSPHATE SYNTHASE 1

(UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1) >gi_2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate

synthase [Citrus unshiu]

Seq. No. 139587

Seq. ID LIB24-033-Q1-E1-D12

Method BLASTX
NCBI GI g3549670
BLAST score 522
E value 2.0e-53
Match length 101



```
% identity
NCBI Description
                  (AL031394) putative protein [Arabidopsis thaliana]
Seq. No.
                   139588
Seq. ID
                   LIB24-033-Q1-E1-E12
Method
                   BLASTX
NCBI GI
                   q4538923
BLAST score
                   202
E value
                   2.0e-16
Match length
                   55
% identity
                   73
NCBI Description
                   (AL049483) predicted protein destination factor
                   [Arabidopsis thaliana]
Seq. No.
                   139589
Seq. ID
                   LIB24-033-Q1-E1-E6
Method
                   BLASTN
NCBI GI
                   g4220635
BLAST score
                   230
E value
                   1.0e-126
Match length
                   394
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MDB19, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139590
Seq. ID
                   LIB24-033-Q1-E1-F1
Method
                   BLASTN
NCBI GI
                   q2244829
BLAST score
                   364
E value
                   0.0e + 00
Match length
                   364
                   100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
Seq. No.
                   139591
Seq. ID
                   LIB24-033-Q1-E1-F12
Method
                   BLASTX
NCBI GI
                   q3953471
BLAST score
                   406
E value
                   9.0e-40
Match length
                   124
% identity
                   56
NCBI Description
                  (AC002328) F2202.16 [Arabidopsis thaliana]
Seq. No.
                   139592
Seq. ID
                   LIB24-034-Q1-E1-C3
Method
                  BLASTX
                   g4755189
                   230
```

NCBI GI BLAST score E value 1.0e-19 Match length 59 % identity 71

NCBI Description (AC007018) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 139593



```
LIB24-034-Q1-E1-C8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3242700
BLAST score
                  240
E value
                  1.0e-132
Match length
                  284
% identity
                  96
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F26B6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139594
Seq. ID
                  LIB24-034-Q1-E1-G12
Method
                  BLASTN
NCBI GI
                  g4159708
BLAST score
                  202
E value
                  1.0e-110
Match length
                  226
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MKP6, complete sequence
                  139595
Seq. No.
Seq. ID
                  LIB24-035-Q1-E1-C2
Method
                  BLASTX
NCBI GI
                  g2408068
BLAST score
                  323
E value
                  6.0e-30
Match length
                  124
% identity
                  48
NCBI Description
                  (Z99165) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                  139596
                  LIB24-035-Q1-E1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4646198
BLAST score
                  101
E value
                  2.0e-36
Match length
                  105
% identity
                  78
NCBI Description
                  (AC007230) T23K8.6 [Arabidopsis thaliana]
Seq. No.
                  139597
Seq. ID
                  LIB24-035-Q1-E1-F8
Method
                  BLASTN
NCBI GI
                  g3335331
                  290
BLAST score
                  1.0e-162
E value
Match length
                  368
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
                  complete sequence [Arabidopsis thaliana]
```

Seq. No. 139598

Seq. ID LIB24-035-Q1-E1-G12

Method BLASTX NCBI GI g2190187 BLAST score 196

E value

Match length

4.0e-49

95

```
E value
                   3.0e-15
Match length
                  91
% identity
                  16
                  (D64087) nuclear matrix constituent protein 1 (NMCP1)
NCBI Description
                   [Daucus carota]
                  139599
Seq. No.
Seq. ID
                  LIB24-036-Q1-E1-A4
Method
                  BLASTX
NCBI GI
                  g2317901
BLAST score
                  477
E value
                  4.0e-48
Match length
                  108
% identity
                  80
NCBI Description
                  (U89959) Similar to vesicle transport protein, PIR
                  Accession Number A55931 [Arabidopsis thaliana]
Seq. No.
                  139600
                  LIB24-036-Q1-E1-A8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1322277
BLAST score
                  220
E value
                  1.0e-121
Match length
                  220
% identity
                  100
NCBI Description
                  Arabidopsis thaliana cyclophilin (ROC4) gene, nuclear gene
                  encoding chloroplast protein, complete cds
Seq. No.
                  139601
Seq. ID
                  LIB24-036-Q1-E1-B2
                  BLASTN
Method
NCBI GI
                  g4691223
BLAST score
                  96
E value
                  4.0e-47
Match length
                  112
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
                   (ESSA project)
Seq. No.
                  139602
Seq. ID
                  LIB24-036-Q1-E1-D2
Method
                  BLASTN
NCBI GI
                  g4519183
BLAST score
                  181
E value
                  2.0e-97
Match length
                  221
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K15C23, complete sequence
Seq. No. Seq. ID
                  139603
                  LIB24-036-Q1-E1-D3
Method
                  BLASTX
NCBI GI
                  g3461814
BLAST score
                  484
```

% identity 97
NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No. 139604

Seq. ID LIB24-036-Q1-E1-E8

Method BLASTN
NCBI GI g2275194
BLAST score 178
E value 2.0e-95
Match length 182
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T08I13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139605

Seq. ID LIB24-036-Q1-E1-F7

Method BLASTX
NCBI GI 94056434
BLAST score 262
E value 5.0e-23
Match length 52
% identity 100

NCBI Description (AC005990) Similar to OBP32pep protein gb U37698 from

Arabidopsis thaliana. [Arabidopsis thaliana]

Seq. No. 139606

Seq. ID LIB24-036-Q1-E1-G3

Method BLASTN
NCBI GI g3831448
BLAST score 110
E value 2.0e-55
Match length 131
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC T32F6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139607

Seq. ID LIB24-036-Q1-E1-G6

Method BLASTX
NCBI GI g1171429
BLAST score 56
E value 2.0e-12
Match length 70
% identity 61

NCBI Description (U44028) CKC [Arabidopsis thaliana]

Seq. No. 139608

Seq. ID LIB24-037-Q1-E1-A12

Method BLASTX
NCBI GI 94586248
BLAST score 363
E value 1.0e-34
Match length 68
% identity 100

NCBI Description (AL049640) growth factor like protein [Arabidopsis

thalianal



```
Seq. No.
                   139609
Seq. ID
                   LIB24-037-Q1-E2-A4
Method
                   BLASTX
NCBI GI
                   g4539404
BLAST score
                   195
                   4.0e-15
E value
Match length
                   106
                   43
% identity
NCBI Description
                  (AL049524) putative protein [Arabidopsis thaliana]
Seq. No.
                   139610
Seq. ID
                   LIB24-037-Q1-E2-B1
Method
                   BLASTN
NCBI GI
                   q2494106
BLAST score
                   132
E value
                   3.0e-68
Match length
                   219
% identity
                   96
                  Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   139611
Seq. ID
                   LIB24-037-Q1-E2-D12
Method
                   BLASTX
NCBI GI
                   g1174592
BLAST score
                   408
E value
                   3.0e-40
Match length
                   74
% identity
                   100
NCBI Description
                   TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin
                   - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                   sativum]
Seq. No.
                   139612
Seq. ID
                   LIB24-037-Q1-E2-E3
Method
                   BLASTX
NCBI GI
                   q4583656
BLAST score
                   170
                   3.0e-12
E value
Match length
                   85
% identity
                   47
NCBI Description
                  (AJ010592) ubiquitin-conjugating enzyme [Guillardia theta]
Seq. No.
                   139613
Seq. ID
                  LIB24-038-Q1-E1-F12
Method
                  BLASTN
NCBI GI
                   g2828278
BLAST score
                   173
E value
                   1.0e-92
Match length
                   311
% identity
```

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16

(ESSAII project)

Seq. No. 139614

LIB24-038-Q1-E1-F9 Seq. ID

Method BLASTN

```
NCBI GI
                   g3309085
BLAST score
                   83
E value
                   6.0e-39
Match length
                   91
% identity
                   98
NCBI Description
                  Arabidopsis thaliana calcineurin B-like protein 3 (CBL3)
                  mRNA, complete cds
Seq. No.
                  139615
Seq. ID
                  LIB24-038-Q1-E1-G6
Method
                  BLASTX
                  g2245070
NCBI GI
BLAST score
                  201
E value
                  1.0e-15
Match length
                  92
% identity
                  43
NCBI Description
                  (Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  139616
Seq. ID
                  LIB24-038-Q1-E1-G7
Method
                  BLASTX
NCBI GI
                  g3924596
BLAST score
                  532
E value
                  1.0e-54
Match length
                  108
                  93
% identity
NCBI Description
                  (AF069442) putative phospho-ser/thr phosphatase
                   [Arabidopsis thaliana]
Seq. No.
                  139617
Seq. ID
                  LIB24-038-Q1-E1-H7
Method
                  BLASTN
NCBI GI
                  g4567259
BLAST score
                  105
E value
                  3.0e-52
Match length
                  205
% identity
                  43
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F3K23 genomic
                  sequence, complete sequence
Seq. No.
                  139618
```

Seq. ID LIB24-038-Q1-E1-H9

Method BLASTX NCBI GI q3885334 BLAST score 352 E value 2.0e-33 Match length 108 % identity 62

(AC005623) putative argonaute protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 139619

Seq. ID LIB24-039-Q1-E1-F10

Method BLASTN NCBI GI g4079614 BLAST score 170 E value 1.0e-90



Match length % identity 98

NCBI Description Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139620

Seq. ID LIB24-039-Q1-E1-G4

Method BLASTX NCBI GI q115783 BLAST score 444 3.0e-44E value Match length 83 100 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 139621

Seq. ID LIB24-039-Q1-E1-H12

Method BLASTX NCBI GI g2347209 BLAST score 404 E value 9.0e-40 Match length 80 % identity 96

NCBI Description (AC002338) EGF receptor like protein isolog [Arabidopsis

thaliana]

Seq. No. 139622

Seq. ID LIB24-040-Q1-E1-B12

Method BLASTXNCBI GI g2317910 BLAST score 292 2.0e-26 E value Match length 54

98 % identity

NCBI Description (U89959) CER1 protein [Arabidopsis thaliana]

Seq. No. 139623

Seq. ID LIB24-040-Q1-E1-F11

Method BLASTN NCBI GI g4309683 BLAST score 251 E value 1.0e-139 Match length 312 % identity 96

NCBI Description Arabidopsis thaliana chromosome 1 BAC T31J12 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 139624

Seq. ID LIB24-040-Q1-E1-G11

Method BLASTN NCBI GI g3128137 BLAST score 328 E value 0.0e + 00Match length 344



% identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana] Seq. No. 139625 Seq. ID LIB24-041-Q1-E1-A6 Method BLASTN NCBI GI g2342673 BLAST score 414 E value 0.0e+00Match length 414 % identity 100 Sequence of BAC F7G19 from Arabidopsis thaliana chromosome NCBI Description 1, complete sequence [Arabidopsis thaliana] Seq. No. 139626 Seq. ID LIB24-041-Q1-E1-C1 Method BLASTN g4454587 NCBI GI BLAST score 75 E value 3.0e-34 Match length 235 % identity 98 Arabidopsis thaliana BAC F21A20 from chromosome V near 61 NCBI Description cM, complete sequence [Arabidopsis thaliana] Seq. No. 139627 Seq. ID LIB24-041-Q1-E1-D3 Method BLASTX NCBI GI g2459421 BLAST score 518 E value 8.0e-53 Match length 111 % identity 88 NCBI Description (AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana] 139628 Seq. No. Seq. ID LIB24-041-Q1-E1-D7 Method BLASTX NCBI GI g3025189 BLAST score 245 E value 6.0e-21 Match length 94 % identity 50 NCBI Description HYPOTHETICAL 67.1 KD PROTEIN SLL1770 >gi_1652753_dbj_BAA17672 (D90908) ABC1-like [Synechocystis

sp.]

Seq. No. 139629

Seq. ID LIB24-041-Q1-E1-E12

Method BLASTX NCBI GI g3212877 BLAST score 541 2.0e-55 E value Match length 123 % identity 89



NCBI Description (AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No. 139630

Seq. ID LIB24-041-Q1-E1-G7

Method BLASTN
NCBI GI g4519183
BLAST score 375
E value 0.0e+00
Match length 402
% identity 98

% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K15C23, complete sequence

Seq. No. 139631

Seq. ID LIB24-042-Q1-E1-B12

Method BLASTN
NCBI GI g4217996
BLAST score 144
E value 1.0e-75
Match length 152
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F24H14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139632

Seq. ID LIB24-042-Q1-E1-D1

Method BLASTN
NCBI GI g4757396
BLAST score 61
E value 1.0e-25
Match length 216
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K8A10, complete sequence

Seq. No. 139633

Seq. ID LIB24-042-Q1-E1-E1

Method BLASTN
NCBI GI 94757662
BLAST score 215
E value 1.0e-117
Match length 413
% identity 99

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10B6 from

chromosome I, complete sequence

Seq. No. 139634

Seq. ID LIB24-042-Q1-E1-E12

Method BLASTX
NCBI GI g1706318
BLAST score 514
E value 2.0e-52
Match length 119
% identity 80

NCBI Description GLUTAMATE DECARBOXYLASE (GAD) (ERT D1)

>gi_1362098_pir__S56177 probable glutamate decarboxylase -

tomato >gi_995555_emb_CAA56812_ (X80840) homology to





pyroxidal-5'-phosphate-dependant glutamate decarboxylases; putative start codon [Lycopersicon esculentum]

Seq. No. 139635 Seq. ID LIB24-042-Q1-E1-E4 Method BLASTN NCBI GI g4063737 BLAST score 198 E value 1.0e-107 Match length 198 100 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F24D13 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 139636 Seq. ID LIB24-042-Q1-E1-E5 Method BLASTN NCBI GI g2191126 BLAST score 179 5.0e-96 E value Match length 400 % identity 100 NCBI Description Arabidopsis thaliana BAC IG002N01 Seq. No. 139637 Seq. ID LIB24-042-Q1-E1-F2 Method BLASTN NCBI GI g4757392 BLAST score 216 E value 1.0e-118 Match length 412 % identity 100 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence Seq. No. 139638 Seq. ID LIB24-042-Q1-E1-F4 Method BLASTX NCBI GI q4760345 BLAST score 156 2.0e-10 E value 90 Match length 38 % identity NCBI Description (AL049769) hypothetical protein [Schizosaccharomyces pombe] Seq. No. 139639 Seq. ID LIB24-042-Q1-E1-F5 Method BLASTX NCBI GI g3426035 BLAST score 478 E value 4.0e-48 Match length 128 % identity 77 NCBI Description (AC005168) putative ripening-associated protein

Seq. No. 139640

[Arabidopsis thaliana]



```
Seq. ID
                   LIB24-042-Q1-E1-F8
Method
                   BLASTX
NCBI GI
                   g1702986
BLAST score
                   508
                   1.0e-51
E value
Match length
                   103
% identity
                   100
NCBI Description
                   14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi
                   isoform [Arabidopsis thaliana] >gi 1256534 (L09112) GF14
                   chi chain [Arabidopsis thaliana]
Seq. No.
                   139641
Seq. ID
                   LIB24-042-Q1-E1-G2
Method
                   BLASTX
NCBI GI
                   q1362007
BLAST score
                   729
E value
                   1.0e-77
Match length
                   136
% identity
                   99
NCBI Description
                   thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana
                   >gi_871992_emb_CAA55787_ (X79195) thioglucosidase
                   [Arabidopsis thaliana]
Seq. No.
                   139642
Seq. ID
                   LIB24-042-Q1-E1-H12
Method
                   BLASTX
NCBI GI
                   q2982583
BLAST score
                   652
E value
                   1.0e-68
Match length
                   126
% identity
                   100
                   (AJ003135) polygalacturonase [Arabidopsis thaliana]
NCBI Description
                   >gi_3152948_emb_CAA06610 (AJ005584) polygalacturonase
                   [Arabidopsis thaliana]
Seq. No.
                   139643
Seq. ID
                   LIB24-042-Q1-E1-H8
Method
                   BLASTX
NCBI GI
                   g416758
BLAST score
                   335
                   7.0e-32
E value
                   73
Match length
% identity
                   79
NCBI Description
                  SERINE CARBOXYPEPTIDASE PRECURSOR >gi 166674 (M81130)
                   carboxypeptidase Y-like protein [Arabidopsis thaliana]
                   >gi 445120 prf 1908426A carboxypeptidase Y [Arabidopsis
                   thaliana]
Seq. No.
                   139644
Seq. ID
                  LIB24-043-Q1-E1-A6
Method
                  BLASTN
NCBI GI
                  g2529657
BLAST score
                  93
E value
                  2.0e-45
Match length
                  114
                  94
% identity
```

16899

NCBI Description Arabidopsis thaliana chromosome II BAC T30B22 genomic

Seq. No.



sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  139645
Seq. ID
                  LIB24-043-Q1-E1-B9
Method
                  BLASTN
NCBI GI
                  g3046852
BLAST score
                  195
E value
                  1.0e-106
Match length
                  199
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQJ16, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139646
Seq. ID
                  LIB24-043-Q1-E1-F8
Method
                  BLASTN
NCBI GI
                  g3420042
BLAST score
                  110
E value
                  4.0e-55
Match length
                  231
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T13E15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139647
Seq. ID
                  LIB24-043-Q1-E1-G4
Method
                  BLASTN
NCBI GI
                  q3449329
BLAST score
                  201
E value
                  1.0e-109
Match length
                  365
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDH9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139648
Seq. ID
                  LIB24-043-Q1-E1-G5
Method
                  BLASTX
NCBI GI
                  q4234768
BLAST score
                  495
                  4.0e-50
E value
Match length
                  92
% identity
                  100
NCBI Description
                  (AF069468) sterol-C5-desaturase [Arabidopsis thaliana]
                  139649
Seq. No.
Seq. ID
                  LIB24-044-Q1-E1-A2
Method
                  BLASTX
NCBI GI
                  g4454037
BLAST score
                  655
                  6.0e-69
E value
                  123
Match length
                  98
% identity
NCBI Description
                  (AL035394) putative major latex protein [Arabidopsis
```

16900

thaliana]



Seq. ID LIB24-044-Q1-E1-A9

Method BLASTX
NCBI GI g418133
BLAST score 265
E value 3.0e-23
Match length 51
% identity 100

NCBI Description ANTHRANILATE SYNTHASE COMPONENT I-1 PRECURSOR >gi_166604

(M92353) anthranilate synthase alpha subunit [Arabidopsis

thaliana]

Seq. No. 139651

Seq. ID LIB24-044-Q1-E1-B8

Method BLASTX
NCBI GI g3403234
BLAST score 328
E value 1.0e-30
Match length 111
% identity 53

NCBI Description (AF071543) ribulose-1,5-bisphosphate carboxylase/oxygenase

N-methyltransferase [Spinacia oleracea] >gi_3403238

(AF071545) ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase II [Spinacia oleracea]

Seq. No. 139652

Seq. ID LIB24-044-Q1-E1-D4

Method BLASTX
NCBI GI g2501603
BLAST score 158
E value 1.0e-10
Match length 44
% identity 66

NCBI Description HYPOTHETICAL 77.0 KD PROTEIN IN HES1-SEC63 INTERGENIC

REGION >gi_2132095_pir__S67136 hypothetical protein YOR243c

yeast (Saccharomyces cerevisiae)

>gi_1420554 emb CAA99464 (Z75151) ORF YOR243c

[Saccharomyces cerevisiae]

Seq. No. 139653

Seq. ID LIB24-044-Q1-E1-E1

Method BLASTN
NCBI GI g1181530
BLAST score 85
E value 5.0e-40
Match length 85
% identity 100

NCBI Description Arabidopsis thaliana thionin (Thi2.1) mRNA, complete cds

Seq. No.

139654

Seq. ID LIB24-044-Q1-E1-F11

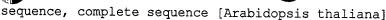
Method BLASTN
NCBI GI g3212846
BLAST score 324
E value 0.0e+00
Match length 328
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic

Seq. No.

Seq. ID





```
Seq. No.
                   139655
 Seq. ID
                   LIB24-044-Q1-E1-G12
Method
                   BLASTN
NCBI GI
                   g2564050
BLAST score
                   221
E value
                   1.0e-121
Match length
                   225
 % identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUA22, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139656
Seq. ID
                   LIB24-044-Q1-E1-G8
Method
                   BLASTN
NCBI GI
                   g4757406
BLAST score
                   80
E value
                   3.0e-37
Match length
                   214
% identity
                   90
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MPF21, complete sequence
Seq. No.
                   139657
Seq. ID
                   LIB24-044-Q1-E1-H3
Method
                   BLASTX
NCBI GI
                   q3608140
BLAST score
                   255
E value
                   5.0e-22
Match length
                   84
% identity
                   61
NCBI Description
                  (AC005314) unknown protein [Arabidopsis thaliana]
Seq. No.
                   139658
Seq. ID
                   LIB24-045-Q1-E1-A4
Method
                   BLASTX
NCBI GI
                   g2244752
BLAST score
                   208
E value
                   5.0e-17
Match length
                   55
% identity
                   75
NCBI Description
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   139659
Seq. ID
                   LIB24-045-Q1-E1-B10
Method
                  BLASTX
NCBI GI
                   g2673917
BLAST score
                   339
E value
                   2.0e-32
Match length
                  68
% identity
                  97
NCBI Description
                  (AC002561) putative ATP-dependent RNA helicase [Arabidopsis
                  thaliana]
```

LIB24-045-Q1-E1-D6



Method BLASTX
NCBI GI g2914700
BLAST score 298
E value 1.0e-27
Match length 60
% identity 95

NCBI Description (AC003974) tRNA-processing protein SEN3-like [Arabidopsis

thaliana]

Seq. No. 139661

Seq. ID LIB24-045-Q1-E1-E4

Method BLASTN
NCBI GI g3608126
BLAST score 362
E value 0.0e+00
Match length 383
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T32F12 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139662

Seq. ID LIB24-045-Q1-E1-F2

Method BLASTX
NCBI GI g3292820
BLAST score 144
E value 4.0e-09
Match length 35
% identity 86

NCBI Description (AL031018) putative MADS Box / AGL protein [Arabidopsis

thaliana]

Seq. No. 139663

Seq. ID LIB24-045-Q1-E1-F4

Method BLASTX
NCBI GI g4580953
BLAST score 316
E value 3.0e-29
Match length 126
% identity 52

NCBI Description (AF117734) glycerol kinase-like protein 2 [Mus musculus]

Seq. No. 139664

Seq. ID MB24-045-Q1-E1-F5

Method BLASTX
NCBI GI g3152585
BLAST score 241
E value 2.0e-20
Match length 64
% identity 72

NCBI Description (AC002986) Contains similarity to auxin-induced protein

TM018A10.6 from A. thaliana BAC gb_AF013294. [Arabidopsis

thaliana]

Seq. No. 139665

Seq. ID LIB24-045-Q1-E1-G8

Method BLASTX NCBI GI q4586117



BLAST score 267 5.0e-24 E value Match length 67 % identity 75

NCBI Description (AL049638) putative protein [Arabidopsis thaliana]

Seq. No. 139666

Seq. ID LIB24-045-Q1-E1-H10

Method BLASTX NCBI GI q4106340 BLAST score 234 E value 4.0e-20 Match length 46 % identity 100

NCBI Description (AF062396) protein phosphatase 2A regulatory subunit

isoform B' delta [Arabidopsis thaliana]

Seq. No. 139667

Seq. ID LIB24-045-Q1-E1-H6

Method BLASTX NCBI GI g1076294 BLAST score 346 E value 1.0e-32 Match length 91 % identity 71

NCBI Description ATAF2 protein - Arabidopsis thaliana

Seq. No. 139668

Seq. ID LIB24-046-Q1-E1-B5

Method BLASTX NCBI GI g1350783 BLAST score 200 E value 1.0e-15 Match length 125 % identity

NCBI Description RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR

>gi_282883_pir__S27756 receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana]

>gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No. 139669

Seq. ID LIB24-046-Q1-E1-B7

Method BLASTN NCBI GI q3641835 BLAST score 336 E value 0.0e + 00Match length 381 % identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20

(ESSAII project)

Seq. No. 139670

Seq. ID LIB24-046-Q1-E1-C11

Method BLASTN NCBI GI g2150022



BLAST score 95 E value 2.0e-46 Match length 155 % identity 95

NCBI Description Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1)

gene, complete cds

Seq. No. 139671

Seq. ID LIB24-046-Q1-E1-C8

Method BLASTN
NCBI GI g2477521
BLAST score 109
E value 7.0e-55
Match length 109
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139672

Seq. ID LIB24-046-Q1-E1-E7

Method BLASTX
NCBI GI g4544445
BLAST score 157
E value 2.0e-10
Match length 81
% identity 48

NCBI Description (AC006592) putative pyrophosphate--fructose 6-phosphate

1-phosphotransferase [Arabidopsis thaliana]

Seq. No. 139673

Seq. ID LIB24-046-Q1-E1-F2

Method BLASTN
NCBI GI g4027862
BLAST score 250
E value 1.0e-138
Match length 262
% identity 99

NCBI Description Arabidopsis thaliana chromosome 1 BAC T7A14 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 139674

Seq. ID LIB24-046-Q1-E1-F3

Method BLASTX
NCBI GI g3668173
BLAST score 576
E value 1.0e-59
Match length 121
% identity 93

NCBI Description (AB006777) vegetative storage protein [Arabidopsis

thaliana]

Seq. No. 139675

Seq. ID LIB24-046-Q1-E1-G5

Method BLASTX
NCBI GI g3738338
BLAST score 243
E value 1.0e-20



Match length 84 % identity 62

NCBI Description (AC005170) putative polygalacturonase [Arabidopsis

thaliana]

Seq. No. 139676

Seq. ID LIB24-046-Q1-E1-H3

Method BLASTN
NCBI GI g2651294
BLAST score 81
E value 2.0e-38

Match length 85 % identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T2P4 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139677

Seq. ID LIB24-046-Q1-E1-H7

Method BLASTX
NCBI GI g2335099
BLAST score 210
E value 6.0e-17
Match length 72
% identity 57

NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

Seq. No. 139678

Seq. ID LIB24-047-Q1-E1-A11

Method BLASTX
NCBI GI g2511590
BLAST score 608
E value 2.0e-63
Match length 119
% identity 100

NCBI Description (Y13692) multicatalytic endopeptidase complex, proteasome

component, beta subunit [Arabidopsis thaliana] >gi_3421111 (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis

thaliana]

Seq. No. 139679

Seq. ID LIB24-047-Q1-E1-A6

Method BLASTN
NCBI GI 94589410
BLAST score 385
E value 0.0e+00
Match length 385
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F2015, complete sequence

Seq. No. 139680

Seq. ID LIB24-047-Q1-E1-B5

Method BLASTX
NCBI GI g2245080
BLAST score 249
E value 3.0e-21
Match length 121

E value

Match length

% identity

4.0e-42

195

94



% identity NCBI Description (Z97343) myosin heavy chain homolog [Arabidopsis thaliana] Seq. No. 139681 Seq. ID LIB24-047-Q1-E1-B8 Method BLASTX NCBI GI g166765 BLAST score 525 E value 1.0e-53 Match length 104 % identity 96 NCBI Description (M23106) heat shock protein HSP70-1 [Arabidopsis thaliana] Seq. No. 139682 Seq. ID LIB24-047-Q1-E1-C4 Method BLASTX NCBI GI g2244987 BLAST score 659 E value 2.0e-69 Match length 134 % identity 92 NCBI Description (Z97340) similarity to protein kinase - slime mold (Dictyostelium) [Arabidopsis thaliana] Seq. No. 139683 Seq. ID LIB24-047-Q1-E1-D6 Method BLASTX NCBI GI g2499607 BLAST score 718 E value 3.0e-76 Match length 138 % identity 99 NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 3 (MAP KINASE 3) (ATMPK3) >gi_629544_pir__S40469 mitogen-activated protein kinase 3 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457398_dbj_BAA04866_ (D21839) MAP kinase [Arabidopsis thaliana] Seq. No. 139684 Seq. ID LIB24-047-Q1-E1-E2 Method BLASTX NCBI GI g3025299 BLAST score 363 E value 1.0e-34 Match length 73 % identity 96 HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi_2088660 NCBI Description (AF002109) ABC1 isolog [Arabidopsis thaliana] Seq. No. 139685 Seq. ID LIB24-047-Q1-E1-E5 Method BLASTN NCBI GI q4220643 BLAST score 88



```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MWD22, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139686
Seq. ID
                   LIB24-047-Q1-E1-E7
Method
                  BLASTX
NCBI GI
                   g399392
BLAST score
                   370
E value
                   2.0e-35
Match length
                   119
% identity
NCBI Description
                  DIHYDROLIPOAMIDE DEHYDROGENASE PRECURSOR (GLYCINE CLEAVAGE
                  SYSTEM L PROTEIN) >gi_100037_pir__S22384 dihydrolipoamide
                  dehydrogenase (EC 1.8.1.4) - garden pea
                  >gi_20806_emb_CAA45066 (X63464) dihydrolipoamide
                  dehydrogenase [Pisum sativum]
Seq. No.
                  139687
Seq. ID
                  LIB24-047-Q1-E1-F5
Method
                  BLASTN
NCBI GI
                  g3063690
BLAST score
                  148
E value
                  1.0e-77
Match length
                  373
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11
                  (ESSAII project)
Seq. No.
                  139688
Seq. ID
                  LIB24-047-Q1-E1-F9
Method
                  BLASTX
NCBI GI
                  g729478
BLAST score
                  624
E value
                  3.0e-65
Match length
                  130
% identity
                  86
NCBI Description
                  FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
                  >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
                  reductase [Oryza sativa]
Seq. No.
                  139689
Seq. ID
                  LIB24-047-Q1-E1-G10
Method
                  BLASTX
                  g4587552
```

NCBI GI BLAST score 685 E value 2.0e-72 Match length 139 % identity 100

NCBI Description (AC006577) Strong similarity to gb_S77096 aldehyde

dehydrogenase homolog from Brassica napus and is a member of PF_00171 Aldehyde dehydrogenase family. ESTs gb_T46213,

gb_T42164, gb_T43682, gb_N96380, gb_T42973, gb

Seq. No. 139690

Seq. ID LIB24-047-Q1-E1-G4

Method BLASTN NCBI GI g3399678



BLAST score 382 E value 0.0e+00 Match length 398 % identity 99

NCBI Description Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139691

Seq. ID LIB24-048-Q1-E1-G10

Method BLASTX
NCBI GI g4185142
BLAST score 572
E value 3.0e-59
Match length 111
% identity 99

NCBI Description (AC005724) putative DNA repair and recombination protein of

the SNF2 family [Arabidopsis thaliana]

Seq. No. 139692

Seq. ID LIB24-048-Q1-E1-G2

Method BLASTN
NCBI GI g3702724
BLAST score 149
E value 1.0e-78
Match length 149
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K17N15, complete sequence [Arabidopsis thaliana]

Seq. No. 139693

Seq. ID LIB24-048-Q1-E1-H3

Method BLASTN
NCBI GI g2914688
BLAST score 92
E value 3.0e-44
Match length 306
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F24L7 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139694

Seq. ID LIB24-048-Q1-E2-A4

Method BLASTN
NCBI GI 94584841
BLAST score 413
E value 0.0e+00
Match length 413
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T23E23,

complete sequence

Seq. No. 139695

Seq. ID LIB24-048-Q1-E2-D3

Method BLASTN
NCBI GI g3510337
BLAST score 237
E value 1.0e-131



```
Match length
                   305
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K19E20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139696
Seq. ID
                   LIB24-048-Q1-E2-D7
Method
                  BLASTX
NCBI GI
                   q99688
BLAST score
                  372
E value
                   1.0e-35
Match length
                   73
% identity
                  100
NCBI Description
                  translation elongation factor eEF-1 alpha chain (gene A4) -
                  Arabidopsis thaliana >gi_295789_emb_CAA34456 (X16432)
                  elongation factor 1-alpha [Arabidopsis thaliana]
Seq. No.
                   139697
Seq. ID
                  LIB24-048-Q1-E2-E8
Method
                  BLASTX
NCBI GI
                  q4325324
BLAST score
                   774
E value
                  8.0e-83
Match length
                  145
% identity
                  100
NCBI Description
                  (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis
                  thaliana]
Seq. No.
                  139698
Seq. ID
                  LIB24-048-Q1-E2-G7
Method
                  BLASTN
NCBI GI
                  g2244991
BLAST score
                  426
E value
                  0.0e+00
Match length
                  426
                  100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  139699
Seq. ID
                  LIB24-049-Q1-E2-C11
Method
                  BLASTN
NCBI GI
                  g4204173
BLAST score
                  158
                  2.0e-83
E value
Match length
                  411
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T2K10 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  139700
```

Seq. ID LIB24-049-Q1-E2-E10

Method BLASTN NCBI GI g2815404 BLAST score 290 E value 1.0e-162 Match length 298



139

% identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana] Seq. No. 139701 Seq. ID LIB24-049-Q1-E2-E11 Method BLASTX NCBI GI g2997767 BLAST score 724 6.0e-77 E value

% identity 34
NCBI Description (AF054906) myrosinase-binding protein homolog [Arabidopsis
thaliana]

 Seq. No.
 139702

 Seq. ID
 LIB24-049-Q1-E2-F9

 Method
 BLASTX

 NCBI GI
 a1912286

NCBI GI g1912286
BLAST score 559
E value 1.0e-57
Match length 106
% identity 100
NCBI Description (M20568)

Match length

NCBI Description (U39568) type 2A serine/threonine protein phosphatase [Arabidopsis thaliana] >gi_2194141 (AC002062) Match to Arabidopsis protein phosphatase PP2A (gb_U39568). EST

gb_T41959 comes from this gene. [Arabidopsis thaliana]

Seq. No. 139703

Seq. ID LIB24-049-Q1-E2-H5

Method BLASTX
NCBI GI g4467147
BLAST score 220
E value 4.0e-18
Match length 103
% identity 52

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 139704

Seq. ID LIB24-050-Q1-E1-B11

Method BLASTN
NCBI GI g1946354
BLAST score 281
E value 1.0e-157
Match length 281
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T06B20 genomic

sequence, complete sequence

Seq. No. 139705

Seq. ID LIB24-050-Q1-E1-H2

Method BLASTN
NCBI GI g2924505
BLAST score 119
E value 2.0e-60
Match length 221
% identity 97



NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13 (ESSAII project) Seq. No. 139706 Seq. ID LIB24-050-Q1-E1-H5 Method BLASTX NCBI GI q3702339 BLAST score 445 E value 2.0e-44 Match length 104 % identity 85 NCBI Description (AC005397) unknown protein [Arabidopsis thaliana] Seq. No. 139707 LIB24-051-Q1-E1-B3 Seq. ID Method BLASTN NCBI GI q3746057 BLAST score 301 E value 1.0e-169 Match length 301 % identity 100 NCBI Description Arabidopsis thaliana chromosome II BAC T16B12 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 139708 Seq. ID LIB24-051-Q1-E1-B9 Method BLASTX NCBI GI q2462749 BLAST score 164 E value 2.0e-14 Match length 54 % identity 76 NCBI Description (AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana] Seq. No. 139709 Seq. ID LIB24-051-Q1-E1-F9 Method BLASTN NCBI GI g4159708 BLAST score 203 E value 1.0e-110 Match length 280 % identity 100 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MKP6, complete sequence Seq. No. 139710 Seq. ID LIB24-051-Q1-E1-G1 Method BLASTX g1076511 352

NCBI GI BLAST score E value 1.0e-33 Match length 86 % identity 73

NCBI Description H+-transporting ATPase (EC 3.6.1.35) - kidney bean

>gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase

[Phaseolus vulgaris]

NCBI Description

thaliana]



```
Seq. No.
                   139711
Seq. ID
                   LIB24-051-Q1-E1-G12
Method
                   BLASTX
NCBI GI
                   g2315451
BLAST score
                   158
E value
                   9.0e-11
Match length
                   88
% identity
                   32
                   (AF016448) No definition line found [Caenorhabditis
NCBI Description
                   elegans]
Seq. No.
                   139712
Seq. ID
                   LIB24-051-Q1-E1-G2
Method
                   BLASTN
NCBI GI
                   g4220632
BLAST score
                   105
E value
                   2.0e-52
Match length
                   146
                   97
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K6M13, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139713
Seq. ID
                   LIB24-052-Q1-E1-B5
Method
                   BLASTN
NCBI GI
                   g3927822
BLAST score
                   79
                   4.0e-37
E value
Match length
                   83
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F8N16 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139714
Seq. ID
                   LIB24-052-Q1-E1-B7
Method
                   BLASTX
NCBI GI
                   g832876
BLAST score
                   437
E value
                   2.0e-43
Match length
                   98
% identity
                  86
NCBI Description
                   (L41345) ascorbate free radical reductase [Solanum
                   lycopersicum] >gi_1097368_prf_ 2113407A ascorbate free
                   radical reductase [Lycopersicon esculentum]
Seq. No.
                   139715
Seq. ID
                  LIB24-052-Q1-E1-F10
Method
                  BLASTX
NCBI GI
                  q2832674
BLAST score
                  248
E value
                  9.0e-22
Match length
                  58
% identity
                  86
```

(AL021712) fibrillin precursor-like protein [Arabidopsis

```
Seq. No.
                    139716
Seq. ID
                    LIB24-052-Q1-E1-H10
Method
                    BLASTX
NCBI GI
                    g2129738
BLAST score
                    448
E value
                    6.0e-45
Match length
                    88
                    97
% identity
                   shaggy-like kinase dzeta - Arabidopsis thaliana
>gi_1225913_emb_CAA64408_ (X94938) shaggy-like kinase dzeta
NCBI Description
                    [Arabidopsis thaliana] >gi_1669653_emb_CAA70483_ (Y09300)
                    serine/threonine kinase [Arabidopsis thaliana]
Seq. No.
                    139717
Seq. ID
                    LIB24-052-Q1-E1-H3
Method
                    BLASTN
NCBI GI
                    g4371278
BLAST score
                    223
E value
                    1.0e-122
Match length
                    227
% identity
                    100
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T2N18 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    139718
Seq. ID
                    LIB24-052-Q1-E1-H8
Method
                   BLASTX
NCBI GI
                    g2129755
BLAST score
                    382
E value
                    3.0e-37
Match length
                    87
                    90
% identity
NCBI Description
```

tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis thaliana >gi_619753 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] >gi_1585768_prf__2201482A Trp

synthase:SUBUNIT=alpha [Arabidopsis thaliana]

Seq. No. 139719

Seq. ID LIB24-052-Q1-E2-C12

Method BLASTN NCBI GI g2880038 BLAST score 159 E value 2.0e-84 Match length 171 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC T11J7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139720

Seq. ID LIB24-052-Q1-E2-H10

Method BLASTX NCBI GI g2129738 BLAST score 371 E value 4.0e-36 Match length 75 % identity 96

NCBI Description shaggy-like kinase dzeta - Arabidopsis thaliana

Seq. No.



>gi_1225913_emb_CAA64408_ (X94938) shaggy-like kinase dzeta
[Arabidopsis thaliana] >gi_1669653_emb_CAA70483_ (Y09300)
serine/threonine kinase [Arabidopsis thaliana]

```
Seq. No.
                   139721
Seq. ID
                   LIB24-053-Q1-E1-B11
Method
                   BLASTX
NCBI GI
                   g3287270
BLAST score
                   655
E value
                   6.0e-69
Match length
                   134
% identity
                   88
                   (Y09533) involved in starch metabalism [Solanum tuberosum]
NCBI Description
Seq. No.
                   139722
Seq. ID
                   LIB24-053-Q1-E1-C3
Method
                   BLASTN
NCBI GI
                   g2696018
BLAST score
                   52
E value
                   1.0e-20
Match length
                   56
% identity
                   98
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MXC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139723
Seq. ID
                   LIB24-053-Q1-E2-C5
Method
                   BLASTX
NCBI GI
                   q4587553
BLAST score
                   300
E value
                   3.0e-27
Match length
                   60
% identity
                   100
NCBI Description
                  (AC006577) F15I1.20 [Arabidopsis thaliana]
Seq. No.
                   139724
Seq. ID
                   LIB24-053-Q1-E2-C6
Method
                   BLASTX
NCBI GI
                   q2129575
BLAST score
                   534
E value
                   1.0e-54
Match length
                   109
% identity
                   93
NCBI Description
                  DNA repair protein homolog XPBara - Arabidopsis thaliana
Seq. No.
                   139725
Seq. ID
                  LIB24-053-Q1-E2-D3
Method
                  BLASTN
NCBI GI
                   g4741184
BLAST score
                  160
E value
                   4.0e-85
Match length
                  160
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7
```

16915

(ESSA project)

```
LIB24-054-Q1-E1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3668173
BLAST score
                   565
                   2.0e-58
E value
Match length
                   120
% identity
                   93
NCBI Description
                   (AB006777) vegetative storage protein [Arabidopsis
                   thaliana]
Seq. No.
                   139727
Seq. ID
                   LIB24-054-Q1-E1-F7
Method
                   BLASTN
NCBI GI
                   q3510336
BLAST score
                   154
E value
                   1.0e-81
Match length
                   166
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K18J17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139728
Seq. ID
                   LIB24-054-Q1-E1-G7
Method
                  BLASTX
NCBI GI
                   g3738302
BLAST score
                   498
E value
                   1.0e-50
Match length
                   103
% identity
                   94
NCBI Description
                   (AC005309) tubby-like protein [Arabidopsis thaliana]
                  >gi 4249398 (AC006072) putative tubby protein [Arabidopsis
                  thaliana]
Seq. No.
                  139729
Seq. ID
                  LIB24-056-Q1-E2-E2
Method
                  BLASTX
NCBI GI
                  q4185511
BLAST score
                   445
E value
                  2.0e-44
Match length
                  88
                  98
% identity
NCBI Description
                   (AF102822) actin depolymerizing factor 4 [Arabidopsis
                  thaliana]
Seq. No.
                  139730
Seq. ID
                  LIB24-056-Q1-E2-E6
Method
                  BLASTN
NCBI GI
                  g2656025
BLAST score
                  38
E value
                  4.0e-12
Match length
                  204
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

Seq. No. 139731

Seq. ID LIB24-056-Q1-E2-E7



```
Method
                   BLASTX
NCBI GI
                   a2459445
BLAST score
                   181
                  2.0e-13
E value
Match length
                  85
% identity
                  21
NCBI Description
                  (AC002332) putative ribonucleoprotein [Arabidopsis
                   thaliana]
                  139732
Seq. No.
Seq. ID
                  LIB24-056-Q1-E2-E8
Method
                  BLASTN
NCBI GI
                  g4589430
BLAST score
                  201
E value
                  1.0e-109
Match length
                  217
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MLD14, complete sequence
                  139733
Seq. No.
Seq. ID
                  LIB24-056-Q1-E2-F7
Method
                  BLASTX
NCBI GI
                  q585536
BLAST score
                  340
E value
                  3.0e-32
Match length
                  82
% identity
                  79
NCBI Description
                  MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)
                  >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) -
                  Arabidopsis thaliana >gi 304115 (L11454) thioglucosidase
                   [Arabidopsis thaliana] >gi 871990 emb CAA55786 (X79194)
                  thioglucosidase [Arabidopsis thaliana]
Seq. No.
                  139734
                  LIB24-058-Q1-E1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2914688
BLAST score
                  164
E value
                  4.0e-87
Match length
                  292
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC F24L7 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139735
Seq. ID
                  LIB24-058-Q1-E1-A3
Method
                  BLASTN
NCBI GI
                  q3158375
BLAST score
                  79
```

E value 6.0e-37 Match length 127 % identity

NCBI Description Arabidopsis thaliana SEN5 mRNA, partial cds

Seq. No. 139736

Seq. ID LIB24-058-Q1-E1-C6

```
BLASTX
```

Method BLASTX
NCBI GI g401213
BLAST score 418
E value 2.0e-41
Match length 93
% identity 88

NCBI Description ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE PRECURSOR >gi 166792

(M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana] >gi_445600_prf__1909347A phosphoribosylanthranilate transferase [Arabidopsis

thaliana]

139737

Seq. No.

Seq. ID

LIB24-058-Q1-E1-D10

Method BLASTN
NCBI GI g2252848
BLAST score 38
E value 6.0e-12
Match length 46

% identity 96

NCBI Description Arabidopsis thaliana BAC TM018A10

Seq. No.

139738

Seq. ID LIB24-058-Q1-E1-D5

Method BLASTN
NCBI GI g1297301
BLAST score 82
E value 2.0e-38
Match length 233
% identity 96

NCBI Description Arabidopsis thaliana phospholipase D mRNA, complete cds

Seq. No.

139739

Seq. ID Method LIB24-058-Q1-E1-D9

Method BLASTN
NCBI GI 94589446
BLAST score 99
E value 1.0e-48
Match length 175
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

T12B11, complete sequence

Seq. No. 139740

Seq. ID LIB24-058-Q1-E1-G10

Method BLASTX
NCBI GI g3461835
BLAST score 176
E value 9.0e-13
Match length 130
% identity 34

NCBI Description (AC005315) putative protein kinase [Arabidopsis thaliana]

>gi_3927840 (AC005727) putative protein kinase [Arabidopsis

thaliana]

Seq. No. 139741

Seq. ID LIB24-059-Q1-E1-A8



```
BLASTN
Method
NCBI GI
                   g2351073
BLAST score
                   115
E value
                   6.0e-58
Match length
                   319
% identity
                   95
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MYJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139742
Seq. ID
                   LIB24-059-Q1-E1-D11
Method
                   BLASTN
NCBI GI
                   q2880038
BLAST score
                   133
                   9.0e-69
E value
Match length
                   301
% identity
                   98
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T11J7 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139743
Seq. ID
                   LIB24-059-Q1-E1-E12
Method
                   BLASTX
NCBI GI
                   g3785977
BLAST score
                   342
E value
                   3.0e-32
Match length
                   122
% identity
                   49
                   (AC005560) putative growth regulator protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   139744
Seq. ID
                   LIB24-059-Q1-E1-F10
Method
                   BLASTN
NCBI GI
                   g4191771
BLAST score
                   173
E value
                   2.0e-92
Match length
                   345
                   97
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F3P11 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139745
Seq. ID
                   LIB24-060-Q1-E1-B7
Method
                  BLASTX
NCBI GI
                   g2598227
BLAST score
                   701
E value
                   3.0e-74
Match length
                   141
% identity
                   98
```

NCBI Description (AJ222585) AT-hook protein 1 [Arabidopsis thaliana]

Seq. No. 139746

Seq. ID LIB24-060-Q1-E1-C5

Method BLASTX NCBI GI g4455159 BLAST score 430



```
E value
                   2.0e-42
Match length
                   114
% identity
                   67
                   (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   139747
Seq. ID
                   LIB24-060-Q1-E1-D2
Method
                   BLASTX
NCBI GI
                   g3402697
BLAST score
                   597
E value
                   3.0e-62
Match length
                   111
% identity
                   32
NCBI Description
                   (AC004261) putative phosphatidylinositol-4-phosphate
                   5-kinase [Arabidopsis thaliana]
Seq. No.
                   139748
Seq. ID
                   LIB24-060-Q1-E1-D8
Method
                  BLASTN
NCBI GI
                   g2760168
BLAST score
                   117
E value
                   5.0e-59
Match length
                   345
% identity
                   83
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MEE6, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139749
Seq. ID
                  LIB24-060-Q1-E1-E7
Method
                  BLASTX
NCBI GI
                  g3776567
BLAST score
                   614
E value
                   4.0e-64
Match length
                  141
% identity
                  87
NCBI Description
                   (AC005388) Strong similarity to F21B7.33 gi 2809264 from A.
                  thaliana BAC gb_AC002560. EST gb_N65119 comes from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  139750
Seq. ID
                  LIB24-060-Q1-E1-G10
Method
                  BLASTN
NCBI GI
                  g2351070
BLAST score
                  176
E value
                  2.0e-94
Match length
                  230
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MTH12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139751
Seq. ID
                  LIB24-060-Q1-E1-G5
Method
                  BLASTX
```

NCBI GI g1617036
BLAST score 427
E value 2.0e-42
Match length 106



```
% identity
NCBI Description (Y08624) Ted2 [Vigna unquiculata]
Seq. No.
                   139752
Seq. ID
                   LIB24-060-Q1-E1-G7
Method
                  BLASTX
NCBI GI
                  g2529668
BLAST score
                  215
E value
                   1.0e-17
Match length
                   89
% identity
                   47
NCBI Description
                   (AC002535) putative photolyase/blue-light receptor
                   [Arabidopsis thaliana] >gi_3319288 (AF053366)
                  photolyase/blue light photoreceptor PHR2 [Arabidopsis
                  thaliana]
Seq. No.
                  139753
Seq. ID
                  LIB24-060-Q1-E1-G8
Method
                  BLASTN
NCBI GI
                  g1946354
BLAST score
                  164
E value
                  2.0e-87
Match length
                  176
% identity
                  98
NCBI Description Arabidopsis thaliana chromosome II BAC T06B20 genomic
                  sequence, complete sequence
Seq. No.
                  139754
Seq. ID
                  LIB24-061-Q1-E1-A11
Method
                  BLASTX
NCBI GI
                  g3228517
BLAST score
                  188
E value
                  1.0e-14
Match length
                  44
% identity
                  84
NCBI Description
                  (AF007788) ETTIN [Arabidopsis thaliana]
Seq. No.
                  139755
Seq. ID
                  LIB24-061-Q1-E1-A6
Method
                  BLASTN
NCBI GI
                  g4521999
BLAST score
                  293
E value
                  1.0e-164
Match length
                  297
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F2G1 genomic
                  sequence, complete sequence
Seq. No.
                  139756
Seq. ID
                  LIB24-061-Q1-E1-A9
Method
                  BLASTN
NCBI GI
                  g3046854
BLAST score
                  108
                  5.0e-54
E value
Match length
                  108
% identity
                  100
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



MRG7, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  139757
Seq. ID
                  LIB24-061-Q1-E1-B7
Method
                  BLASTN
NCBI GI
                  g3449329
BLAST score
                  393
E value
                  0.0e+00
Match length
                  393
                  50
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDH9, complete sequence [Arabidopsis thaliana]
                  139758
Seq. No.
Seq. ID
                  LIB24-061-Q1-E1-B8
Method
                  BLASTX
NCBI GI
                  g4432846
BLAST score
                  298
                  2.0e-27
E value
Match length
                  78
                  76
% identity
NCBI Description
                  (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                  139759
Seq. ID
                  LIB24-061-Q1-E1-C11
Method
                  BLASTX
NCBI GI
                  g585012
BLAST score
                  425
E value
                  6.0e-42
Match length
                  84
                  100
% identity
NCBI Description
                  PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE)
                  >gi_289205 (L16237) phytoene desaturase [Arabidopsis
                  thaliana] >gi_2244777_emb_CAB10200_ (Z97335) unnamed
                  protein product [Arabidopsis thaliana]
Seq. No.
                  139760
Seq. ID
                  LIB24-061-Q1-E1-C12
Method
                  BLASTX
NCBI GI
                  g4567263
BLAST score
                  534
E value
                  1.0e-54
Match length
                  103
% identity
                  100
NCBI Description
                  (AC006841) putative cell division inhibitor [Arabidopsis
                  thaliana]
Seq. No.
                  139761
Seq. ID
                  LIB24-061-Q1-E1-D10
Method
                  BLASTN
NCBI GI
                  g4512656
BLAST score
                  159
E value
                  4.0e-84
Match length
                  345
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
```

16922

sequence, complete sequence



```
Seq. No.
                   139762
Seq. ID
                   LIB24-061-Q1-E1-D9
Method
                   BLASTX
NCBI GI
                   g2342690
BLAST score
                   235
E value
                  1.0e-19
Match length
                  88
% identity
                   35
NCBI Description
                   (AC000106) Similar to Homo copine I (gb U83246).
                   [Arabidopsis thaliana]
Seq. No.
                  139763
Seq. ID
                  LIB24-061-Q1-E1-F3
Method
                  BLASTX
NCBI GI
                  q3056584
BLAST score
                   240
                  3.0e-20
E value
Match length
                  90
% identity
                   48
NCBI Description
                  (AC004255) T1F9.5 [Arabidopsis thaliana]
Seq. No.
                  139764
Seq. ID
                  LIB24-062-Q1-E1-A11
Method
                  BLASTN
NCBI GI
                  g2623294
BLAST score
                  150
E value
                  9.0e-79
Match length
                  404
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20B5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139765
Seq. ID
                  LIB24-062-Q1-E1-A12
Method
                  BLASTN
NCBI GI
                  g2623294
BLAST score
                  32
                  7.0e-09
E value
Match length
                  56
% identity
                  89
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20B5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139766
Seq. ID
                  LIB24-062-Q1-E1-A4
Method
                  BLASTX
NCBI GI
                  g3688193
BLAST score
                  196
E value
                  4.0e-15
Match length
                  126
% identity
                  40
NCBI Description (AJ010091) MAP3K alpha 1 protein kinase [Brassica napus]
```

Seq. No. 139767

Seq. ID LIB24-062-Q1-E1-C6

Method BLASTN



NCBI GI g2924732
BLAST score 120
E value 3.0e-61
Match length 144
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUA2, complete sequence [Arabidopsis thaliana]

Seq. No. 139768

Seq. ID LIB24-062-Q1-E1-D9

Method BLASTN
NCBI GI g4263753
BLAST score 326
E value 0.0e+00
Match length 350
% identity 98

NCBI Description Arabidopsis thaliana chromosome V map near 60.5 cM,

complete sequence [Arabidopsis thaliana]

Seq. No. 139769

Seq. ID LIB24-062-Q1-E1-E6

Method BLASTN
NCBI GI g4572664
BLAST score 58
E value 7.0e-24
Match length 183
% identity 86

NCBI Description Arabidopsis thaliana chromosome II BAC F25P17 genomic

sequence, complete sequence

Seq. No. 139770

Seq. ID LIB24-062-Q1-E1-G7

Method BLASTX
NCBI GI g2052383
BLAST score 280
E value 4.0e-25
Match length 91
% identity 58

NCBI Description (U66345) calreticulin [Arabidopsis thaliana]

Seq. No. 139771

Seq. ID LIB24-062-Q1-E1-G8

Method BLASTX
NCBI GI g544424
BLAST score 191
E value 2.0e-14
Match length 36
% identity 97

NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir_ S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana

>gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding

97 ×

protein [Arabidopsis thaliana]

>gi 4567224 gb AAD23639.1 AC007119 5 (AC007119)

glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No. 139772



```
Seq. ID
                   LIB24-063-Q1-E1-C12
                  BLASTX
Method
                  g625977
NCBI GI
BLAST score
                   605
E value
                   5.0e-63
Match length
                   117
% identity
                  100
                  p40 protein homolog - Arabidopsis thaliana >gi 402904
NCBI Description
                   (U01955) laminin receptor-like protein [Arabidopsis
                  thaliana]
Seq. No.
                   139773
Seq. ID
                  LIB24-063-Q1-E1-C9
Method
                  BLASTN
NCBI GI
                  q3449333
BLAST score
                   134
                   3.0e-69
E value
Match length
                   396
% identity
                   96
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXF12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139774
Seq. ID
                  LIB24-063-Q1-E1-E1
Method
                  BLASTN
NCBI GI
                   q3128137
BLAST score
                   159
E value
                   4.0e-84
Match length
                   410
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9I9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139775
Seq. ID
                   LIB24-063-Q1-E1-F12
Method
                  BLASTN
NCBI GI
                   q2564051
BLAST score
                   154
E value
                   2.0e-81
Match length
                   253
% identity
                   93
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MWD9, complete sequence [Arabidopsis thaliana]
                   139776
Seq. No.
Seq. ID
                   LIB24-063-Q1-E1-F2
Method
                   BLASTX
NCBI GI
                   g4646203
BLAST score
                   190
                   2.0e-14
E value
                   65
Match length
                   52
% identity
                   (AC007230) Belongs to PF 00026 Eukaryotic aspartyl protease
NCBI Description
                   family. [Arabidopsis thaliana]
```

Seq. No. 139777

Seq. ID LIB24-063-Q1-E1-F8



```
BLASTX
Method
NCBI GI
                  g4732123
BLAST score
                  667
E value
                  2.0e-70
Match length
                  128
                  95
% identity
                   (AF129087) mitogen-activated protein kinase homologue
NCBI Description
                   [Medicago sativa]
                  139778
Seq. No.
Seq. ID
                  LIB24-063-Q1-E1-H11
Method
                  BLASTN
NCBI GI
                  g2264304
BLAST score
                  115
                  3.0e-58
E value
Match length
                  155
% identity
                  94
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBG8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139779
Seq. ID
                  LIB24-063-Q1-E1-H7
Method
                  BLASTX
NCBI GI
                  g1117780
BLAST score
                  224
                  6.0e-19
E value
Match length
                  53
% identity
                  83
NCBI Description
                  (D49367) 4-coumarate:CoA ligase [Lithospermum
                  erythrorhizon]
Seq. No.
                  139780
Seq. ID
                  LIB24-063-Q1-E1-H8
Method
                  BLASTX
NCBI GI
                  g1174470
BLAST score
                  386
E value
                  1.0e-39
Match length
                  133
                  62
% identity
                  OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)
NCBI Description
                  (INTEGRAL MEMBRANE PROTEIN 1) >gi 508543 (L34260) integral
                  membrane protein 1 [Mus musculus] >gi 1588285 prf 2208301A
                  integral membrane protein [Mus musculus]
Seq. No.
                  139781
Seq. ID
                  LIB24-064-Q1-E1-A10
Method
                  BLASTX
NCBI GI
                  q4468980
BLAST score
                  348
E value
                  4.0e-33
```

Match length 91 % identity 75

NCBI Description (AL035605) formamidase-like protein [Arabidopsis thaliana]

Seq. No. 139782

Seq. ID LIB24-064-Q1-E1-B5

Method BLASTX



```
NCBI GI
                   q2129670
BLAST score
                  363
                  1.0e-34
E value
Match length
                  70
                  100
% identity
                  {\tt phosphoinositide-specific\ phospholipase\ C\ -\ Arabidopsis}
NCBI Description
                  thaliana >gi_857374 dbj_BAA09432 (D50804) phosphoinositide
                  specific phospholipase C [Arabidopsis thaliana]
                  139783
Seq. No.
Seq. ID
                  LIB24-064-Q1-E1-C11
Method
                  BLASTX
NCBI GI
                  q4567231
                  320
BLAST score
                  1.0e-29
E value
Match length
                  61
% identity
                  100
NCBI Description
                   (AC007119) putative glucose-1-phosphate adenylyltransferase
                   [Arabidopsis thaliana]
                  139784
Seq. No.
Seq. ID
                  LIB24-064-Q1-E1-C4
Method
                  BLASTN
NCBI GI
                  g2351096
BLAST score
                  56
E value
                  3.0e-23
Match length
                  100
                  90
% identity
NCBI Description Arabidopsis thaliana mRNA for ATMRK1, complete cds
Seq. No.
                  139785
Seq. ID
                  LIB24-064-Q1-E1-D12
Method
                  BLASTX
NCBI GI
                  g3983665
BLAST score
                  329
E value
                  1.0e-30
Match length
                  87
% identity
                  74
NCBI Description
                  (AB011271) importin-beta2 [Oryza sativa]
Seq. No.
                  139786
Seq. ID
                  LIB24-064-Q1-E1-D5
Method
                  BLASTX
NCBI GI
                  g3617741
BLAST score
                  249
E value
                  2.0e-21
Match length
                  51
% identity
                  100
NCBI Description
                   (AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis
                  thaliana]
```

139787 Seq. No.

Seq. ID LIB24-064-Q1-E1-D7

BLASTN Method NCBI GI g3985949 BLAST score 257 1.0e-143 E value



```
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MOB24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139788
Seq. ID
                  LIB24-064-Q1-E1-E1
Method
                  BLASTN
                  g4455262
NCBI GI
BLAST score
                  106
E value
                  1.0e-52
Match length
                  282
% identity
                  90
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
NCBI Description
                   (ESSAII project)
Seq. No.
                  139789
Seq. ID
                  LIB24-064-Q1-E1-F1
Method
                  BLASTN
NCBI GI
                  g4249393
BLAST score
                  359
E value
                  0.0e+00
Match length
                  380
% identity
                  98
                  Arabidopsis thaliana chromosome II BAC T9J23 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139790
Seq. ID
                  LIB24-064-Q1-E1-G12
Method
                  BLASTX
NCBI GI
                  g4467096
BLAST score
                  544
E value
                  6.0e-56
Match length
                  112
% identity
                  56
NCBI Description
                  (AL035538) putative protein [Arabidopsis thaliana]
Seq. No.
                  139791
Seq. ID
                  LIB24-064-Q1-E1-G3
Method
                  BLASTN
                  g1877523
NCBI GI
BLAST score
                  270
E value
                  1.0e-150
Match length
                  282
% identity
                  99
                  Arabidopsis thaliana BAC T7I23, complete sequence
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  139792
Seq. ID
                  LIB24-064-Q1-E1-G9
Method
                  BLASTN
NCBI GI
                  q2760172
```

BLAST score 197

E value 1.0e-107 Match length 273 100 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



MUB3, complete sequence [Arabidopsis thaliana]

139793 Seq. No. Seq. ID LIB24-064-Q1-E1-H4 Method BLASTX NCBI GI q2209087 BLAST score 292 2.0e-26 E value Match length 108 53 % identity (AF000309) putative serine/threonine kinase [Colletotrichum NCBI Description lindemuthianum] Seq. No. 139794 Seq. ID LIB24-065-Q1-E1-C8 Method BLASTX NCBI GI q1170606 BLAST score 193 E value 7.0e-15 Match length 53 70 % identity NCBI Description ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) >gi 629863 pir S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a) >gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor P1, P5-Bis (Adenosine-5'-)pentaphosphate (Ap5a) 139795 Seq. No. Seq. ID LIB24-065-Q1-E1-C9 Method BLASTN NCBI GI g3033373 BLAST score 259 E value 1.0e-144 Match length 263 % identity 100 Arabidopsis thaliana chromosome II BAC F19I3 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 139796 Seq. No. Seq. ID LIB24-065-Q1-E1-E6 Method BLASTN NCBI GI g3080406 BLAST score 76 E value 8.0e-35 Match length 247 % identity 100 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12 (ESSA project) Seq. No. 139797

Seq. ID LIB24-065-Q1-E1-G4

Method BLASTN
NCBI GI g4490324
BLAST score 226



E value 1.0e-124 Match length 280 % identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14

(ESSA project)

Seq. No. 139798

Seq. ID LIB24-066-Q1-E1-C5

Method BLASTX
NCBI GI g2119848
BLAST score 422
E value 1.0e-41
Match length 80
% identity 100

NCBI Description chlorophyll a/b-binding protein type I precursor LhblB1 -

Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]

Seq. No. 139799

Seq. ID LIB24-066-Q1-E1-C9

Method BLASTN
NCBI GI g4220643
BLAST score 114
E value 3.0e-57
Match length 391
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 139800

Seq. ID LIB24-066-Q1-E1-F2

Method BLASTX
NCBI GI g1169201
BLAST score 439
E value 1.0e-43
Match length 112
% identity 81

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR

>gi 421830 pir S33707 DRT112 protein - Arabidopsis

thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No. 139801

Seq. ID LIB24-066-Q1-E1-F5

Method BLASTX
NCBI GI g3204134
BLAST score 380
E value 4.0e-51
Match length 119
% identity 76

NCBI Description (AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No. 139802

Seq. ID

Method



```
Seq. ID
                  LIB24-066-Q1-E1-F7
Method
                  BLASTN
NCBI GI
                  q3985934
BLAST score
                  87
E value
                  1.0e-41
Match length
                  127
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJE7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139803
Seq. ID
                  LIB24-066-Q1-E1-H5
Method
                  BLASTN
NCBI GI
                  a4432829
BLAST score
                  100
E value
                   3.0e - 49
                  217
Match length
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC T1B3 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139804
Seq. ID
                  LIB24-067-Q1-E1-C10
Method
                  BLASTN
                  g2358139
NCBI GI
BLAST score
                  167
                   5.0e-89
E value
                   304
Match length
% identity
                   98
                  Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete
NCBI Description
                   sequence [Arabidopsis thaliana]
Seq. No.
                   139805
Seq. ID
                   LIB24-067-Q1-E1-C2
Method
                   BLASTN
                   q3046854
NCBI GI
BLAST score
                   19
                   4.7e-01
E value
Match length
                   124
% identity
                   86
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRG7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139806
Seq. ID
                   LIB24-067-Q1-E1-D11
Method
                   BLASTX
NCBI GI
                   q3522956
BLAST score
                   424
E value
                   4.0e-42
Match length
                   89
% identity
                   96
                   (AC004411) putative pectinacetylesterase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   139807
Seq. No.
```

16931

LIB24-067-Q1-E1-E11

BLASTX



358

382

0.0e + 00

BLAST score

E value Match length

```
a4580393
NCBI GI
BLAST score
                   301
                  2.0e-27
E value
                  104
Match length
                  58
% identity
                  (AC007171) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  139808
                  LIB24-067-Q1-E1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3766248
BLAST score
                  440
E value
                  1.0e-43
Match length
                  102
                  81
% identity
                   (Y18227) blue copper binding-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  139809
                  LIB24-067-Q1-E1-F1
Seq. ID
Method
                  BLASTX
                  g2253583
NCBI GI
BLAST score
                  184
E value
                  1.0e-13
Match length
                  63
% identity
                  62
                  (U78721) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  139810
                  LIB24-067-01-E1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2618601
BLAST score
                   170
E value
                   6.0e-91
Match length
                   218
% identity
                   93
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MHJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139811
Seq. ID
                   LIB24-067-01-E1-G12
Method
                  BLASTX
NCBI GI
                   g4586106
BLAST score
                   653
E value
                   9.0e-69
Match length
                   120
% identity
                   100
NCBI Description
                   (ALO49638) putative disease resistance protein (TMV N-like)
                   [Arabidopsis thaliana]
Seq. No.
                   139812
Seq. ID
                   LIB24-067-Q1-E1-G2
Method
                   BLASTN
NCBI GI
                   g4467131
```

1.5



92

% identity

NCBI Description

```
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13
                   (ESSA project)
                  139813
Seq. No.
Seq. ID
                  LIB24-067-Q1-E1-G6
Method
                  BLASTN
NCBI GI
                  q3510347
BLAST score
                  121
                  2.0e-61
E value
Match length
                  334
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139814
                  LIB24-067-Q1-E1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g166708
BLAST score
                  639
                  5.0e-67
E value
                  130
Match length
% identity
                  98
NCBI Description
                  (M64118) glyceraldehyde-3-phosphate dehydrogenase
                   [Arabidopsis thaliana]
Seq. No.
                  139815
Seq. ID
                  LIB24-069-Q1-E1-B12
Method
                  BLASTX
NCBI GI
                  q3281866
BLAST score
                  536
E value
                  5.0e-55
Match length
                  100
% identity
                  100
NCBI Description
                  (AL031004) putative protein [Arabidopsis thaliana]
Seq. No.
                  139816
Seq. ID
                  LIB24-069-Q1-E1-C6
Method
                  BLASTX
NCBI GI
                  q4006887
BLAST score
                  388
E value
                  6.0e-38
Match length
                  80
% identity
                  93
NCBI Description
                 (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                  139817
Seq. ID
                  LIB24-069-Q1-E1-D7
Method
                  BLASTN
                  g2264312
NCBI GI
BLAST score
                  93
E value
                  3.0e-45
Match length
                  137
```

16933

MOK16, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



```
Seq. No.
                  139818
Seq. ID
                  LIB24-069-Q1-E1-E12
Method
                  BLASTX
NCBI GI
                  q4586433
BLAST score
                  193
                  8.0e-15
E value
Match length
                  51
                  67
% identity
                  (AB016798) ribosomal protein L29/cell surface heparin
NCBI Description
                  binding protein HIP [Sus scrofa]
                  >gi_4586439_dbj_BAA76404.1_ (AB017196) ribosomal protein
                  L29/heparin/heparan sulfate interacting protein [Sus
                  scrofa]
Seq. No.
                  139819
Seq. ID
                  LIB24-069-Q1-E1-F11
Method
                  BLASTX
NCBI GI
                  g2632103
BLAST score
                  655
                  7.0e-69
E value
Match length
                  126
                  100
% identity
NCBI Description
                  (Z98759) arginyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.
                  139820
                  LIB24-069-Q1-E1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2335108
BLAST score
                  548
                  2.0e-56
E value
Match length
                  127
% identity
                  82
                  (AC002339) putative isulinase [Arabidopsis thaliana]
NCBI Description
                  139821
Seq. No.
Seq. ID
                  LIB24-069-Q1-E1-G1
Method
                  BLASTN
NCBI GI
                  q4803835
BLAST score
                  90
E value
                  1.0e-43
Match length
                  90
                  100
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for a dynamin-like protein ADL3,
                  complete cds
Seq. No.
                  139822
Seq. ID
                  LIB24-069-Q1-E1-G12
Method
                  BLASTX
NCBI GI
                  g417383
```

BLAST score 619 E value 1.0e-64 Match length 125 % identity 98

NITRILASE 2 >gi_322548_pir__S31969 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_22656_emb_CAA48377_ (X68305) NCBI Description

nitrilase II [Arabidopsis thaliana] >gi_508733 (U09958)

nitrilase [Arabidopsis thaliana]

% identity

100



```
Seq. No.
                  139823
                  LIB24-069-Q1-E1-H2
Seq. ID
Method
                  BLASTN
                  g3510341
NCBI GI
BLAST score
                  72
E value
                  1.0e-32
Match length
                  140
                  88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFC16, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139824
Seq. ID
                  LIB24-070-Q1-E1-A3
Method
                  BLASTX
                  g3915023
NCBI GI
BLAST score
                  546
                  3.0e-56
E value
Match length
                  121
% identity
                  84
                  SUCROSE-PHOSPHATE SYNTHASE 1
NCBI Description
                  (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1)
                  >gi_2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate
                  synthase [Citrus unshiu]
Seq. No.
                  139825
Seq. ID
                  LIB24-070-Q1-E1-A5
Method
                  BLASTX
                  g1480078
NCBI GI
BLAST score
                  479
                  3.0e-48
E value
Match length
                  96
                  99
% identity
NCBI Description
                  (X99696) shaggy-like protein kinase iota [Arabidopsis
                  thaliana] >gi_2444277_gb_AAB71545.1_ (AF019927)
                  GSK3/shaggy-like protein kinase [Arabidopsis thaliana]
Seq. No.
                  139826
Seq. ID
                  LIB24-070-Q1-E1-A7
Method
                  BLASTX
                  q4510356
NCBI GI
                  433
BLAST score
                  6.0e-43
E value
Match length
                  84
% identity
                  100
                   (AC006921) putative kinesin-related protein TKRP125
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  139827
Seq. ID
                  LIB24-070-Q1-E1-C9
Method
                  BLASTN
NCBI GI
                  q4454447
BLAST score
                  262
                  1.0e-145
E value
Match length
                  413
```

16935

NCBI Description Arabidopsis thaliana chromosome II BAC F5H14 genomic



sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  139828
                  LIB24-070-Q1-E1-G10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3513725
BLAST score
                  388
E value
                  0.0e+00
Match length
                  412
                  98
% identity
NCBI Description Arabidopsis thaliana BAC F8M12
Seq. No.
                  139829
Seq. ID
                  LIB24-070-Q1-E1-H2
Method
                  BLASTX
NCBI GI
                  q2501056
BLAST score
                  492
E value
                  7.0e-50
                  99
Match length
                  100
% identity
                  SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)
NCBI Description
                  >gi 2129737_pir__S71293 seryl-tRNA synthetase - Arabidopsis
                  thaliana >gi_1359497_emb_CAA94388_ (Z70313) seryl-tRNA
                  Synthetase [Arabidopsis thaliana]
Seq. No.
                  139830
Seq. ID
                  LIB24-071-Q1-E1-A1
Method
                  BLASTX
NCBI GI
                  q2244859
BLAST score
                  305
E value
                  3.0e-28
Match length
                  84
                  68
% identity
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  139831
Seq. ID
                  LIB24-071-Q1-E1-C5
                  BLASTN
Method
NCBI GI
                  g3702736
                   42
BLAST score
                  3.0e-14
E value
Match length
                   66
% identity
                   91
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRI1, complete sequence [Arabidopsis thaliana]
                  139832
Seq. No.
Seq. ID
                  LIB24-071-Q1-E1-C8
Method
                  BLASTX
NCBI GI
                  g1352663
BLAST score
                   607
                  3.0e-63
E value
Match length
                  116
                  100
% identity
                  SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-3 CATALYTIC
NCBI Description
```

16936

(EC 3.1.3.16) 2A isoform 3 - Arabidopsis thaliana

SUBUNIT >gi_1076388_pir__S52659 phosphoprotein phosphatase



139833

>gi_466441 (M96841) Ser/Thr protein phosphatase
[Arabidopsis thaliana]
>gi_4559341_gb_AAD23003.1_AC007087_22 (AC007087)
serine/threonine protein phosphatase PP2A-3 catalytic
subunit [Arabidopsis thaliana]
>gi_4567320_gb_AAD23731.1_AC005956_20 (AC005956)
serine/threonine protein phosphatase [Arabidopsis thaliana]

Seq. ID LIB24-071-Q1-E1-E7
Method BLASTN
NCBI GI g4079614
BLAST score 138
E value 1.0e-71
Match length 372
% identity 96

Seq. No.

NCBI Description Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

 Seq. No.
 139834

 Seq. ID
 LIB24-071-Q1-E1-G11

 Method
 BLASTX

 NCBI GI
 g4586254

 BLAST, game
 207

BLAST score 207
E value 2.0e-16
Match length 73
% identity 60

NCBI Description (AL049640) auxilin-like protein [Arabidopsis thaliana]

Seq. No. 139835

Seq. ID LIB24-071-Q1-E1-G12

Method BLASTN
NCBI GI g3299824
BLAST score 98
E value 3.0e-48
Match length 134
% identity 93

NCBI Description Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,

near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No. 139836

Seq. ID LIB24-071-Q1-E1-H7

Method BLASTN
NCBI GI g3080406
BLAST score 86
E value 3.0e-41
Match length 86
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12

(ESSA project)

Seq. No. 139837

Seq. ID LIB24-071-Q1-E1-H9

Method BLASTX
NCBI GI g2832619
BLAST score 559
E value 1.0e-57

NCBI Description



```
Match length
% identity
                  62
                   (AL021711) major intrinsic protein (MIP) - like [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  139838
Seq. ID
                  LIB24-072-Q1-E1-A12
Method
                  BLASTN
NCBI GI
                  g3608126
BLAST score
                  114
E value
                  1.0e-57
Match length
                  158
% identity
                  93
                  Arabidopsis thaliana chromosome II BAC T32F12 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139839
Seq. ID
                  LIB24-072-Q1-E1-B3
Method
                  BLASTX
NCBI GI
                  q4191789
BLAST score
                  415
E value
                  5.0e-41
Match length
                  93
% identity
                  88
                   (AC005917) putative transmembrane transport protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  139840
Seq. ID
                  LIB24-072-01-E1-B9
Method
                  BLASTX
NCBI GI
                  g681904
BLAST score
                  464
E value
                  2.0e-46
Match length
                  108
% identity
                  86
                  (D31711) cp29 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  139841
Seq. ID
                  LIB24-072-Q1-E1-C12
Method
                  BLASTX
NCBI GI
                  g2827700
BLAST score
                  657
E value
                  4.0e-69
Match length
                  132
                  100
% identity
NCBI Description
                   (AL021684) DEAD box ATP dependent helicase protein
                   [Arabidopsis thaliana]
Seq. No.
                  139842
Seq. ID
                  LIB24-072-Q1-E1-E3
Method
                  BLASTX
NCBI GI
                  g2911057
BLAST score
                  152
                  1.0e-32
E value
Match length
                  76
                  99
% identity
```

16938

(AL021961) caffeoyl-CoA O-methyltransferase - like protein



[Arabidopsis thaliana]

```
139843
Seq. No.
Seq. ID
                  LIB24-072-Q1-E1-F10
Method
                  BLASTX
NCBI GI
                  q3482918
BLAST score
                  446
                  2.0e-44
E value
                  91
Match length
                  100
% identity
NCBI Description
                  (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
                  thaliana]
                  139844
Seq. No.
                  LIB24-072-Q1-E1-F9
Seq. ID
Method
                  BLASTX
                  q115783
NCBI GI
                  595
BLAST score
E value
                  7.0e-62
Match length
                  113
                  99
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  139845
Seq. No.
                  LIB24-072-Q1-E1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1946367
BLAST score
                  356
                  7.0e-34
E value
Match length
                  128
% identity
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
                  139846
Seq. ID
                  LIB24-072-Q1-E1-G5
Method
                  BLASTN
NCBI GI
                  q2618604
BLAST score
                  348
                  0.0e + 00
E value
Match length
                  394
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTG13, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139847
Seq. ID
                  LIB24-072-Q1-E1-G9
Method
                  BLASTX
                  g2623307
NCBI GI
BLAST score
                  760
                  3.0e-81
E value
Match length
                  141
                  99
% identity
                   (AC002409) putative ubiquitin protease [Arabidopsis
NCBI Description
```

thaliana]



```
Seq. No.
                  139848
Seq. ID
                  LIB24-072-Q1-E1-H4
Method
                  BLASTN
NCBI GI
                  g2342673
BLAST score
                  202
E value
                  1.0e-110
Match length
                  313
                  100
% identity
                  Sequence of BAC F7G19 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139849
Seq. ID
                  LIB24-073-Q1-E1-A12
Method
                  BLASTN
NCBI GI
                  q3201608
BLAST score
                  251
E value
                  1.0e-139
                  263
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC F7F1 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139850
                  LIB24-073-Q1-E1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3719211
                  448
BLAST score
E value
                  1.0e-44
                  110
Match length
% identity
                  81
NCBI Description
                  (U97021) UIP2 [Arabidopsis thaliana]
Seq. No.
                  139851
Seq. ID
                  LIB24-073-Q1-E1-D1
Method
                  BLASTN
NCBI GI
                   q3763915
BLAST score
                   105
E value
                   4.0e-52
Match length
                   269
% identity
                   97
                  Arabidopsis thaliana chromosome II BAC F14B2 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   139852
Seq. No.
                  LIB24-074-Q1-E1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2623296
BLAST score
                   360
E value
                   3.0e-34
                   105
Match length
                   71
% identity
                  (AC002409) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 139853

Seq. ID LIB24-074-Q1-E1-C11

Method BLASTX



NCBI GI g3876247 BLAST score 366 E value 5.0e-35 Match length 133 % identity 54

NCBI Description (Z71262) similar to serine/threonine kinase; cDNA EST EMBL:D27596 comes from this gene; cDNA EST EMBL:D75765 comes from this gene; cDNA EST EMBL:D34336 comes from this gene; cDNA EST EMBL:D34931 comes from this gene; cDNA EST E

Seq. No. 139854

Seq. ID LIB24-074-Q1-E1-C12

Method BLASTX
NCBI GI 94585974
BLAST score 592
E value 2.0e-61
Match length 129
% identity 88

NCBI Description (AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 139855

Seq. ID LIB24-074-Q1-E1-D4

Method BLASTX
NCBI GI g3668173
BLAST score 670
E value 1.0e-70
Match length 139
% identity 94

NCBI Description (AB006777) vegetative storage protein [Arabidopsis

thaliana]

Seq. No. 139856

Seq. ID LIB24-074-Q1-E1-D9

Method BLASTN
NCBI GI g2281081
BLAST score 95
E value 6.0e-46
Match length 338
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F18019 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139857

Seq. ID LIB24-074-Q1-E1-E5

Method BLASTN
NCBI GI g3212846
BLAST score 115
E value 5.0e-58
Match length 115
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139858

Seq. ID LIB24-074-Q1-E1-F8

Method BLASTX NCBI GI g4558591



BLAST score 516 E value 1.0e-52 Match length 105 % identity 98

NCBI Description (AC006555) putative beta-1,3-glucanase [Arabidopsis

thaliana] >gi_4662638_gb_AAD26909.1_AC007233_1 (AC007233)

putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No. 139859

Seq. ID LIB24-074-Q1-E1-G1

Method BLASTN
NCBI GI g3449317
BLAST score 228
E value 1.0e-125
Match length 390
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MKM21, complete sequence [Arabidopsis thaliana]

Seq. No. 139860

Seq. ID LIB24-074-Q1-E1-G11

Method BLASTX
NCBI GI g2499611
BLAST score 384
E value 4.0e-37
Match length 72
% identity 100

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7)

(ATMPK7) >gi_629548_pir__S40473 mitogen-activated protein

kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana

>gi 457406 dbj BAA04870 (D21843) MAP kinase [Arabidopsis

thaliana]

Seq. No. 139861

Seq. ID LIB24-075-Q1-E1-A3

Method BLASTX
NCBI GI g4557060
BLAST score 623
E value 4.0e-65
Match length 123
% identity 100

NCBI Description (AC007154) putative chromosome-associated polypeptide, 5'

partial [Arabidopsis thaliana]

Seq. No. 139862

Seq. ID LIB24-075-Q1-E1-A7

Method BLASTN
NCBI GI g3869069
BLAST score 269
E value 1.0e-150
Match length 390
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 139863

Seq. ID LIB24-075-Q1-E1-B10



```
Method BLASTX
NCBI GI g3790567
BLAST score 347
E value 3.0e-33
Match length 69
% identity 97
```

NCBI Description (AF078821) RING-H2 finger protein RHA1b [Arabidopsis

thaliana]

Seq. No. 139864

Seq. ID LIB24-075-Q1-E1-D7

Method BLASTN
NCBI GI g3212846
BLAST score 149
E value 4.0e-78
Match length 390
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139865

Seq. ID LIB24-075-Q1-E1-E3

Method BLASTX
NCBI GI g586080
BLAST score 498
E value 1.0e-50
Match length 98
% identity 100

NCBI Description TUBULIN GAMMA-2 CHAIN >qi 460131 (U03990) q2-tubulin

[Arabidopsis thaliana]

Seq. No. 139866

Seq. ID LIB24-075-Q1-E1-E8

Method BLASTX
NCBI GI 94262149
BLAST score 633
E value 3.0e-66
Match length 122
% identity 99

NCBI Description (AC005275) putative xyloglucan endotransglycosylase

[Arabidopsis thaliana]

Seq. No. 139867

Seq. ID LIB24-075-Q1-E1-F9

Method BLASTX
NCBI GI g3157947
BLAST score 460
E value 5.0e-46
Match length 89
% identity 53

NCBI Description (AC002131) Similar to protein gb Z74962 from Brassica

oleracea which is similar to bacterial YRN1 and HEAHIO proteins. ESTs gb_T21954, gb_T04283, gb_Z37609, gb_N37366, gb_R90704, gb_F15500 and gb_F14353 come from this gene.

[Arabidopsis tha

Seq. No. 139868



```
Seq. ID
                  LIB24-075-Q1-E1-G10
Method
                  BLASTX
NCBI GI
                  q115783
BLAST score
                  557
E value
                  2.0e-57
Match length
                  105
% identity
                   99
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  139869
                  LIB24-075-Q1-E1-G3
Seq. ID
Method
                  BLASTX
                  q3868857
NCBI GI
BLAST score
                   530
E value
                   3.0e-54
                  101
Match length
% identity
                  100
NCBI Description (AB013886) RAV1 [Arabidopsis thaliana]
Seq. No.
                  139870
Seq. ID
                  LIB24-076-Q1-E1-B11
Method
                  BLASTX
                   q1001603
NCBI GI
BLAST score
                   160
                   6.0e-11
E value
Match length
                   101
% identity
                   37
                  (D64000) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No. Seq. ID
                   139871
                  LIB24-076-Q1-E1-B9
Method
                  BLASTN
NCBI GI
                   q4538895
BLAST score
                   103
E value
                   6.0e-51
Match length
                   228
% identity
                   88
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8
NCBI Description
                   (ESSA project)
Seq. No.
                   139872
                   LIB24-076-Q1-E1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1709970
BLAST score
                   180
                   8.0e-14
E value
```

Match length 42 % identity 86

NCBI Description 60S RIBOSOMAL PROTEIN L10A

Seq. No. 139873

Seq. ID LIB24-076-Q1-E1-D5

BLASTN Method NCBI GI g3063438



BLAST score 285 E value 1.0e-159 Match length 359 % identity 97

NCBI Description Complete sequence of Arabidopsis F22013, complete sequence

[Arabidopsis thaliana]

Seq. No. 139874

Seq. ID LIB24-076-Q1-E1-D8

Method BLASTX
NCBI GI g4006941
BLAST score 259
E value 1.0e-22
Match length 52
% identity 100

NCBI Description (AJ131391) voltage-dependent anion-selective channel

protein [Arabidopsis thaliana]

Seq. No. 139875

Seq. ID <LIB24-076-Q1-E1-F1

Method BLASTX
NCBI GI g543841
BLAST score 580
E value 4.0e-60
Match length 113
% identity 99

NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 322518 pir S28875

ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236)

ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No. 139876

Seq. ID LIB24-076-Q1-E1-F7

Method BLASTN
NCBI GI g4519191
BLAST score 333
E value 0.0e+00
Match length 414
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9P8, complete sequence

Seq. No. 139877

Seq. ID LIB24-076-Q1-E1-G7

Method BLASTN
NCBI GI g2264310
BLAST score 177
E value 7.0e-95
Match length 366
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MKP11, complete sequence [Arabidopsis thaliana]

Seq. No. 139878

Seq. ID LIB24-077-Q1-E1-A12

Method NCBI GI

BLAST score



```
Method
                  BLASTN
NCBI GI
                  g2191126
BLAST score
                  257
E value
                  1.0e-142
Match length
                  432
                  100
% identity
NCBI Description Arabidopsis thaliana BAC IG002N01
Seq. No.
                  139879
Seq. ID
                  LIB24-077-Q1-E1-D12
Method
                  BLASTX
NCBI GI
                  g3522950
BLAST score
                  600
E value
                  2.0e-62
Match length
                  131
                  88
% identity
NCBI Description
                  (AC004411) hypothetical protein [Arabidopsis thaliana]
                  139880
Seq. No.
Seq. ID
                  LIB24-077-Q1-E1-D9
Method
                  BLASTX
NCBI GI
                  q2851577
BLAST score
                  143
E value
                  8.0e-09
                  55
Match length
% identity
                  51
                  SERINE CARBOXYPEPTIDASE III PRECURSOR (CP-MIII)
NCBI Description
                  >gi_1877219_emb_CAA70817_ (Y09604) serine carboxypeptidase
                  III, CP-MIII [Hordeum vulgare]
Seq. No.
                  139881
Seq. ID
                  LIB24-077-Q1-E1-H5
Method
                  BLASTN
NCBI GI
                  g2275194
BLAST score
                  200
E value
                  1.0e-108
Match length
                  387
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC T08I13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  139882
Seq. No.
                  LIB24-078-Q1-E1-C7
Seq. ID
Method
                  BLASTN
                  g4589436
NCBI GI
BLAST score
                  434
E value
                  0.0e + 00
Match length
                  434
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MPA22, complete sequence
                  139883
Seq. No.
Seq. ID
                  LIB24-078-Q1-E1-E9
```

16946

BLASTX

394

g2244985



```
E value
                   2.0e-38
 Match length
                   73
 % identity
                   100
NCBI Description (Z97340) similarity to peroxidase [Arabidopsis thaliana]
 Seq. No.
                   139884
                   LIB24-078-Q1-E1-F11
 Seq. ID
Method
                   BLASTX
 NCBI GI
                   q2961389
 BLAST score
                   491
E value
                   1.0e-49
Match length
                   135
 % identity
 NCBI Description
                   (AL022141) purple acid phosphatase like protein
                   [Arabidopsis thaliana] >qi 4006925 emb CAB16853.1 (Z99708)
                   purple acid phosphatase like protein [Arabidopsis thaliana]
 Seq. No.
                   139885
 Seq. ID
                   LIB24-078-Q1-E1-F6
 Method
                   BLASTN
 NCBI GI
                   q2749918
 BLAST score
                   108
 E value
                   3.0e-54
 Match length
                   140
                   94
 % identity
                   Arabidopsis thaliana chromosome I BAC F3I6 genomic
 NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   139886
                   LIB24-078-Q1-E1-H5
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g1653767
 BLAST score
                   508
 E value
                   1.0e-51
 Match length
                   149
 % identity
                   62
                   (D90916) oligopeptidase A [Synechocystis sp.]
 NCBI Description
 Seq. No.
                   139887
                   LIB24-078-Q1-E1-H8
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g3236261
 BLAST score
                   420
                   3.0e-41
 E value
 Match length
                   146
                   49
 % identity
                   (AC004684) putative zinc finger protein [Arabidopsis
 NCBI Description
                   thaliana]
                   139888
 Seq. No.
 Seq. ID
                   LIB24-079-Q1-E1-B11
                   BLASTX
 Method
 NCBI GI
                   g4455185
```

NCBI GI g4455185
BLAST score 204
E value 2.0e-16
Match length 76
% identity 58



NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 139889

Seq. ID LIB24-079-Q1-E1-C6

Method BLASTN
NCBI GI 94756963
BLAST score 134
E value 2.0e-69
Match length 205
% identity 93

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23

(ESSA project)

Seq. No. 139890

Seq. ID LIB24-079-Q1-E1-D3

Method BLASTX
NCBI GI g1769568
BLAST score 519
E value 6.0e-53
Match length 103
% identity 95

NCBI Description (U82202) fumarase; fumarate hydratase [Arabidopsis

thaliana]

Seq. No. 139891

Seq. ID LIB24-079-Q1-E1-E11

Method BLASTN
NCBI GI g4757397
BLAST score 372
E value 0.0e+00
Match length 372
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MBG14, complete sequence

Seq. No. 139892

Seq. ID LIB24-079-Q1-E1-E9

Method BLASTX
NCBI GI g3688182
BLAST score 643
E value 1.0e-67
Match length 123
% identity 100

NCBI Description (AL031804) P-Protein - like protein [Arabidopsis thaliana]

Seq. No. 139893

Seq. ID LIB24-079-Q1-E1-G5

Method BLASTX
NCBI GI g4512698
BLAST score 414
E value 4.0e-41
Match length 81
% identity 94

NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No. 139894

Seq. ID LIB24-079-Q1-E1-G6

```
Method
NCBI GI
                  a2660677
BLAST score
                  752
E value
                  3.0e-80
Match length
                  142
% identity
                  100
NCBI Description
                  (AC002342) unknown protein [Arabidopsis thaliana]
Seq. No.
                  139895
                  LIB24-080-Q1-E1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539944
BLAST score
                  201
                  1.0e-15
E value
Match length
                  61
% identity
                  64
NCBI Description
                  (AF133841) aldose reductase ALDRXV4 [Xerophyta viscosa]
Seq. No.
                  139896
                  LIB24-080-Q1-E1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3335347
BLAST score
                  335
E value
                  1.0e-31
Match length
                  88
% identity
                  62
                  (AC004512) Contains similarity to ARI, RING finger protein
NCBI Description
                  gb X98309 from Drosophila melanogaster. ESTs gb T44383,
                  gb W43120, gb N65868, gb H36013, gb AA042241, gb T76869 and
                  gb AA042359 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  139897
Seq. ID
                  LIB24-081-Q1-E1-A10
Method
                  BLASTX
                  g1399380
NCBI GI
BLAST score
                  421
E value
                  1.0e-41
Match length
                  94
% identity
                  83
NCBI Description
                  (U43683) S-adenosyl-L-methionine:delta24-sterol-C-
                  methyltransferase [Glycine max]
Seq. No.
                  139898
Seq. ID
                  LIB24-081-Q1-E1-A6
Method
                  BLASTX
NCBI GI
                  q4835245
BLAST score
                  151
```

Method BLASTX
NCBI GI g4835245
BLAST score 151
E value 4.0e-10
Match length 84
% identity 33

NCBI Description (AL049862) putative mitochondrial protein [Arabidopsis

thaliana]

Seq. No. 139899

Seq. ID LIB24-081-Q1-E1-C9

Method BLASTX NCBI GI g119194



```
BLAST score
                    3.0e-44
E value
Match length
                    96
% identity
                    88
NCBI Description
                    ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
                    >gi_81607 pir S09152 translation elongation factor Tu
                    precursor, chloroplast - Arabidopsis thaliana >gi_22565_emb_CAA36498_ (X52256) elongation factor Tu precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A
                    elongation factor Tu [Arabidopsis thaliana]
Seq. No.
                    139900
Seq. ID
                    LIB24-081-Q1-E1-D10
Method
                    BLASTN
NCBI GI
                    g3928542
BLAST score
                    85
E value
                    4.0e-40
Match length
                    249
% identity
                    Arabidopsis thaliana mRNA for UDP-glucose
NCBI Description
                    glucosyltransferase, complete cds
Seq. No.
                    139901
Seq. ID
                    LIB24-081-Q1-E1-F5
Method
                    BLASTN
NCBI GI
                    q3402671
BLAST score
                    133
E value
                    1.0e-68
Match length
                    392
                    100
% identity
                    Arabidopsis thaliana chromosome II BAC T16B24 genomic
NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
                    139902
Seq. No.
Seq. ID
                    LIB24-081-Q1-E1-F7
Method
                    BLASTX
NCBI GI
                    g3335371
BLAST score
                    657
E value
                    4.0e-69
Match length
                    142
% identity
                    91
                    (AC003028) putative ethylene-inducible protein [Arabidopsis
NCBI Description
                    thaliana]
                    139903
Seq. No.
Seq. ID
                    LIB24-081-Q1-E1-G2
Method
                    BLASTX
NCBI GI
                    g2632254
BLAST score
                    283
                    9.0e-26
E value
```

72 Match length 76 % identity

NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.

139904

Seq. ID

LIB24-081-Q1-E1-G3

Method

BLASTX

```
NCBI GI
                  q2832679
BLAST score
                  427
                  4.0e-42
E value
                  83
Match length
                  100
% identity
                  (AL021712) putative protein [Arabidopsis thaliana]
NCBI Description
                  139905
Seq. No.
                  LIB24-081-Q1-E1-G9
Seq. ID
Method
                  BLASTX
                  g1931642
NCBI GI
BLAST score
                  756
E value
                  1.0e-80
Match length
                  144
                  100
% identity
                  (U95973) Ser/Thr protein kinase isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  139906
                  LIB24-082-Q1-E1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263795
BLAST score
                  166
E value
                  1.0e-11
Match length
                  48
% identity
                  60
                  (AC006068) putative glucosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  139907
Seq. No.
Seq. ID
                  LIB24-082-Q1-E1-C11
Method
                  BLASTN
NCBI GI
                  g2062691
BLAST score
                  33
                  7.0e-09
E value
Match length
                  58
% identity
                  48
NCBI Description Human sodium phosphate transporter (NPT4) mRNA, complete
                  cds
Seq. No.
                  139908
Seq. ID
                  LIB24-082-Q1-E1-C2
Method
                  BLASTN
NCBI GI
                  g2244991
BLAST score
                  96
                   4.0e-47
E value
Match length
                  124
% identity
                  94
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
                  139909
Seq. No.
Seq. ID
                  LIB24-082-Q1-E1-D3
```

Method BLASTN
NCBI GI g4584841
BLAST score 92
E value 2.0e-44



Match length 203 % identity 92

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T23E23,

complete sequence

Seq. No. 139910

Seq. ID LIB24-082-Q1-E1-D7

Method BLASTX
NCBI GI g4204274
BLAST score 211
E value 5.0e-17
Match length 39
% identity 100

NCBI Description (AC004146) ribulose bisphosphate carboxylase, small subunit

[Arabidopsis thaliana]

Seq. No. 139911

Seq. ID LIB24-082-Q1-E1-E4

Method BLASTN
NCBI GI 94220640
BLAST score 199
E value 1.0e-108
Match length 299
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MPE11, complete sequence [Arabidopsis thaliana]

Seq. No. 139912

Seq. ID LIB24-082-Q1-E1-G1

Method BLASTX
NCBI GI g135406
BLAST score 525
E value 1.0e-53
Match length 98
% identity 100

NCBI Description TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi 99768 pir A32712 tubulin

alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)

alpha-5 tubulin [Arabidopsis thaliana]

Seq. No. 139913

Seq. ID LIB24-082-Q1-E1-G10

Method BLASTN
NCBI GI g2098816
BLAST score 373
E value 0.0e+00
Match length 377
% identity 100

NCBI Description Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No. 139914

Seq. ID LIB24-082-Q1-E1-G9

Method BLASTN
NCBI GI g3236234
BLAST score 272
E value 1.0e-151
Match length 383

```
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13M22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  139915
Seq. No.
Seq. ID
                  LIB24-082-Q1-E1-H10
Method
                  BLASTX
NCBI GI
                  q4741942
BLAST score
                  400
E value
                  4.0e-39
Match length
                  103
                  81
% identity
NCBI Description
                  (AF134121) Lhca5 protein [Arabidopsis thaliana]
```

Seq. No. 139916 Seq. ID LIB24-083-Q1-E1-C4

Method BLASTX
NCBI GI g600855
BLAST score 327
E value 7.0e-31
Match length 76
% identity 84

NCBI Description (U17887) bZIP protein [Arabidopsis thaliana]

Seq. No. 139917 Seq. ID LIB24-083-Q1-E1-D6

Method BLASTX
NCBI GI 94455332
BLAST score 217
E value 4.0e-18
Match length 72
% identity 56

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 139918

Seq. ID LIB24-083-Q1-E1-E1

Method BLASTN
NCBI GI g3292807
BLAST score 270
E value 1.0e-150
Match length 274
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19

(ESSAII project)

Seq. No. 139919

Seq. ID LIB24-083-Q1-E1-E5

Method BLASTX
NCBI GI g4006867
BLAST score 320
E value 3.0e-30
Match length 64
% identity 95

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 139920

Seq. ID LIB24-083-Q1-E1-G8



```
Method
                  BLASTN
NCBI GI
                  q4220640
BLAST score
                  177
E value
                   4.0e-95
Match length
                  213
                   95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MPE11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139921
Seq. ID
                  LIB24-084-Q1-E1-C10
Method
                  BLASTN
NCBI GI
                  q4589426
BLAST score
                  175
                  1.0e-93
E value
Match length
                   403
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDE13, complete sequence
                  139922
Seq. No.
Seq. ID
                  LIB24-084-Q1-E1-D11
Method
                  BLASTN
NCBI GI
                  q4263753
BLAST score
                  81
E value
                  7.0e-38
Match length
                   220
% identity
                   98
                  Arabidopsis thaliana chromosome V map near 60.5 cM,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                   139923
Seq. No.
Seq. ID
                   LIB24-084-Q1-E1-D6
Method
                  BLASTN
NCBI GI
                   g4519194
BLAST score
                   187
                   1.0e-101
E value
                   325
Match length
% identity
                   98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHM17, complete sequence
                   139924
Seq. No.
Seq. ID
                   LIB24-084-Q1-E1-D8
                  BLASTN
Method
NCBI GI
                   g2264318
BLAST score
                   214
E value
                   1.0e-117
                   316
Match length
                   100
% identity
```

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MUP24, complete sequence [Arabidopsis thaliana]

139925 Seq. No.

Seq. ID LIB24-084-Q1-E1-F11

Method BLASTN NCBI GI g1931636



BLAST score 115 E value 4.0e-58 Match length 155 % identity 94

NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No. 139926

Seq. ID LIB24-085-Q1-E1-A4

Method BLASTX
NCBI GI g3549672
BLAST score 700
E value 4.0e-74
Match length 138
% identity 100

NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. No. 139927

Seq. ID LIB24-085-Q1-E1-B11

Method BLASTX
NCBI GI g136636
BLAST score 399
E value 7.0e-39
Match length 73
% identity 100

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -

Arabidopsis thaliana >gi 442594 pdb 1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi 2981894 pdb 2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi 431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 139928

Seq. ID LIB24-085-Q1-E1-C10

Method BLASTN
NCBI GI g4063735
BLAST score 318
E value 1.0e-179
Match length 431
% identity 68

NCBI Description Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5

cM, complete sequence [Arabidopsis thaliana]

Seq. No. 139929

Seq. ID LIB24-085-Q1-E1-C8

Method BLASTX
NCBI GI g1906830
BLAST score 744
E value 3.0e-79
Match length 147
% identity 98

NCBI Description (Y11829) heat shock protein [Arabidopsis thaliana]

Seq. No. 139930

Seq. ID LIB24-085-Q1-E1-D11



Method BLASTN NCBI GI g3128136 BLAST score 282 1.0e-157 E value Match length 417 96 % identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K1F13, complete sequence [Arabidopsis thaliana]

139931 Seq. No. LIB24-085-Q1-E1-D12 Seq. ID Method BLASTX g4507067 NCBI GI BLAST score 332 3.0e-42 E value 140 Match length % identity 62

SWI/SNF related, matrix associated, actin dependent NCBI Description

regulator of chromatin, subfamily a, member 1 >gi 134584 sp P28370 SN21 HUMAN POSSIBLE GLOBAL

TRANSCRIPTION ACTIVATOR SNF2L1 >gi_479804_pir__S35457 SNF2 protein homolog - human >gi 292496 (M88163) transcription

activator [Homo sapiens]

Seq. No. 139932

LIB24-085-Q1-E1-D2 Seq. ID

Method BLASTX g4512122 NCBI GI BLAST score 671 E value 1.0e-70 146 Match length 90 % identity

(AF131219) chorismate mutase 3 [Arabidopsis thaliana] NCBI Description

139933 Seq. No.

LIB24-085-Q1-E1-D8 Seq. ID

Method BLASTN g2980787 NCBI GI BLAST score 301 E value 1.0e-169 Match length 441 100 % identity

Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 NCBI Description

(ESSAII project)

139934 Seq. No.

LIB24-085-Q1-E1-E5 Seq. ID

Method BLASTX NCBI GI q115783 BLAST score 595 7.0e-62 E value Match length 113 % identity 99

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b bind $\overline{\text{ing}}$ protein (LHCP $\overline{\text{AB}}$ 140) [Arabidopsis

thaliana]



```
Seq. No.
                  139935
Seq. ID
                  LIB24-085-Q1-E1-E9
Method
                  BLASTN
                  q1297184
NCBI GI
                  50
BLAST score
E value
                  4.0e-19
Match length
                  392
                  98
% identity
                  Arabidopsis thaliana chromosome I cosmid g8261 DNA
NCBI Description
                  (cytosine-5-) methyltransferase, zinc finger protein 1,
                  nucleoporin 98, poly A+ RNA export protein, plasma membrane
                  ATPase 2, and serine/threonine protein kinase genes, co
                  139936
Seq. No.
                  LIB24-085-Q1-E1-F2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2894557
BLAST score
                  310
E value
                  1.0e-174
Match length
                  355
                  96
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T805
NCBI Description
                  (ESSAII project)
Seq. No.
                  139937
                  LIB24-086-Q1-E1-B12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4589440
                  138
BLAST score
                  1.0e-71
E value
                  138
Match length
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSD21, complete sequence
Seq. No.
                  139938
Seq. ID
                  LIB24-086-Q1-E1-D1
Method
                  BLASTN
NCBI GI
                  q2351066
BLAST score
                  303
E value
                  1.0e-170
Match length
                  411
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOP9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139939
Seq. ID
                  LIB24-086-Q1-E1-D12
```

Method BLASTN
NCBI GI g4455168
BLAST score 323
E value 0.0e+00
Match length 323
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10

(ESSAII project)



```
Seq. No.
                  139940
                  LIB24-086-Q1-E1-D8
Seq. ID
                  BLASTX
Method
                  g3281850
NCBI GI
                  783
BLAST score
E value
                  8.0e-84
                  150
Match length
                  99
% identity
                  (ALO31004) monogalactosyldiacylglycerol synthase - like
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  139941
                  LIB24-086-Q1-E1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3688195
BLAST score
                  367
E value
                  2.0e-35
Match length
                  98
                  42
% identity
                  (AJ010092) MAP3K beta 3 protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  139942
Seq. ID
                  LIB24-086-Q1-E1-F5
Method
                  BLASTN
NCBI GI
                  g4467094
BLAST score
                  422
E value
                  0.0e+00
Match length
                  422
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10
                   (ESSA project)
                  139943
Seq. No.
Seq. ID
                  LIB24-086-Q1-E1-H8
Method
                  BLASTN
NCBI GI
                  g4220635
BLAST score
                   45
E value
                   3.0e-16
                   215
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDB19, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139944
Seq. ID
                   LIB24-087-Q1-E1-E1
Method
                  BLASTX
NCBI GI
                   g3292821
BLAST score
                   172
                   2.0e-12
E value
Match length
                   76
% identity
                   53
                  (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
```

16958

139945

LIB24-087-Q1-E1-F3

Seq. No.

Seq. ID



```
Method
                  BLASTN
NCBI GI
                  q4678258
BLAST score
                  193
E value
                  1.0e-105
                  193
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F617
                  (ESSA project)
Seq. No.
                  139946
Seq. ID
                  LIB24-088-Q1-E1-B2
Method
                  BLASTN
NCBI GI
                  g4371278
BLAST score
                  63
                  7.0e-27
E value
Match length
                  139
                  86
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T2N18 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  139947
Seq. No.
Seq. ID
                  LIB24-088-Q1-E1-D1
Method
                  BLASTN
NCBI GI
                  g4159712
BLAST score
                  199
E value
                  1.0e-108
Match length
                  367
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MWI23, complete sequence
Seq. No.
                  139948
                  LIB24-088-Q1-E1-G6
Seq. ID
Method
                  BLASTN
                  g4757388
NCBI GI
BLAST score
                  122
E value
                  3.0e-62
                  142
Match length
% identity
                  96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  F15L12, complete sequence
Seq. No.
                  139949
Seq. ID
                  LIB24-089-Q1-E1-A1
Method
                  BLASTN
NCBI GI
                  q3763944
BLAST score
                  345
E value
                  0.0e + 00
```

Match length 345 100 % identity

Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 NCBI Description

(ESSAII project)

139950 Seq. No.

Seq. ID LIB24-089-Q1-E1-C1

Method BLASTX NCBI GI g3281866



BLAST score 635 E value 1.0e-66 Match length 126 % identity 100

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 139951

Seq. ID LIB24-089-Q1-E1-C3

Method BLASTN
NCBI GI g4510360
BLAST score 33
E value 7.0e-09
Match length 65

Match length 65 % identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic

sequence, complete sequence

Seq. No. 139952

Seq. ID LIB24-089-Q1-E1-E2

Method BLASTX
NCBI GI g2832683
BLAST score 349
E value 6.0e-33
Match length 68
% identity 100

NCBI Description (AL021712) putative protein [Arabidopsis thaliana]

Seq. No. 139953

Seq. ID LIB24-089-Q1-E1-F2

Method BLASTN
NCBI GI g3928074
BLAST score 365
E value 0.0e+00
Match length 386
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T7F6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139954

Seq. ID LIB24-089-Q1-E1-G9

Method BLASTN
NCBI GI g4544381
BLAST score 67
E value 1.0e-29
Match length 153
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC F16F14 genomic

sequence, complete sequence

Seq. No. 139955

Seq. ID LIB24-090-Q1-E1-A3

Method BLASTN
NCBI GI g3128134
BLAST score 335
E value 0.0e+00
Match length 339
% identity 100



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18G13, complete sequence [Arabidopsis thaliana]

Seq. No. 139956

LIB24-090-Q1-E1-C2 Seq. ID

Method BLASTX NCBI GI g2462929 709 BLAST score 3.0e-75 E value Match length 137 % identity 100

(Y12295) glutathione transferase [Arabidopsis thaliana] NCBI Description

Seq. No. 139957

LIB24-090-Q1-E1-E3 Seq. ID

Method BLASTX g132074 NCBI GI BLAST score 349 1.0e-33 E value Match length 70 99 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

139958 Seq. No.

LIB24-090-Q1-E1-F11 Seq. ID

Method BLASTX NCBI GI q4567271 290 BLAST score 4.0e-26 E value Match length 101 % identity 63

(AC006841) putative kinesin protein [Arabidopsis thaliana] NCBI Description

Seq. No. 139959

Seq. ID LIB24-090-Q1-E1-F12

Method BLASTN NCBI GI q2341023 BLAST score 275 E value 1.0e-153 Match length 275 100 % identity

Sequence of BAC F19P19 from Arabidopsis thaliana chromosome NCBI Description

1, complete sequence [Arabidopsis thaliana]

Seq. No. 139960

LIB24-090-Q1-E1-F2 Seq. ID

82

Method BLASTX g3152603 NCBI GI BLAST score 317 2.0e-29 E value Match length 71

% identity (AC004482) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

Seq. ID

139966

LIB24-091-Q1-E1-D8



```
Seq. No.
                   139961
Seq. ID
                  LIB24-090-Q1-E1-F4
Method
                  BLASTN
NCBI GI
                  g3449321
BLAST score
                   61
                   5.0e-26
E value
Match length
                  161
                  89
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MTG10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139962
Seq. ID
                  LIB24-090-Q1-E1-G6
Method
                  BLASTX
NCBI GI
                  g3915639
BLAST score
                   510
E value
                  7.0e-52
Match length
                  117
% identity
                  87
                  ALTERNATIVE OXIDASE 1A PRECURSOR >gi 2506083_dbj_BAA22625
NCBI Description
                   (D89875) alternative oxidase [Arabidopsis thaliana]
Seq. No.
                  139963
Seq. ID
                  LIB24-090-Q1-E1-H5
Method
                  BLASTN
NCBI GI
                  q4204173
BLAST score
                  95
E value
                  1.0e-46
Match length
                  95
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T2K10 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  139964
Seq. ID
                  LIB24-091-Q1-E1-B10
Method
                  BLASTN
NCBI GI
                  g4538990
BLAST score
                  294
E value
                  1.0e-165
Match length
                  313
                  98
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19
                  (ESSA project)
Seq. No.
                  139965
Seq. ID
                  LIB24-091-Q1-E1-C12
Method
                  BLASTX
NCBI GI
                  q2827712
BLAST score
                  645
E value
                  1.0e-67
Match length
                  122
% identity
                  100
NCBI Description
                  (AL021684) endoxyloglucan tranferase-like protein
                  [Arabidopsis thaliana]
```



```
Method
                   BLASTX
NCBI GI
                   q115767
BLAST score
                   443
                   4.0e-44
E value
Match length
                   84
% identity
                   100
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir_A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541 (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   139967
Seq. ID
                   LIB24-091-01-E1-E11
Method
                   BLASTX
NCBI GI
                   g1563719
BLAST score
                   352
E value
                   2.0e-33
Match length
                   104
% identity
                   66
NCBI Description
                   (Y08320) cyclophylin [Digitalis lanata]
Seq. No.
                   139968
Seq. ID
                   LIB24-091-Q1-E1-F12
Method
                   BLASTN
NCBI GI
                   g1877523
BLAST score
                   329
                   0.0e+00
E value
Match length
                   337
% identity
                   99
NCBI Description
                   Arabidopsis thaliana BAC T7I23, complete sequence
                   [Arabidopsis thaliana]
Seq. No.
                   139969
Seq. ID
                   LIB24-091-Q1-E1-F2
Method
                   BLASTN
NCBI GI
                   q3241927
BLAST score
                   314
                   1.0e-176
E value
Match length
                   385
% identity
                   98
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MTE17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   139970
                   LIB24-091-Q1-E1-F4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3128142
BLAST score
                   181
```

NCBI GI g312814:
BLAST score 181
E value 3.0e-97
Match length 376
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQN23, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                   139971
Seq. ID
                   LIB24-091-Q1-E1-G9
Method
                   BLASTX
NCBI GI
                   q136636
BLAST score
                   475
E value
                   8.0e-48
Match length
                   87
% identity
                   100
NCBI Description
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
                   LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                   >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 -
                   Arabidopsis thaliana >gi_442594 pdb 1AAK Ubiquitin
                   Conjugating Enzyme (E.C.\overline{6}.3.2.19) >\overline{g}i 29\overline{8}1894 pdb 2AAK
                   Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                   >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis
                   thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
                   [Arabidopsis thaliana]
Seq. No.
                   139972
                   LIB24-091-Q1-E1-H8
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4567300
BLAST score
                   124
E value
                   9.0e-64
Match length
                   124
                   100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II P1 MHK10 genomic
                   sequence, complete sequence
Seq. No.
                   139973
Seq. ID
                   LIB24-092-Q1-E1-C11
Method
                   BLASTX
NCBI GI
                   g4206206
BLAST score
                   342
                   3.0e-32
E value
Match length
                   91
                   79
% identity
NCBI Description
                   (AF071527) putative M-type thioredoxin [Arabidopsis
                   thaliana] >gi_4263039_gb_AAD15308 (AC005142) putative
                   M-type thioredoxin [Arabidopsis thaliana]
Seq. No.
                   139974
Seq. ID
                   LIB24-092-Q1-E1-C8
Method
                   BLASTN
NCBI GI
                   g3548797
BLAST score
                   39
E value
                   1.0e-13
Match length
                   39
% identity
                   100
```

NCBI Description Arabidopsis thaliana chromosome II BAC T18E12 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.

139975

Seq. ID LIB24-092-Q1-E1-D4 Method

BLASTX NCBI GI g1491712 BLAST score 254



```
E value
                   7.0e-22
Match length
                  109
% identity
                   47
NCBI Description
                  (X99961) unknown [Homo sapiens]
Seq. No.
                  139976
Seq. ID
                  LIB24-092-Q1-E1-D8
Method
                  BLASTX
NCBI GI
                  g1906830
BLAST score
                  718
E value
                  3.0e-76
Match length
                  141
% identity
                   99
NCBI Description
                  (Y11829) heat shock protein [Arabidopsis thaliana]
Seq. No.
                  139977
Seq. ID
                  LIB24-092-Q1-E1-F6
Method
                  BLASTN
NCBI GI
                  q3869074
BLAST score
                  169
                  3.0e-90
E value
Match length
                  271
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MMI9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139978
Seq. ID
                  LIB24-092-Q1-E1-G1
Method
                  BLASTX
NCBI GI
                  g4406384
BLAST score
                  369
E value
                  3.0e-35
Match length
                  70
% identity
                  100
NCBI Description (AF112303) serine acetyltransferase [Arabidopsis thaliana]
Seq. No.
                  139979
Seq. ID
                  LIB24-092-Q1-E1-H2
Method
                  BLASTX
NCBI GI
                  q3687249
BLAST score
                  467
E value
                  5.0e-47
Match length
                  98
% identity
                  96
NCBI Description
                   (AC005169) putative copia-like transposable element
                   [Arabidopsis thaliana]
Seq. No.
                  139980
Seq. ID
                  LIB24-092-Q1-E1-H5
Method
                  BLASTX
NCBI GI
                  g3258570
BLAST score
                  58
E value
                  4.0e-62
Match length
                  135
% identity
                  94
NCBI Description
                  (U89959) Unknown protein [Arabidopsis thaliana]
```



Seq. No. 139981 Seq. ID LIB24-092-Q1-E1-H6 Method BLASTN NCBI GI g2244829 BLAST score 197 1.0e-107 E value Match length 281 100 % identity Arabidopsis thaliana DNA chromosome 4, ESSA I contig NCBI Description fragment No Seq. No. 139982 Seq. ID LIB24-093-Q1-E1-A9 Method BLASTX q3688799 NCBI GI 160 BLAST score 2.0e-11 E value Match length 32 100 % identity (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis NCBI Description thaliana] Seq. No. 139983 Seq. ID LIB24-093-Q1-E1-B8 Method BLASTX NCBI GI q4539423 BLAST score 460 E value 4.0e-46 Match length 109 85 % identity (AL049171) pyrophosphate-dependent phosphofructo-1-kinase NCBI Description [Arabidopsis thaliana] Seq. No. 139984 LIB24-093-Q1-E1-B9 Seq. ID Method BLASTN NCBI GI g4432811 BLAST score 405 E value 0.0e+00Match length 405 % identity 100 Arabidopsis thaliana chromosome II BAC F16D14 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139985

Seq. ID LIB24-093-Q1-E1-C11

Method BLASTX NCBI GI q4406765 BLAST score 544 7.0e-56 E value 120 Match length 92 % identity

(AC006836) putative cold-regulated protein cor15 NCBI Description

[Arabidopsis thaliana]

139986 Seq. No.

LIB24-093-Q1-E1-C7 Seq. ID



Method BLASTN NCBI GI q4490291 BLAST score 283 E value 1.0e-158 Match length 366 97 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5

(ESSA project)

Seq. No. 139987

Seq. ID LIB24-093-Q1-E1-D12

Method BLASTX NCBI GI g4506387 BLAST score 150 1.0e-09 E value 73 Match length % identity 41

NCBI Description RAD23 (S. cerevisiae) homolog B

>gi_1709985_sp_P54727_R23B_HUMAN UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG B (HHR23B) (XP-C REPAIR COMPLEMENTING COMPLEX 58 KD PROTEIN) (P58) >gi_1082758_pir__\$44346 RAD23 protein homolog - human >gi_498148_dbj_BAA04652_ (D21090)

XP-C repair complementing protein (p58/HHR23B) [Homo

sapiens]

139988 Seq. No.

LIB24-093-Q1-E1-F11 Seq. ID

Method BLASTN NCBI GI q2245073 BLAST score 84 2.0e-39 E value 100 Match length % identity 49

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 139989

Seq. ID LIB24-093-Q1-E1-H4

Method BLASTX NCBI GI q4056433 BLAST score 178 E value 4.0e-13 Match length 54 % identity

NCBI Description (AC005990) Similar to anter-specific proline-rich protein

(CEX) gb X60376 from Brassica napus. [Arabidopsis thaliana]

Seq. No. 139990

Seq. ID LIB24-093-Q1-E1-H8

Method BLASTX NCBI GI g3860247 BLAST score 49 E value 4.0e-26 Match length 87 % identity 70

(AC005824) unknown protein [Arabidopsis thaliana] NCBI Description



```
Seq. No.
                  139991
Seq. ID
                  LIB24-094-Q1-E1-A1
Method
                  BLASTN
NCBI GI
                  q4406805
BLAST score
                  247
E value
                  1.0e-136
Match length
                  377
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T27K22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  139992
Seq. ID
                  LIB24-094-Q1-E1-B11
Method
                  BLASTN
NCBI GI
                  q4581161
BLAST score
                  202
E value
                  1.0e-110
Match length
                  387
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC T20G20 genomic
NCBI Description
                  sequence, complete sequence
                  139993
Seq. No.
Seq. ID
                  LIB24-094-Q1-E1-D3
Method
                  BLASTX
NCBI GI
                  q1621539
BLAST score
                  657
                  4.0e-69
E value
Match length
                  129
% identity
                  42
                  (U28415) annexin-like protein [Arabidopsis thaliana]
NCBI Description
                  139994
Seq. No.
Seq. ID
                  LIB24-094-Q1-E1-E11
Method
                  BLASTX
NCBI GI
                  g2497753
BLAST score
                  263
E value
                  6.0e-23
                  95
Match length
% identity
                  49
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
NCBI Description
                  >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein
                   [Prunus dulcis]
Seq. No.
                   139995
Seq. ID
                   LIB24-094-Q1-E1-G3
Method
                  BLASTX
NCBI GI
                   g3258569
BLAST score
                  569
E value
                   7.0e-59
```

Match length 119 % identity 100

NCBI Description (U89959) Similar to yeast general negative regulator of

transcription subunit 1 [Arabidopsis thaliana]

Seq. No. 139996

Seq. ID LIB24-094-Q1-E1-H7



Method BLASTX
NCBI GI g2129550
BLAST score 436
E value 3.0e-43
Match length 113
% identity 76
NCBI Description calciumArabidop
calcium>gi 8369

calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -

Arabidopsis thaliana >gi_2129554_pir__S71901

calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi 836940 (U20623) calcium-dependent protein kinase

[Arabidopsis thaliana] >gi_836944 (U20625)

calcium-dependent protein kinase [Arabidopsis thaliana]
>gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent

protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No. 139997

Seq. ID LIB24-095-Q1-E1-C1

Method BLASTN
NCBI GI g2351066
BLAST score 331
E value 0.0e+00
Match length 339
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOP9, complete sequence [Arabidopsis thaliana]

Seq. No. 139998

Seq. ID LIB24-095-Q1-E1-D10

Method BLASTX
NCBI GI g3643611
BLAST score 647
E value 5.0e-68
Match length 123
% identity 98

NCBI Description (AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No. 139999

Seq. ID LIB24-095-Q1-E1-E12

Method BLASTN
NCBI GI g4371278
BLAST score 99
E value 2.0e-48
Match length 347
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC T2N18 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140000

Seq. ID LIB24-095-Q1-E1-E7

Method BLASTN
NCBI GI g4581084
BLAST score 71
E value 9.0e-32
Match length 227
% identity 90

NCBI Description Arabidopsis thaliana chromosome I BAC T30F21 genomic

sequence, complete sequence



```
Seq. No.
                  140001
Seq. ID
                  LIB24-095-Q1-E1-F3
Method
                  BLASTX
NCBI GI
                  g1053047
BLAST score
                  267
E value
                  5.0e-24
Match length
                  54
                  98
% identity
                  (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
NCBI Description
                  histone H3 [Glycine max] >gi 1053051 (U38427) histone H3
                  [Glycine max]
                  140002
Seq. No.
                  LIB24-095-Q1-E1-F4
Seq. ID
Method
                  BLASTN
                  q4589438
NCBI GI
BLAST score
                  92
                  7.0e-45
E value
Match length
                  92
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQJ2, complete sequence
Seq. No.
                  140003
                  LIB24-095-Q1-E1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q479413
BLAST score
                  654
                  9.0e-69
E value
                  131
Match length
                  100
% identity
NCBI Description myosin-like protein - Arabidopsis thaliana
                  140004
Seq. No.
Seq. ID
                  LIB24-095-Q1-E1-H12
Method
                  BLASTN
NCBI GI
                  q3212846
BLAST score
                  68
E value
                  7.0e-30
Match length
                  132
% identity
                  88
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140005
Seq. ID
                  LIB24-095-Q1-E1-H7
Method
                  BLASTN
NCBI GI
                  q4263753
BLAST score
                  118
E value
                  6.0e-60
Match length
                  207
```

% identity NCBI Description

Arabidopsis thaliana chromosome V map near 60.5 cM,

complete sequence [Arabidopsis thaliana]

Seq. No. 140006

100



Seq. ID LIB24-096-Q1-E1-A11

Method BLASTX
NCBI GI g1171978
BLAST score 440
E value 9.0e-44
Match length 106
% identity 35

NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)

(PABP 2) >gi_304109 (L19418) poly(A)-binding protein

[Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)

poly(A)-binding protein [Arabidopsis thaliana]

Seq. No. 140007

Seq. ID LIB24-096-Q1-E1-A6

Method BLASTN
NCBI GI g2673901
BLAST score 378
E value 0.0e+00
Match length 403
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T24P15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140008

Seq. ID LIB24-096-Q1-E1-C9

Method BLASTX
NCBI GI g3062791
BLAST score 325
E value 3.0e-30
Match length 84
% identity 73

NCBI Description (AB010433) Lipid transfer protein [Brassica rapa]

Seq. No. 140009

Seq. ID LIB24-096-Q1-E1-E5

Method BLASTN
NCBI GI g4589433
BLAST score 55
E value 2.0e-22
Match length 120
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNI5, complete sequence

Seq. No. 140010

Seq. ID LIB24-096-Q1-E1-E6

Method BLASTX
NCBI GI g585536
BLAST score 615
E value 3.0e-64
Match length 111
% identity 100

NCBI Description MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)

>gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase
[Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194)

thioglucosidase [Arabidopsis thaliana]



Seq. No. 140011

Seq. ID LIB24-096-Q1-E1-G12

Method BLASTX
NCBI GI g115783
BLAST score 479
E value 2.0e-48
Match length 90
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 140012

Seq. ID LIB24-096-Q1-E1-G6

Method BLASTX
NCBI GI g2213594
BLAST score 697
E value 8.0e-74
Match length 132
% identity 100

NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No. 140013

Seq. ID LIB24-097-Q1-E1-A2

Method BLASTX
NCBI GI g2826900
BLAST score 487
E value 4.0e-49
Match length 146
% identity 68

NCBI Description (AB004461) DNA polymerase alpha catalytic subunit [Oryza

satival

Seq. No. 140014

Seq. ID LIB24-097-Q1-E1-A4

Method BLASTN
NCBI GI g3241927
BLAST score 423
E value 0.0e+00
Match length 423
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTE17, complete sequence [Arabidopsis thaliana]

Seq. No. 140015

Seq. ID LIB24-097-Q1-E1-B2

Method BLASTX
NCBI GI g3927837
BLAST score 423
E value 9.0e-42
Match length 81
% identity 100

NCBI Description (AC005727) putative core protein [Arabidopsis thaliana]

Seq. No. 140016

Method

NCBI GI



```
Seq. ID
                   LIB24-097-Q1-E1-B4
Method
                  BLASTX
NCBI GI
                   q99741
BLAST score
                   491
E value
                   1.0e-49
Match length
                   103
% identity
                   95
NCBI Description P-glycoprotein pgp1 - Arabidopsis thaliana
Seq. No.
                   140017
Seq. ID
                  LIB24-097-Q1-E1-B8
Method
                  BLASTX
NCBI GI
                   q4262228
BLAST score
                   319
E value
                   2.0e-29
Match length
                   124
                   52
% identity
NCBI Description
                  (AC006200) putative receptor protein kinase [Arabidopsis
                   thaliana]
                   140018
Seq. No.
Seq. ID
                  LIB24-097-Q1-E1-C2
Method
                  BLASTN
NCBI GI
                   q4063737
BLAST score
                   116
E value
                   5.0e-59
Match length
                   116
% identity
                   100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F24D13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   140019
Seq. ID
                   LIB24-097-Q1-E1-C6
Method
                  BLASTN
NCBI GI
                   q4741184
BLAST score
                   420
E value
                   0.0e + 00
Match length
                   420
% identity
                   100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7
                   (ESSA project)
Seq. No.
                   140020
Seq. ID
                  LIB24-097-Q1-E1-C7
Method
                  BLASTN
NCBI GI
                  g2760169
BLAST score
                   341
E value
                  0.0e + 00
Match length
                   408
                  95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFB13, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140021
Seq. ID
```

16973

LIB24-097-Q1-E1-E5

BLASTX

g1362003



BLAST score 735 E value 3.0e-78 Match length 143 % identity 99

NCBI Description protein phosphatase 2A B regulatory chain 55K - Arabidopsis

thaliana >gi_710330 (U18129) 55 kDa B regulatory subunit of

phosphatase ZA [Arabidopsis thaliana]

Seq. No. 140022

Seq. ID LIB24-097-Q1-E1-F1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36

% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 140023

Seq. ID LIB24-097-Q1-E1-F5

Method BLASTN
NCBI GI g4249393
BLAST score 292
E value 1.0e-163
Match length 394
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T9J23 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140024

Seq. ID LIB24-097-Q1-E1-F7

Method BLASTX
NCBI GI g3367534
BLAST score 629
E value 8.0e-66
Match length 143
% identity 90

NCBI Description (AC004392) Strong similarity to coatamer alpha subunit

(HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis

thaliana]

Seq. No. 140025

Seq. ID LIB24-097-Q1-E1-H6

Method BLASTX
NCBI GI g1350680
BLAST score 731
E value 9.0e-78
Match length 142
% identity 99

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 140026

Seq. ID LIB24-097-Q1-E1-H8

MethodBLASTXNCBI GIg4585981BLAST score292E value2.0e-26

% identity



```
Match length
% identity
                  88
NCBI Description
                  (AC005287) similar to Na+/H+-exchanging proteins
                  [Arabidopsis thaliana]
                  140027
Seq. No.
Seq. ID
                  LIB24-099-Q1-E1-A1
Method
                  BLASTX
NCBI GI
                  g3885340
BLAST score
                  562
E value
                  3.0e-58
Match length
                  101
% identity
                  99
                  (AC005623) unknown protein [Arabidopsis thaliana]
NCBI Description
                  140028
Seq. No.
                  LIB24-099-Q1-E1-A4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4371278
                  149
BLAST score
                  2.0e-78
E value
Match length
                  197
                  94
% identity
NCBI Description
                 Arabidopsis thaliana chromosome II BAC T2N18 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  140029
Seq. No.
                  LIB24-099-Q1-E1-C6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3241917
BLAST score
                  153
E value
                  7.0e-81
Match length
                  193
% identity
                  95
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19B1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140030
Seq. ID
                  LIB24-099-Q1-E1-F10
Method
                  BLASTN
NCBI GI
                  q4455339
BLAST score
                  46
E value
                  3.0e-17
Match length
                  85
% identity
                  95
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5
                  (ESSAII project)
Seq. No.
                  140031
Seq. ID
                  LIB24-099-Q1-E1-F3
Method
                  BLASTN
NCBI GI
                  g2924732
BLAST score
                  273
E value
                  1.0e-152
Match length
                  281
                  99
```

16975

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

Match length

% identity

123

93



MUA2, complete sequence [Arabidopsis thaliana]

```
140032
Seq. No.
Seq. ID
                  LIB24-099-Q1-E1-F5
Method
                  BLASTX
NCBI GI
                  q4567286
BLAST score
                   74
                  2.0e-15
E value
Match length
                  57
                  84
% identity
NCBI Description
                  (AC006841) putative coatomer alpha subunit [Arabidopsis
                  140033
Seq. No.
                  LIB24-099-Q1-E1-G8
Seq. ID
Method
                  BLASTX
                  g464524
NCBI GI
BLAST score
                  139
E value
                  8.0e-09
Match length
                  31
                  87
% identity
                  RAS-RELATED PROTEIN RAB-1A >gi_345404_pir__S32206 RAB1
NCBI Description
                  protein - great pond snail >gi_481217_pir__S38339 rab1
                  protein - great pond snail >gi_288934_emb_CAA51233_
                   (X72688) RAB1 [Lymnaea stagnalis]
                  140034
Seq. No.
                  LIB24-099-Q1-E1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132939
BLAST score
                   461
                   2.0e-46
E value
Match length
                   91
% identity
                   96
                   60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal
NCBI Description
                   protein L3 (ARP1) - Arabidopsis thaliana >gi_166858
                   (M32654) ribosomal protein [Arabidopsis thaliana]
                   140035
Seq. No.
Seq. ID
                  LIB24-099-Q1-E1-H12
Method
                   BLASTX
NCBI GI
                   g3702314
BLAST score
                   606
E value
                   3.0e-63
Match length
                   116
                   100
% identity
                   (AC002535) similar to SWI/SNF complex subunit BAF170
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   140036
Seq. ID
                   LIB24-100-Q1-E1-A11
Method
                  BLASTX
NCBI GI
                   g1345594
BLAST score
                   546
E value
                   4.0e-56
```





```
NCBI Description 14-3-3-LIKE PROTEIN GF14 KAPPA >gi_1022780 (U36447) GF14 Kappa isoform [Arabidopsis thaliana]
```

Seq. No. 140037

Seq. ID LIB24-100-Q1-E1-A6

Method BLASTX
NCBI GI g1903347
BLAST score 308
E value 2.0e-28
Match length 93
% identity 73

NCBI Description (AC000104) EST gb ATTS5672 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 140038

Seq. ID LIB24-100-Q1-E1-B8

Method BLASTN
NCBI GI g2760168
BLAST score 337
E value 0.0e+00
Match length 412
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MEE6, complete sequence [Arabidopsis thaliana]

Seq. No. 140039

Seq. ID LIB24-100-Q1-E1-D12

Method BLASTN

NCBI GI g4757662

BLAST score 277

E value 1.0e-154

Match length 301

% identity 98

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10B6 from

chromosome I, complete sequence

Seq. No. 140040

Seq. ID LIB24-100-Q1-E1-D6

Method BLASTN
NCBI GI 94757417
BLAST score 207
E value 1.0e-113
Match length 271
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

T30G6, complete sequence

Seq. No. 140041

Seq. ID LIB24-100-Q1-E1-F9

Method BLASTN
NCBI GI g3599967
BLAST score 254
E value 1.0e-141
Match length 254
% identity 100

NCBI Description Arabidopsis thaliana clp protease (CLP) mRNA, partial cds

NCBI Description



```
Seq. No.
                  140042
Seq. ID
                  LIB24-100-Q1-E1-G10
Method
                  BLASTN
NCBI GI
                  g2264316
BLAST score
                  65
E value
                  2.0e-28
Match length
                  77
                  96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRO11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140043
Seq. ID
                  LIB24-100-Q1-E1-G12
Method
                  BLASTX
NCBI GI
                  q2688544
BLAST score
                  201
E value
                  1.0e-15
Match length
                  101
                  39
% identity
                  (AE001163) 4-methyl-5(b-hydroxyethyl)-thiazole
NCBI Description
                  monophosphate biosynthesis protein (thiJ) [Borrelia
                  burgdorferi]
Seq. No.
                  140044
                  LIB24-101-Q1-E1-F2
Seq. ID
Method
                  BLASTX
                  a2507587
NCBI GI
                  284
BLAST score
E value
                  2.0e-25
                  57
Match length
% identity
                  88
                  METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G)
NCBI Description
                  >gi_1361998_pir__S57861 metallothionein 2a - Arabidopsis
                  thaliana >gi_555976 (U15108) metallothionein-like protein
                   [Arabidopsis thaliana] >gi_1580892_prf__2116236A
                  metallothionein 1 [Arabidopsis thaliana]
Seq. No.
                  140045
Seq. ID
                  LIB24-101-Q1-E1-G5
Method
                  BLASTX
                  q3298327
NCBI GI
BLAST score
                  345
                  7.0e-33
E value
Match length
                  71
% identity
                  100
NCBI Description
                  (AB010416) delta-VM23 [Raphanus sativus]
Seq. No.
                  140046
Seq. ID
                  LIB24-102-Q1-E1-A10
Method
                  BLASTN
NCBI GI
                  q2832639
BLAST score
                  71
                  3.0e-32
E value
Match length
                  114
% identity
                  91
```

16978

(ESSAII project)

Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12

Seq. No.

Seq. ID

140052

LIB24-102-Q1-E1-H12



```
Seq. No.
                  140047
Seq. ID
                  LIB24-102-Q1-E1-B11
Method
                  BLASTX
NCBI GI
                  g3292821
BLAST score
                  272
E value
                  5.0e-24
                  105
Match length
% identity
                  54
NCBI Description
                  (AL031018) putative protein [Arabidopsis thaliana]
Seq. No.
                  140048
Seq. ID
                  LIB24-102-Q1-E1-D4
Method
                  BLASTN
NCBI GI
                  q3540210
BLAST score
                  124
E value
                  1.0e-63
Match length
                  172
% identity
                  93
                  Arabidopsis thaliana chromosome I BAC F5A8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140049
Seq. ID
                  LIB24-102-Q1-E1-E8
Method
                  BLASTX
NCBI GI
                  q4249382
BLAST score
                  209
E value
                  9.0e-17
Match length
                  55
% identity
                  80
NCBI Description
                  (AC005966) Strong similarity to gi_3337350 F13P17.3
                  putative permease from Arabidopsis thaliana BAC
                  gb_AC004481. [Arabidopsis thaliana]
Seq. No.
                  140050
Seq. ID
                  LIB24-102-Q1-E1-F4
Method
                  BLASTX
NCBI GI
                  q1710549
BLAST score
                  277
E value
                  1.0e-24
                  51
Match length
                  98
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L39
Seq. No.
                  140051
Seq. ID
                  LIB24-102-Q1-E1-G10
Method
                  BLASTN
NCBI GI
                  g4455229
BLAST score
                  261
E value
                  1.0e-145
Match length
                  294
% identity
                  99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23
                  (ESSAII project)
```



Method BLASTX
NCBI GI g486784
BLAST score 581
E value 3.0e-60
Match length 130
% identity 27

NCBI Description Golgi-associated particle 102K chain - human

Seq. No. 140053

Seq. ID LIB24-102-Q1-E1-H8

Method BLASTN
NCBI GI g4263753
BLAST score 117
E value 4.0e-59
Match length 327
% identity 61

NCBI Description Arabidopsis thaliana chromosome V map near 60.5 cM,

complete sequence [Arabidopsis thaliana]

Seq. No. 140054

Seq. ID LIB24-103-Q1-E1-A1

Method BLASTX
NCBI GI g3850587
BLAST score 343
E value 6.0e-33
Match length 68
% identity 97

NCBI Description (AC005278) Strong similarity to gi_2244780 hypothetical

protein from Arabidopsis thaliana chromosome 4 contig

gb_Z97335. [Arabidopsis thaliana]

Seq. No. 140055

Seq. ID LIB24-103-Q1-E1-A5

Method BLASTX
NCBI GI g585421
BLAST score 524
E value 1.0e-53
Match length 97
% identity 100

NCBI Description LIPOXYGENASE, CHLOROPLAST PRECURSOR >gi 541879 pir JQ2391

lipoxygenase (EC 1.13.11.12) AtLox2 - Arabidopsis thaliana

>gi 431258 (L23968) lipoxygenase [Arabidopsis thaliana]

Seq. No. 140056

Seq. ID LIB24-103-Q1-E1-B8

Method BLASTX
NCBI GI g1669389
BLAST score 545
E value 6.0e-56
Match length 100
% identity 100

NCBI Description (U42007) actin 8 [Arabidopsis thaliana]

Seq. No. 140057

Seq. ID LIB24-103-Q1-E1-G5

Method BLASTX NCBI GI g1169599



```
BLAST score
E value
                  8.0e-35
Match length
                  87
                  80
% identity
                  OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_541883_pir__JQ2336 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CFD - Arabidopsis thaliana >gi_408481 (L22961)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi_468434_dbj_BAA05040_ (D26019) plastid fatty acid
                  desaturase [Arabidopsis thaliana] >gi_541653_dbj_BAA03106_
                  (D14007) omega-3-desaturase [Arabidopsis thaliana]
Seq. No.
                  140058
                  LIB24-103-Q1-E1-G8
Seq. ID
Method
                  BLASTX
                  g2443755
NCBI GI
BLAST score
                  573
E value
                  3.0e-59
Match length
                  125
                  83
% identity
NCBI Description (AF020433) cyclophilin [Arabidopsis thaliana]
                  140059
Seq. No.
Seq. ID
                  LIB24-104-Q1-E2-A11
Method
                  BLASTX
                  g267073
NCBI GI
BLAST score
                  144
                  1.0e-09
E value
Match length
                  29
% identity
                  86
                  TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin
NCBI Description
                  beta chain - Arabidopsis thaliana >gi_166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
Seq. No.
                  140060
Seq. ID
                  LIB24-104-Q1-E2-C7
Method
                  BLASTX
NCBI GI
                  g3337366
BLAST score
                  469
                  4.0e-47
E value
Match length
                  121
% identity
                  42
NCBI Description
                  (AC004481) unknown protein [Arabidopsis thaliana]
Seq. No.
                  140061
                  LIB24-104-Q1-E2-D5
Seq. ID
Method
                  BLASTN
                  q1905875
NCBI GI
BLAST score
                  96
                  4.0e-47
E value
                  96
```

Match length % identity 100

Arabidopsis thaliana biotin carboxylase subunit (CAC2) NCBI Description

mRNA, complete cds

Seq. No. 140062

NCBI GI BLAST score



```
Seq. ID
                  LIB24-104-Q1-E2-F10
Method
                  BLASTX
NCBI GI
                  q4510346
BLAST score
                  400
E value
                  5.0e-39
Match length
                  124
% identity
                   62
                  (AC006921) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  140063
Seq. ID
                  LIB24-106-Q1-E1-B12
Method
                  BLASTN
NCBI GI
                  q3176694
BLAST score
                  225
E value
                   1.0e-123
Match length
                   368
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T14N5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  140064
Seq. No.
Seq. ID
                  LIB24-106-Q1-E1-C10
Method
                  BLASTX
                  q4589965
NCBI GI
BLAST score
                  503
                  5.0e-51
E value
Match length
                  100
                   100
% identity
NCBI Description
                  (AC007169) putative glyoxalase II [Arabidopsis thaliana]
Seq. No.
                   140065
Seq. ID
                   LIB24-106-Q1-E1-D12
Method
                  BLASTX
NCBI GI
                   g2244904
BLAST score
                   166
                   1.0e-11
E value
Match length
                   139
% identity
NCBI Description
                   (Z97339) similar to hypothetical protein C02F5.7 - Caenorha
                   [Arabidopsis thaliana]
                   140066
Seq. No.
Seq. ID
                   LIB24-106-Q1-E1-E1
Method
                  BLASTN
                   g2264318
NCBI GI
BLAST score
                   387
E value
                  0.0e + 00
Match length
                   387
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUP24, complete sequence [Arabidopsis thaliana]
                  140067
Seq. No.
Seq. ID
                  LIB24-106-Q1-E1-E5
                  BLASTN
Method
```

16982

g4159706



```
1.0e-57
E value
Match length
                  184
% identity
                   97
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGL6, complete sequence
                  140068
Seq. No.
Seq. ID
                  LIB24-106-Q1-E1-F1
Method
                  BLASTX
NCBI GI
                  g3395588
BLAST score
                  149
E value
                   5.0e-10
Match length
                   58
% identity
                   45
NCBI Description
                   (AL031179) serine-threonine protein phosphatase
                   [Schizosaccharomyces pombe]
Seq. No.
                   140069
Seq. ID
                  LIB24-106-Q1-E1-F4
Method
                  BLASTN
NCBI GI
                  g3236479
BLAST score
                  245
E value
                  1.0e-135
Match length
                   302
% identity
                   95
NCBI Description
                  Arabidopsis thaliana BAC F9H3, from chromosome IV near 18.8
                  cM, complete sequence
                  140070
Seq. No.
Seq. ID
                  LIB24-106-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                  g4510424
BLAST score
                  512
E value
                   4.0e-52
Match length
                  99
                  100
% identity
                  (AC006929) putative carboxypeptidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  140071
Seq. ID
                  LIB24-107-Q1-E1-A10
Method
                  BLASTX
NCBI GI
                  g4539383
BLAST score
                  474
E value
                  7.0e-48
                  93
Match length
                  97
% identity
                   (AL035526) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                  140072
Seq. No.
Seq. ID
                  LIB24-107-Q1-E1-B12
Method
                  BLASTN
NCBI GI
                  g2245073
```

Method BLASTN
NCBI GI g2245073
BLAST score 173
E value 1.0e-92
Match length 258
% identity 100



NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 140073

Seq. ID LIB24-107-Q1-E1-C9

Method BLASTX
NCBI GI g4539314
BLAST score 251
E value 1.0e-21
Match length 114
% identity 43

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 140074

Seq. ID LIB24-107-Q1-E1-D7

Method BLASTX
NCBI GI g2443890
BLAST score 354
E value 1.0e-33
Match length 125
% identity 58

NCBI Description (AC002294) similar to NAM (gp_X92205_1321924) and CUC2

(gp_AB002560_1944132) proteins [Arabidopsis thaliana]

Seq. No. 140075

Seq. ID LIB24-107-Q1-E1-E8

Method BLASTX
NCBI GI g4049351
BLAST score 515
E value 1.0e-52
Match length 96
% identity 99

NCBI Description (AL034567) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 140076

Seq. ID LIB24-107-Q1-E1-F12

Method BLASTN
NCBI GI g4263586
BLAST score 269
E value 1.0e-150
Match length 342
% identity 91

NCBI Description Arabidopsis thaliana chromosome 1 BAC F28K20 sequence,

complete sequence

Seq. No. 140077

Seq. ID LIB24-107-Q1-E1-G11

Method BLASTN
NCBI GI g2570223
BLAST score 160
E value 9.0e-85
Match length 368
% identity 98

NCBI Description Arabidopsis thaliana chromosome 1 BAC F20D22 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 140078



```
Seq. ID
                  LIB24-107-Q1-E1-G6
Method
                  BLASTN
NCBI GI
                  q3738275
BLAST score
                  188
E value
                  1.0e-101
Match length
                  352
% identity
                  Arabidopsis thaliana chromosome II BAC F17A22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  140079
Seq. No.
Seq. ID
                  LIB24-107-Q1-E1-H12
Method
                  BLASTX
NCBI GI
                  q3149952
BLAST score
                  491
E value
                  1.0e-49
Match length
                  126
% identity
                  77
                  (AB010259) DRH1 [Arabidopsis thaliana]
NCBI Description
                  140080
Seq. No.
                  LIB24-108-Q1-E1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4159705
                  300
BLAST score
                  1.0e-168
E value
Match length
                  382
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGD8, complete sequence
                  140081
Seq. No.
                  LIB24-108-Q1-E1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4580454
BLAST score
                  308
E value
                  1.0e-173
Match length
                  312
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T2G17 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  140082
Seq. ID
                  LIB24-108-Q1-E1-F12
Method
                  BLASTN
NCBI GI
                  g2564051
BLAST score
                  98
E value
                  2.0e-48
Match length
                  98
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MWD9, complete sequence [Arabidopsis thaliana]
```

Seq. No. 140083

Seq. ID LIB24-108-Q1-E1-H1

Method BLASTX NCBI GI g4587549



BLAST score 363 E value 1.0e-34 Match length 75 % identity 84

NCBI Description (AC006577) Similar to gb U55861 RNA binding protein

nucleolysin (TIAR) from Mus musculus and contains several PF_00076 RNA recognition motif domains. ESTs gb_T21032 and

gb T44127 come from this gene. [Arabidopsis t

Seq. No. 140084

Seq. ID LIB24-109-Q1-E1-B10

Method BLASTN
NCBI GI g3335356
BLAST score 366
E value 0.0e+00
Match length 404
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F16M14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140085

Seq. ID LIB24-109-Q1-E1-B3

Method BLASTX
NCBI GI g4006880
BLAST score 435
E value 3.0e-43
Match length 100
% identity 87

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 140086

Seq. ID LIB24-109-Q1-E1-C1

Method BLASTN
NCBI GI g4519194
BLAST score 145
E value 4.0e-76
Match length 193
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MHM17, complete sequence

Seq. No. 140087

Seq. ID LIB24-109-Q1-E1-E10

Method BLASTX
NCBI GI g3522948
BLAST score 682
E value 5.0e-72
Match length 137
% identity 92

NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No. 140088

Seq. ID LIB24-109-Q1-E1-E12

Method BLASTX
NCBI GI g115783
BLAST score 598
E value 3.0e-62



Match length 113 % identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 140089

Seq. ID LIB24-109-Q1-E1-E9

Method BLASTX
NCBI GI g818849
BLAST score 230
E value 2.0e-19
Match length 77
% identity 52

NCBI Description (U25430) nucleotide pyrophosphatase precursor [Oryza

sativa]

Seq. No. 140090

Seq. ID LIB24-109-Q1-E1-F1

Method BLASTN
NCBI GI g4519197
BLAST score 219
E value 1.0e-120
Match length 235
% identity 51

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MTC11, complete sequence

Seq. No. 140091

Seq. ID LIB24-109-Q1-E1-F10

Method BLASTN
NCBI GI g4454004
BLAST score 124
E value 2.0e-63
Match length 128
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6

(ESSAII project)

Seq. No. 140092

Seq. ID LIB24-109-Q1-E1-F12

Method BLASTN
NCBI GI g3831448
BLAST score 414
E value 0.0e+00
Match length 414
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T32F6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140093

Seq. ID LIB24-109-Q1-E1-F6

Method BLASTX
NCBI GI g4539383
BLAST score 191
E value 2.0e-14

% identity

71

NCBI Description beta-glucosidase (EC 3.2.1.21) - rape



```
Match length
% identity
                  29
NCBI Description
                  (AL035526) putative protein (fragment) [Arabidopsis
                  thaliana]
                  140094
Seq. No.
                  LIB24-109-Q1-E1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4678280
BLAST score
                  263
                  7.0e-23
E value
                  140
Match length
% identity
                  41
NCBI Description
                  (AL049660) zinc finger-like protein [Arabidopsis thaliana]
                  140095
Seq. No.
                  LIB24-109-Q1-E1-G5
Seq. ID
Method
                  BLASTN
                  g3212846
NCBI GI
BLAST score
                  294
                  1.0e-164
E value
                  437
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140096
                  LIB24-109-Q1-E1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2494125
BLAST score
                  702
E value
                  2.0e-74
Match length
                  139
                  100
% identity
NCBI Description
                  (AC002376) Strong similarity to Cucumis acetyl-CoA
                  acyltransferase (gb_D70895). [Arabidopsis thaliana]
                  140097
Seq. No.
Seq. ID
                  LIB24-110-Q1-E1-A7
Method
                  BLASTN
NCBI GI
                  g4519193
BLAST score
                  212
E value
                  1.0e-116
Match length
                  415
% identity
                  51
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDC11, complete sequence
Seq. No.
                  140098
Seq. ID
                  LIB24-110-Q1-E1-A9
Method
                  BLASTX
NCBI GI
                  q1076442
BLAST score
                  271
                  5.0e-24
E value
Match length
                  68
```



>gi_757740_emb_CAA57913_ (X82577) beta-glucosidase [Brassica napus]

140099 Seq. No. Seq. ID

LIB24-110-Q1-E1-B7

Method BLASTX NCBI GI q3395426 459 BLAST score 6.0e-46 E value 102 Match length % identity 86

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

140100 Seq. No.

LIB24-110-Q1-E1-D4 Seq. ID

Method BLASTN q4581103 NCBI GI BLAST score 67 3.0e-29 E value 67 Match length

% identity Arabidopsis thaliana chromosome II BAC T24I21 genomic NCBI Description

sequence, complete sequence

Seq. No. 140101

Seq. ID LIB24-110-Q1-E1-F10

100

Method BLASTN NCBI GI g2264313 BLAST score 34 E value 2.0e-09 110 Match length 83 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MOP10, complete sequence [Arabidopsis thaliana]

Seq. No. 140102

Seq. ID LIB24-110-Q1-E1-F8

Method BLASTX NCBI GI q4204257 BLAST score 438 E value 2.0e-43 Match length 97 % identity 82

NCBI Description (AC005223) 5493 [Arabidopsis thaliana]

Seq. No. 140103

Seq. ID LIB24-110-Q1-E1-H11

Method BLASTN NCBI GI g3241922 BLAST score 120 E value 7.0e-61 374 Match length % identity 95

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MLM24, complete sequence [Arabidopsis thaliana]

Seq. No. 140104

Seq. ID

Method



```
LIB24-110-Q1-E1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006856
BLAST score
                  565
                  3.0e-58
E value
Match length
                  146
                  77
% identity
                  (Z99707) receptor kinase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  140105
Seq. No.
Seq. ID
                  LIB24-111-Q1-E1-B7
Method
                  BLASTX
NCBI GI
                  q4415914
BLAST score
                  79
E value
                  6.0e-18
                  139
Match length
                  45
% identity
                  (AC006282) unknown protein [Arabidopsis thaliana]
NCBI Description
                  140106
Seq. No.
                  LIB24-111-Q1-E1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914658
BLAST score
                  595
                  8.0e-62
E value
Match length
                  143
                  83
% identity
                  50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_1694974_emb_CAA70851_ (Y09635) plastid ribosomal
                  protein [Arabidopsis thaliana]
Seq. No.
                  140107
Seq. ID
                  LIB24-111-Q1-E1-B9
Method
                  BLASTN
NCBI GI
                  g4589439
BLAST score
                  309
E value
                  1.0e-173
Match length
                  454
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQM1, complete sequence
Seq. No.
                  140108
Seq. ID
                  LIB24-111-Q1-E1-C6
Method
                  BLASTN
NCBI GI
                  g3980374
BLAST score
                  155
                  1.0e-81
E value
Match length
                  414
% identity
                  98
                  Arabidopsis thaliana chromosome II BAC F16P2 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140109
```

16990

LIB24-111-Q1-E1-C7

BLASTX

BLAST score

E value

536

5.0e-55



```
a4406819
NCBI GI
BLAST score
                  321
                  1.0e-29
E value
Match length
                  144
                  49
% identity
NCBI Description
                  (AC006201) unknown protein [Arabidopsis thaliana]
                  140110
Seq. No.
Seq. ID
                  LIB24-111-Q1-E1-C8
Method
                  BLASTN
NCBI GI
                  g2459406
BLAST score
                  136
                  9.0e-71
E value
Match length
                  176
% identity
                  95
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F4P9 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140111
Seq. ID
                  LIB24-111-Q1-E1-D11
Method
                  BLASTN
NCBI GI
                  g2760173
BLAST score
                  293
E value
                  1.0e-164
Match length
                  409
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MYH19, complete sequence [Arabidopsis thaliana]
                  140112
Seq. No.
Seq. ID
                  LIB24-111-Q1-E1-F11
                  BLASTN
Method
NCBI GI
                  q4028969
BLAST score
                  250
E value
                  1.0e-138
                  420
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana pollenless3 (178) gene, complete cds;
                  beta-9 tubulin (TUB9) gene, partial cds; and unknown gene
Seq. No.
                  140113
Seq. ID
                  LIB24-111-Q1-E1-F12
Method
                  BLASTX
NCBI GI
                  g3395443
BLAST score
                  357
E value
                  6.0e-34
Match length
                  87
% identity
                  84
NCBI Description
                  (AC004683) putative ammonium transporter, 3' partial
                   [Arabidopsis thaliana]
Seq. No.
                  140114
Seq. ID
                  LIB24-111-Q1-E1-F2
Method
                  BLASTX
NCBI GI
                  g2827621
```



```
Match length
% identity
                  90
NCBI Description
                  (AL021636) putative protein [Arabidopsis thaliana]
Seq. No.
                  140115
Seq. ID
                  LIB24-111-Q1-E1-F6
Method
                  BLASTN
NCBI GI
                  q4325336
BLAST score
                  389
E value
                  0.0e+00
Match length
                  442
% identity
                  99
NCBI Description Arabidopsis thaliana BAC F15P23
Seq. No.
                  140116
Seq. ID
                  LIB24-111-Q1-E1-G10
Method
                  BLASTX
NCBI GI
                  q3881133
BLAST score
                  178
E value
                  6.0e-13
Match length
                  123
                  28
% identity
NCBI Description
                  (Z99278) similar to WD domain, G-beta repeats (4 domains)
                  [Caenorhabditis elegans]
Seq. No.
                  140117
Seq. ID
                  LIB24-111-Q1-E1-H3
Method
                  BLASTX
NCBI GI
                  g1345595
BLAST score
                  598
E value
                  3.0e-62
Match length
                  122
% identity
                  100
NCBI Description
                  14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1)
                  >gi_1084332_pir__S53727 14-3-3-like protein (ATF1) -
                  Arabidopsis thaliana >gi_953221 (U02565) 14-3-3-like
                  protein 1 [Arabidopsis thaliana] >gi 1549404 (U68545) GF14
                  lambda [Arabidopsis thaliana]
Seq. No.
                  140118
Seq. ID
                  LIB24-112-01-E1-B5
Method
                  BLASTX
NCBI GI
                  g1170503
BLAST score
                  568
E value
                  1.0e-58
Match length
                  109
% identity
                  100
NCBI Description
                  EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
```

>gi 322503 pir JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554 emb CAA46188 (X65052) eukaryotic translation initiation factor 4A-1

[Arabidopsis thaliana]

Seq. No. 140119

Seq. ID LIB24-112-Q1-E1-B7

Method BLASTN NCBI GI g16353



BLAST score 253 E value 1.0e-140 Match length 253 % identity 100

NCBI Description A.thaliana kin2 gene

Seq. No. 140120

Seq. ID LIB24-112-Q1-E1-C4

Method BLASTX
NCBI GI g2635703
BLAST score 290
E value 4.0e-26
Match length 135
% identity 50

NCBI Description (Z99120) similar to hypothetical proteins [Bacillus

subtilis]

Seq. No. 140121

Seq. ID LIB24-112-Q1-E1-D1

Method BLASTN
NCBI GI g3510347
BLAST score 387
E value 0.0e+00
Match length 387
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No. 140122

Seq. ID LIB24-112-Q1-E1-D11

Method BLASTN
NCBI GI g2564050
BLAST score 140
E value 8.0e-73
Match length 312
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUA22, complete sequence [Arabidopsis thaliana]

Seq. No. 140123

Seq. ID LIB24-112-Q1-E1-E12

Method BLASTN
NCBI GI g3152947
BLAST score 115
E value 3.0e-58
Match length 139
% identity 96

NCBI Description Arabidopsis thaliana mRNA for polygalacturonase

Seq. No. 140124

Seq. ID LIB24-112-Q1-E1-E3

Method BLASTN
NCBI GI g2924651
BLAST score 334
E value 0.0e+00
Match length 398
% identity 100



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No. 140125

Seq. ID LIB24-112-Q1-E1-E4

Method BLASTN
NCBI GI g710625
BLAST score 380
E value 0.0e+00
Match length 401
% identity 98

NCBI Description Arabidopsis thaliana mRNA for ERD15 protein, complete cds

Seq. No. 140126

Seq. ID LIB24-112-Q1-E1-F5

Method BLASTN
NCBI GI g2264321
BLAST score 398
E value 0.0e+00
Match length 398
% identity 33

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXM12, complete sequence [Arabidopsis thaliana]

Seq. No. 140127

Seq. ID LIB24-113-Q1-E1-C6

Method BLASTX
NCBI GI g280386
BLAST score 479
E value 3.0e-48
Match length 98
% identity 98

NCBI Description ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana

>gi_166930 (J05507) ubiquitin extension protein (UBQ1)
[Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin

extension protein (UBQ2) [Ārabidopsis thaliana] >gi 4678227 gb AAD26972.1 AC007135_8 (AC007135)

ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]

Seq. No. 140128

Seq. ID LIB24-113-Q1-E1-D9

Method BLASTN
NCBI GI g4584841
BLAST score 246
E value 1.0e-136
Match length 246
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T23E23,

complete sequence

Seq. No. 140129

Seq. ID LIB24-113-Q1-E1-F7

Method BLASTX
NCBI GI g3549654
BLAST score 263
E value 6.0e-23
Match length 141



```
% identity
                  (AL031394) metal-transporting P-type ATPase (fragment)
NCBI Description
                  [Arabidopsis thaliana]
                  140130
Seq. No.
                  LIB24-113-Q1-E1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2832629
                  295
BLAST score
                  8.0e-27
E value
Match length
                  111
% identity
                  45
                  (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis
NCBI Description
                  thaliana]
                  140131
Seq. No.
                  LIB24-113-Q1-E1-H1
Seq. ID
                  BLASTN
Method
                  q3449333
NCBI GI
                  223
BLAST score
                  1.0e-122
E value
                  227
Match length
                  52
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXF12, complete sequence [Arabidopsis thaliana]
                  140132
Seq. No.
                  LIB24-113-Q1-E1-H3
Seq. ID
Method
                  BLASTX
                  g4309728
NCBI GI
BLAST score
                  379
                  2.0e-36
E value
Match length
                  109
                  72
% identity
                  (ACO06439) putative ADP-ribosylation factor [Arabidopsis
NCBI Description
                  thaliana]
                  140133
Seq. No.
                  LIB24-114-Q1-E1-A4
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2505873
BLAST score
                  71
E value
                  1.0e-31
Match length
                  96
                  100
% identity
NCBI Description Arabidopsis thaliana DNA, 40 kb surrounding ACS1 locus
                   140134
Seq. No.
                  LIB24-114-Q1-E1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                   g972918
BLAST score
                   211
E value
                   1.0e-115
                   231
Match length
% identity
NCBI Description Arabidopsis thaliana IAA8 (IAA8) gene complete cds
```



```
Seq. No.
                   140135
                   LIB24-114-Q1-E1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4249386
                   193
BLAST score
                   5.0e-15
E value
                   37
Match length
                   100
% identity
                   (AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1
NCBI Description
                   from Arabidopsis thaliana. EST gb_H37393 comes from this
                   gene. [Arabidopsis thaliana]
                   140136
Seq. No.
                   LIB24-114-Q1-E1-E1
Seq. ID
Method
                   BLASTX
                   g3851584
NCBI GI
BLAST score
                   260
                   1.0e-22
E value
Match length
                   61
                   84
 % identity
                   (AF092563) chromosome-associated protein-E [Homo sapiens]
NCBI Description
 Seq. No.
                   140137
                   LIB24-114-Q1-E1-H11
 Seq. ID
Method
                   BLASTX
                   g464621
NCBI GI
 BLAST score
                   408
                   4.0e-40
 E value
Match length
                   97
                   79
 % identity
                   60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586
 NCBI Description
                   ribosomal protein ML16 - common ice plant
                   >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                    [Mesembryanthemum crystallinum]
                   140138
 Seq. No.
                   LIB24-115-Q1-E1-A11
 Seq. ID
 Method
                   BLASTX
                   q2880048
 NCBI GI
 BLAST score
                   644
                   1.0e-67
 E value
 Match length
                   122
 % identity
                   (AC002340) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   140139
 Seq. No.
                   LIB24-115-Q1-E1-A5
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q99688
                   690
 BLAST score
 E value
                    5.0e-73
                   133

    Match length
```

100 % identity

NCBI Description translation elongation factor eEF-1 alpha chain (gene A4) -

Arabidopsis thaliana >gi 295789 emb CAA34456 (X16432)

elongation factor 1-alpha [Arabidopsis thaliana]



```
140140
Seq. No.
Seq. ID
                  LIB24-115-Q1-E1-A7
Method
                  BLASTX
NCBI GI
                  q4406756
                  657
BLAST score
                  4.0e-69
E value
Match length
                  129
% identity
                  100
                  (AC006836) putative integral membrane protein A3
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  140141
Seq. ID
                  LIB24-115-Q1-E1-A8
Method
                  BLASTN
                  q3789706
NCBI GI
                  333
BLAST score
                  0.0e+00
E value
Match length
                  341
% identity
                  99
                  Arabidopsis thaliana chromosome 1 BAC F15K9 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  140142
Seq. No.
Seq. ID
                  LIB24-115-Q1-E1-A9
Method
                  BLASTN
NCBI GI
                  q166589
BLAST score
                   287
                  1.0e-160
E value
                   303
Match length
% identity
                   99
                  Arabidopsis thaliana transcription factor (AGL2) mRNA,
NCBI Description
                  complete cds
Seq. No.
                   140143
                  LIB24-115-Q1-E1-C1
Seq. ID
                  BLASTN
Method
NCBI GI
                   q3292807
BLAST score
                   211
                   1.0e-115
E value
Match length
                   369
                   100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19
NCBI Description
                   (ESSAII project)
Seq. No.
                   140144
                   LIB24-115-Q1-E1-D12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4662609
BLAST score
                   153
E value
                   2.0e-80
Match length
                   427
```

complete sequence

% identity 🚁

Seq. No.

NCBI Description

Seq. ID LIB24-115-Q1-E1-D8

99

140145

16997

Genomic sequence for Arabidopsis thaliana BAC F10A5,

Seq. No.

140150



```
Method
                   BLASTX
NCBI GI
                   g115767
BLAST score
                   317
                   1.0e-29
E value
Match length
                   65
                   94
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi_81603_pir_A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   140146
                   LIB24-115-Q1-E1-F4
Seq. ID
                   BLASTN
Method
                   g2435510
NCBI GI
BLAST score
                   186
                   1.0e-100
E value
                   194
Match length
                   99
% identity
NCBI Description Arabidopsis thaliana BAC TM017A05
Seq. No.
                   140147
                   LIB24-115-Q1-E1-F5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2864607
BLAST score
                   260
E value
                   1.0e-144
                   356
Match length
                   100
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
NCBI Description
                    (ESSAII project)
Seq. No.
                   140148
                   LIB24-115-Q1-E1-F9
Seq. ID
Method
                   BLASTN
NCBI GI
                    q3985958
BLAST score
                    290
E value
                    1.0e-162
Match length
                    358
                    94
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MZN1, complete sequence [Arabidopsis thaliana]
                    140149
Seq. No.
                    LIB24-115-Q1-E1-G10
Seq. ID
Method
                    BLASTX
                    g1762935
NCBI GI
BLAST score
                    199
                    5.0e-16
E value
                    45
Match length
% identity
                   (U66264) ubiquitin [Nicotiana tabacum]
NCBI Description
```



```
LIB24-115-Q1-E1-G5
Seq. ID
Method
                  BLASTN
                  g3869074
NCBI GI
                  129
BLAST score
                  2.0e-66
E value
                  249
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MMI9, complete sequence [Arabidopsis thaliana]
                  140151
Seq. No.
                  LIB24-116-Q1-E1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4538963
                  271
BLAST score
                  3.0e-24
E value
                  53
Match length
                  100
% identity
                  (AL049488) chlorophyll a/b-binding protein-like
NCBI Description
                  [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129_1
                   (AF134129) Lhcb5 protein [Arabidopsis thaliana]
                  140152
Seq. No.
                  LIB24-116-Q1-E1-A8
Seq. ID
Method
                  BLASTN
                  g2244747
NCBI GI
                  205
BLAST score
                  1.0e-111
E value
                  396
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
                   140153
Seq. No.
                   LIB24-116-Q1-E1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1402904
BLAST score
                   657
                   4.0e-69
E value
                   126
Match length
                   100
% identity
                  (X98313) peroxidase [Arabidopsis thaliana]
NCBI Description
                   140154
Seq. No.
                   LIB24-116-Q1-E1-C4
Seq. ID
                   BLASTN
Method
                   q4757392
NCBI GI
BLAST score
                   84
                   8.0e-40
E value
                   148
Match length
% identity
                   97
                   Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                   K14A17, complete sequence
```

Seq. No. 140155

Seq. ID LIB24-116-Q1-E1-D7

Method BLASTN



q4581084 NCBI GI BLAST score 373 0.0e + 00E value Match length 377 100 % identity Arabidopsis thaliana chromosome I BAC T30F21 genomic NCBI Description sequence, complete sequence 140156 Seq. No. LIB24-116-Q1-E1-D8 Seq. ID Method BLASTX NCBI GI q2618725 BLAST score 637 9.0e-67 E value Match length 144 89 % identity NCBI Description (U49074) IAA18 [Arabidopsis thaliana] Seq. No. 140157 LIB24-116-Q1-E1-D9 Seq. ID Method BLASTN q4159712 NCBI GI BLAST score 119 E value 1.0e-60 Match length 214 89 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MWI23, complete sequence Seq. No. 140158 LIB24-116-Q1-E1-E10 Seq. ID BLASTX Method q464707 NCBI GI BLAST score 582 2.0e-60 E value Match length 115 % identity 100 40S RIBOSOMAL PROTEIN S18 >qi 480908 pir S37496 ribosomal NCBI Description protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >qi 434343 emb CAA82273 (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi 434345 emb CAA82274 (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi 434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
[Arabidopsis thaliana] >gi_3287678 (AC003979) Match to
ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs qb T21121, qb Z17755, gb R64776 and qb R30430 come from this gene. [Arabidopsis thaliana] >qi 4538910 emb CAB39647.1 (AL049482) S18.A ribosomal

Seq. No. 140159

Seq. ID LIB24-116-Q1-E1-E4

Method BLASTX NCBI GI g2623990

protein [Arabidopsis thaliana]



```
BLAST score
                  419
E value
                  3.0e-41
Match length
                  121
% identity
                  71
                  (Y13156) ferrochelatase [Arabidopsis thaliana]
NCBI Description
                  140160
Seq. No.
                  LIB24-116-Q1-E1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2104538
BLAST score
                  710
E value
                  3.0e-75
Match length
                  142
% identity
                  49
                  (AF001308) AtKAP alpha [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  140161
                  LIB24-116-Q1-E1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4741184
BLAST score
                  405
E value
                  0.0e+00
Match length
                  428
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7
                  (ESSA project)
                  140162
Seq. No.
                  LIB24-116-Q1-E1-H3
Seq. ID
Method
                  BLASTX
                  g4559384
NCBI GI
BLAST score
                  223
                  3.0e-18
E value
Match length
                  81
% identity
                  57
                  (AC006526) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  140163
Seq. ID
                  LIB24-116-Q1-E1-H4
Method
                  BLASTN
NCBI GI
                  q3869067
BLAST score
                  359
E value
                  0.0e+00
Match length
                  359
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCK7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140164
Seq. ID
                  LIB24-117-Q1-E1-A7
Method
                  BLASTN
NCBI GI
                  q4678258
BLAST score
                  225
```

E value 1.0e-123 Match length 317 % identity 93

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F617

Seq. ID



(ESSA project)

```
Seq. No.
                  140165
                  LIB24-117-Q1-E1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3449331
BLAST score
                  153
                  9.0e-81
E value
Match length
                  241
                  83
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNC17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140166
Seq. ID
                  LIB24-117-Q1-E1-D12
Method
                  BLASTN
NCBI GI
                  q4757415
BLAST score
                  56
E value
                  1.0e-22
Match length
                  135
                  89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYN21, complete sequence
Seq. No.
                  140167
Seq. ID
                  LIB24-117-Q1-E1-D4
Method
                  BLASTN
NCBI GI
                  g2252848
BLAST score
                   368
                   0.0e+00
E value
Match length
                  372
                  100
% identity
NCBI Description Arabidopsis thaliana BAC TM018A10
                  140168
Seq. No.
Seq. ID
                  LIB24-117-Q1-E1-D8
Method
                  BLASTX
NCBI GI
                   g4539340
BLAST score
                   321
E value
                   8.0e-30
Match length
                   60
                   100
% identity
NCBI Description
                  (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                   140169
Seq. ID
                  LIB24-117-Q1-E1-E4
Method
                  BLASTN
NCBI GI
                   g4662609
BLAST score
                   68
E value
                   2.0e-30
Match length
                   121
% identity
                   90
                  Genomic sequence for Arabidopsis thaliana BAC F10A5,
NCBI Description
                   complete sequence
Seq. No.
                   140170
```

17002

LIB24-117-Q1-E1-F2



```
Method
                  BLASTN
NCBI GI
                  q4725940
BLAST score
                  221
                  1.0e-121
E value
Match length
                  321
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T1P17
NCBI Description
                  (ESSA project)
Seq. No.
                  140171
Seq. ID
                  LIB24-118-Q1-E1-B2
Method
                  BLASTX
NCBI GI
                  q479831
BLAST score
                  628
E value
                  1.0e-65
Match length
                  137
% identity
                  91
NCBI Description high mobility group protein - Arabidopsis thaliana
Seq. No.
                  140172
Seq. ID
                  LIB24-118-Q1-E1-B5
Method
                  BLASTX
NCBI GI
                  q2980764
BLAST score
                  245
E value
                  8.0e-21
Match length
                  59
% identity
                  73
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]
Seq. No.
                  140173
Seq. ID
                  LIB24-118-Q1-E1-C2
Method
                  BLASTX
NCBI GI
                  g2746341
BLAST score
                  664
E value
                  6.0e-70
Match length
                  137
% identity
                  91
NCBI Description
                  (AF037590) ATA27 [Arabidopsis thaliana]
Seq. No.
                  140174
Seq. ID
                  LIB24-118-Q1-E1-C8
Method
                  BLASTX
NCBI GI
                  g4206767
                  155
BLAST score
E value
                  3.0e-10
Match length
                  26
                  96
% identity
                  (AF104330) glycine-rich protein 3 short isoform
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  140175
Seq. ID
                  LIB24-118-Q1-E1-D10
Method
                  BLASTN
```

NCBI GI g3449326 BLAST score 327 E value 0.0e+00Match length 363



```
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19M22, complete sequence [Arabidopsis thaliana]
                  140176
Seq. No.
Seq. ID
                  LIB24-118-Q1-E1-E12
Method
                  BLASTN
NCBI GI
                  g2645198
BLAST score
                  60
                  4.0e-25
E value
Match length
                  228
                  89
% identity
                  Arabidopsis thaliana chromosome I BAC T26J12 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  140177
Seq. No.
                  LIB24-118-Q1-E1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q124871
BLAST score
                  215
                  3.0e-17
E value
Match length
                  86
                  50
% identity
NCBI Description
                  INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE)
                  (PPASE) >gi_67792_pir__PWVKL inorganic pyrophosphatase (EC
                  3.6.1.1) - yeast (Kluyveromyces marxianus var. lactis)
                  >gi_2903_emb_CAA32446_ (X14230) inorganic pyrophosphatase
                  (AA 1-287) [Kluyveromyces lactis]
Seq. No.
                  140178
Seq. ID
                  LIB24-118-Q1-E1-F8
Method
                  BLASTX
                  q3875451
NCBI GI
BLAST score
                  243
                  1.0e-20
E value
Match length
                  120
% identity
                  38
                  (Z66496) cDNA EST EMBL: D71941 comes from this gene; cDNA
NCBI Description
                  EST EMBL:D74691 comes from this gene; cDNA EST EMBL:D76330
                  comes from this gene; cDNA EST EMBL: D65192 comes from this
                  gene; cDNA EST EMBL: D68540 comes from this gene; cDN
Seq. No.
                  140179
Seq. ID
                  LIB24-118-Q1-E1-G2
Method
                  BLASTX
NCBI GI
                  q452593
BLAST score
                  485
```

E value 6.0e-49 Match length 137 % identity 66

NCBI Description (D21814) ORF [Lilium longiflorum]

Seq. No. 140180

Seq. ID LIB24-118-Q1-E1-H4

Method BLASTN NCBI GI g4096078

BLAST score 58



E value 2.0e-24
Match length 97
% identity 97

NCBI Description Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140181

Seq. ID LIB24-119-Q1-E1-B7

Method BLASTX
NCBI GI g585536
BLAST score 655
E value 6.0e-69
Match length 122
% identity 99

NCBI Description MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)

>gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase
[Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194)

thioglucosidase [Arabidopsis thaliana]

Seq. No. 140182

Seq. ID LIB24-119-Q1-E1-D1

Method BLASTX
NCBI GI g4585966
BLAST score 229
E value 4.0e-19
Match length 50
% identity 84

NCBI Description (AC005287) Putative dihyrdolipoamide acetyltransferase

[Arabidopsis thaliana]

Seq. No. 140183

Seq. ID LIB24-119-Q1-E1-D6

Method BLASTX
NCBI GI g1145697
BLAST score 537
E value 4.0e-55
Match length 108
% identity 55

NCBI Description (U39485) delta tonoplast integral protein [Arabidopsis

thaliana]

Seq. No. 140184

Seq. ID LIB24-119-Q1-E1-G6

Method BLASTN
NCBI GI g4220643
BLAST score 65
E value 3.0e-28
Match length 238
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 140185

Seq. ID LIB24-119-Q1-E1-H4

Method BLASTN NCBI GI g3033373



BLAST score 132
E value 3.0e-68
Match length 184
% identity 93
NCBI Description Arabido sequenc

CBI Description Arabidopsis thaliana chromosome II BAC F1913 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140186

Seq. ID LIB24-120-Q1-E1-A4

Method BLASTN
NCBI GI 94757414
BLAST score 35
E value 3.0e-10
Match length 95
% identity 74

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYF24, complete sequence

Seq. No. 140187

Seq. ID LIB24-120-Q1-E1-B2

Method BLASTN
NCBI GI g16302
BLAST score 72
E value 3.0e-32
Match length 534
% identity 23

NCBI Description A.thaliana mRNA encoding glycine rich protein

Seq. No. 140188

Seq. ID LIB24-120-Q1-E1-B5

Method BLASTN
NCBI GI g2264317
BLAST score 155
E value 4.0e-82
Match length 163
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUG13, complete sequence [Arabidopsis thaliana]

Seq. No. 140189

Seq. ID LIB24-120-Q1-E1-D10

Method BLASTN
NCBI GI g3702728
BLAST score 135
E value 3.0e-70
Match length 167
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19M13, complete sequence [Arabidopsis thaliana]

Seq. No. 140190

Seq. ID LIB24-120-Q1-E1-E2

Method BLASTN
NCBI GI g4512690
BLAST score 148
E value 1.0e-77
Match length 405



% identity NCBI Description Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence Seq. No. 140191 Seq. ID LIB24-120-Q1-E1-E4 Method BLASTX NCBI GI q1785851 BLAST score 159 9.0e-11 E value Match length 61 % identity 51 NCBI Description (D50692) c-myc binding protein [Homo sapiens] >gi_2443310 dbj BAA22408 (AB007191) AMY-1 [Homo sapiens] 140192 Seq. No. Seq. ID LIB24-120-Q1-E1-H1 Method BLASTX NCBI GI q4406807 BLAST score 471 2.0e-47 E value Match length 93 % identity 100 NCBI Description (AC006201) putative elongation factor beta-1 [Arabidopsis thaliana] Seq. No. 140193 Seq. ID LIB24-121-Q1-E1-B12 Method BLASTX NCBI GI q4678297 BLAST score 253 6.0e-22 E value Match length 108 % identity 50 (AL049655) protein disulfide-isomerase-like protein NCBI Description [Arabidopsis thaliana] Seq. No. 140194 Seq. ID LIB24-121-Q1-E1-E5 Method BLASTN NCBI GI q2494110 BLAST score 61 E value 3.0e-26 Match length 105 % identity 90 NCBI Description Sequence of BAC T1G11 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 140195 Seq. ID LIB24-121-Q1-E1-F12

Method BLASTX q3874447 NCBI GI BLAST score 179 4.0e-13 E value Match length 121 % identity 39

NCBI Description (Z81039) predicted using Genefinder; cDNA EST EMBL:T01209

% identity

80



comes from this gene; cDNA EST yk278all.3 comes from this gene; cDNA EST yk278all.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com

140196 Seq. No. LIB24-121-Q1-E1-G4 Seq. ID Method BLASTN g2245073 NCBI GI BLAST score 139 2.0e-72 E value Match length 272 93 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No 140197 Seq. No. LIB24-121-Q1-E1-G9 Seq. ID BLASTN Method NCBI GI q3212846 94 BLAST score 2.0e-45 E value Match length 241 85 % identity Arabidopsis thaliana chromosome II BAC F6E13 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 140198 Seq. No. LIB24-122-Q1-E1-A10 Seq. ID BLASTX Method NCBI GI q1708464 BLAST score 422 E value 1.0e-41 Match length 134 62 % identity PUTATIVE DIHYDROXY-ACID DEHYDRATASE PRECURSOR (DAD) NCBI Description (2,3-DIHYDROXY ACID HYDROLYASE) >gi 1213255 emb CAA93689_ (Z69795) unknown [Schizosaccharomyces pombe] 140199 Seq. No. Seq. ID LIB24-122-Q1-E1-A7 BLASTN Method NCBI GI q3821780 BLAST score 25 1.0e-04 E value Match length 49 % identity 51 NCBI Description Xenopus laevis cDNA clone 27A6-1 Seq. No. 140200 Seq. ID LIB24-122-Q1-E1-B1 Method BLASTN NCBI GI q2749918 BLAST score 20 2.7e-01 E value Match length 218

17008

NCBI Description Arabidopsis thaliana chromosome I BAC F3I6 genomic

Seq. ID



sequence, complete sequence [Arabidopsis thaliana]

```
140201
Seq. No.
                  LIB24-122-Q1-E1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3983663
BLAST score
                  211
                  2.0e-17
E value
Match length
                  69
                  62
% identity
                  (AB011270) importin-betal [Oryza sativa]
NCBI Description
                  140202
Seq. No.
Seq. ID
                  LIB24-123-Q1-E1-A8
Method
                  BLASTN
NCBI GI
                  g4589435
BLAST score
                  145
                  9.0e-76
E value
Match length
                  396
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MOE17, complete sequence
                  140203
Seq. No.
                  LIB24-123-Q1-E1-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g405130
BLAST score
                  147
                  2.0e-77
E value
                  151
Match length
% identity
                  99
                  Arabidopsis thaliana nuclear-encoded chloroplast stromal
NCBI Description
                  cyclophilin (ROC4) mRNA, complete cds
Seq. No.
                  140204
                  LIB24-123-Q1-E1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3805760
BLAST score
                  256
E value
                  4.0e-22
Match length
                  88
                  69
% identity
NCBI Description (AC005693) unknown protein [Arabidopsis thaliana]
                  140205
Seq. No.
                  LIB24-123-Q1-E2-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q405130
BLAST score
                  151
                  8.0e-80
E value
Match length
                  151
% identity
                  100
                  Arabidopsis thaliana nuclear-encoded chloroplast stromal
NCBI Description
                  cyclophilin (ROC4) mRNA, complete cds
Seq. No.
                  140206
```

17009

LIB24-124-Q1-E1-B5



```
Method
                  BLASTN
NCBI GI
                  g4544435
BLAST score
                  181
                  2.0e-97
E value
Match length
                  267
% identity
                  98
NCBI Description Arabidopsis thaliana chromosome II BAC F14M13 genomic
                  sequence, complete sequence
Seq. No.
                  140207
                  LIB24-124-Q1-E1-C8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2191126
BLAST score
                  347
E value
                  0.0e+00
Match length
                  409
% identity
                  100
NCBI Description Arabidopsis thaliana BAC IG002N01
Seq. No.
                  140208
                  LIB24-124-Q1-E1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4521999
BLAST score
                  58
E value
                  2.0e-24
Match length
                  130
% identity
                  86
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F2G1 genomic
                  sequence, complete sequence
Seq. No.
                  140209
Seq. ID
                  LIB24-125-Q1-E1-A4
Method
                  BLASTN
NCBI GI
                  g2262097
BLAST score
                  125
E value
                  3.0e-64
Match length
                  157
% identity
                  95
NCBI Description Arabidopsis thaliana chromosome IV BAC T19F6 genomic
                  sequence, complete sequence
Seq. No.
                  140210
                  LIB24-125-Q1-E1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263781
BLAST score
                  369
E value
                  2.0e-35
Match length
                  104
% identity
                  61
NCBI Description
                  (AC006068) putative membrane transport protein [Arabidopsis
                  thaliana]
```

Seq. No. 140211

Seq. ID LIB24-125-Q1-E1-D2 Method BLASTX

NCBI GI g2853078 BLAST score 693



```
E value
                  2.0e-73
Match length
                  135
% identity
                  100
NCBI Description
                  (AL021768) TMV resistance protein N-like [Arabidopsis
                  thaliana]
                  140212
Seq. No.
Seq. ID
                  LIB24-125-Q1-E1-F5
Method
                  BLASTX
NCBI GI
                  g1617013
BLAST score
                  326
                  2.0e-30
E value
Match length
                  66
% identity
                  97
                  (Y07745) histone H2B like protein [Arabidopsis thaliana]
NCBI Description
                  140213
Seq. No.
Seq. ID
                  LIB24-126-Q1-E1-A10
Method
                  BLASTN
NCBI GI
                  q4159704
BLAST score
                  92
                  3.0e-44
E value
Match length
                  184
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MCB17, complete sequence
Seq. No.
                  140214
                  LIB24-126-Q1-E1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g643469
BLAST score
                  173
E value
                  2.0e-12
Match length
                  47
% identity
                   68
NCBI Description
                  (U19886) unknown [Lycopersicon esculentum]
Seq. No.
                  140215
                  LIB24-126-Q1-E1-B6
Seq. ID
Method
                  BLASTN
NCBI GI
                   q3522932
BLAST score
                   374
E value
                   0.0e + 00
Match length
                   374
% identity
                   100
                  Arabidopsis thaliana chromosome II BAC F14M4 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   140216
Seq. ID
                  LIB24-126-Q1-E1-C9
Method
                   BLASTN
NCBI GI
                   q4454004
BLAST score
                   244
                   1.0e-135
E value
Match length
                   368
                   100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6
```



(ESSAII project)

Seq. No. 140217

Seq. ID LIB24-126-Q1-E1-D2

Method BLASTN
NCBI GI g4585890
BLAST score 175
E value 1.0e-93
Match length 399
% identity 86

NCBI Description Arabidopsis thaliana chromosome II BAC T3G21 genomic

sequence, complete sequence

Seq. No. 140218

Seq. ID LIB24-126-Q1-E1-D6

Method BLASTX
NCBI GI g544424
BLAST score 217
E value 1.0e-17
Match length 43
% identity 98

NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755_pir__S30147

glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding

protein [Arabidopsis thaliana]

>gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)

glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No. 140219

Seq. ID LIB24-126-Q1-E1-D9

Method BLASTN
NCBI GI g4558586
BLAST score 334
E value 0.0e+00
Match length 334
% identity 100

NCBI Description Arabidopsis thaliana chromosome 1 BAC T518 sequence,

complete sequence

Seq. No. 140220

Seq. ID LIB24-126-Q1-E1-E11

Method BLASTN
NCBI GI g3241921
BLAST score 73
E value 5.0e-33
Match length 235
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCM23, complete sequence [Arabidopsis thaliana]

Seq. No. 140221

Seq. ID LIB24-126-Q1-E1-E6

MethodBLASTNNCBI GIg2477521BLAST score214E value1.0e-117



Match length 367 % identity 97

NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140222

Seq. ID LIB24-126-Q1-E1-F2

Method BLASTN
NCBI GI g3643588
BLAST score 244
E value 1.0e-135
Match length 244
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140223

Seq. ID LIB24-126-Q1-E1-G4

Method BLASTN
NCBI GI g3688169
BLAST score 151
E value 1.0e-79
Match length 253
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21

(ESSAII project)

Seq. No. 140224

Seq. ID LIB24-126-Q1-E1-G6

Method BLASTX
NCBI GI g1170711
BLAST score 686
E value 1.0e-72
Match length 129
% identity 99

NCBI Description SHAGGY RELATED PROTEIN KINASE ASK-ALPHA

>gi_541901_pir__S41596 protein kinase ASK-alpha (EC
2.7.1.-) - Arabidopsis thaliana >gi_460832_emb_CAA53181_
(X75432) shaggy related kinase [Arabidopsis thaliana]
>gi_1769889_emb_CAA48538_ (X68525) serine /threonine

protein kinase [Arabidopsis thaliana]

Seq. No. 140225

Seq. ID LIB24-126-Q1-E1-H11

Method BLASTX
NCBI GI g3461833
BLAST score 411
E value 3.0e-40
Match length 77
% identity 100

NCBI Description (AC004138) putative expansin [Arabidopsis thaliana]

Seq. No. 140226

Seq. ID LIB24-127-Q1-E1-B12

Method BLASTX
NCBI GI g3150403
BLAST score 181



E value 3.0e-13 Match length 102 % identity 39

NCBI Description (AC004165) hypothetical protein [Arabidopsis thaliana]

Seq. No. 140227

Seq. ID LIB24-127-Q1-E1-B5

Method BLASTX
NCBI GI g3169173
BLAST score 341
E value 2.0e-56
Match length 112
% identity 99

NCBI Description (AC004401) putative serine carboxypeptidase I [Arabidopsis

thaliana] >gi_3445215 (AC004786) putative serine

carboxypeptidase I [Arabidopsis thaliana]

Seq. No. 140228

Seq. ID LIB24-127-Q1-E1-D6

Method BLASTX
NCBI GI g2244763
BLAST score 401
E value 2.0e-39
Match length 97
% identity 75

NCBI Description (Z97335) A6 anther-specific protein [Arabidopsis thaliana]

Seq. No. 140229

Seq. ID LIB24-127-Q1-E1-F5

Method BLASTX
NCBI GI g1352243
BLAST score 528
E value 4.0e-54
Match length 119
% identity 86

NCBI Description LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1

>gi_625972_pir__A54841 DET1 protein - Arabidopsis thaliana
>gi_510275 (L33695) DET1 [Arabidopsis thaliana] >gi_3695414
(AF096373) Arabidopsis thaliana light-mediated development

protein DET1 (SP:P48732) [Arabidopsis thaliana]

>gi_4538982_emb_CAB39770.1_ (AL049487) Deetiolated1 (DET1)
light signal transduction protein [Arabidopsis thaliana]

Seq. No. 140230

Seq. ID LIB24-127-Q1-E1-H4

Method BLASTX
NCBI GI g2160158
BLAST score 274
E value 1.0e-24
Match length 62
% identity 98

NCBI Description (AC000132) Similar to elongation factor 1-gamma

(gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come

from this gene. [Arabidopsis thaliana]

Seq. No. 140231

Seq. ID LIB24-128-Q1-E1-A12



Method BLASTX
NCBI GI g1345973
BLAST score 492
E value 7.0e-50
Match length 107
% identity 83

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 140232

Seq. ID LIB24-128-Q1-E1-A6

Method BLASTN
NCBI GI g4454004
BLAST score 400
E value 0.0e+00
Match length 400
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6

(ESSAII project)

Seq. No. 140233

Seq. ID LIB24-128-Q1-E1-B3

Method BLASTX
NCBI GI g3335365
BLAST score 496
E value 3.0e-50
Match length 139
% identity 76

NCBI Description (AC003028) high affinity calcium antiporter [Arabidopsis

thaliana]

Seq. No. 140234

Seq. ID LIB24-128-Q1-E1-G7

Method BLASTX
NCBI GI g2970034
BLAST score 381
E value 9.0e-37
Match length 115
% identity 57

NCBI Description (D88536) delta 9 desaturase [Arabidopsis thaliana]

Seq. No. 140235

Seq. ID LIB24-128-Q1-E1-H3

Method BLASTN
NCBI GI 94454022
BLAST score 185
E value 1.0e-99
Match length 306
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16



(ESSAII project)

```
Seq. No.
                   140236
Seq. ID
                  LIB24-129-Q1-E1-H1
Method
                  BLASTN
NCBI GI
                   q3860243
BLAST score
                   137
                   4.0e-71
E value
Match length
                  204
% identity
                   63
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F15K20 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   140237
Seq. ID
                  LIB24-130-Q1-E1-C5
Method
                  BLASTN
NCBI GI
                  g166787
BLAST score
                  130
                   2.0e-67
E value
                                                               - الجيولا
Match length
                   130
% identity
                   100
NCBI Description A.thaliana chloroplast ATP synthase gamma subunit (atpC2)
                  gene, complete cds
Seq. No.
                  140238
Seq. ID
                  LIB24-130-Q1-E1-C7
Method
                  BLASTX
NCBI GI
                   q4586116
BLAST score
                   436
E value
                   3.0e-43
Match length
                   107
% identity
                   81
NCBI Description
                   (AL049638) putative C-4 sterol methyl oxidase [Arabidopsis
                   thaliana]
                   140239
Seq. No.
Seq. ID
                   LIB24-130-Q1-E1-F4
Method
                  BLASTN
NCBI GI
                   q1234869
BLAST score
                   271
E value
                   1.0e-151
Match length
                   362
% identity
                   94
NCBI Description A.thaliana PSST gene
                   140240
Seq. No.
Seq. ID
                  LIB24-131-Q1-E1-A10
Method
                  BLASTN
NCBI GI
                  g3643588
BLAST score
                  110
E value
                  7.0e-55
                  379
Match length
                   99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F17H15 genomic
```

Seq. No. 140241

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.

Seq. ID

140246

LIB24-131-Q1-E1-G6



```
LIB24-131-Q1-E1-A11
 Seq. ID
 Method
                   BLASTN
                    g4469002
 NCBI GI
                    349
 BLAST score
                    0.0e+00
 E value
 Match length
                    370
                    98
 % identity
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
                    (ESSA project)
                    140242
 Seq. No.
 Seq. ID
                    LIB24-131-Q1-E1-A9
 Method
                    BLASTN
 NCBI GI
                    g3243214
 BLAST score
                    184
 E value
                    4.0e-99
 Match length
                    289
                    98
 % identity
 NCBI Description
                   Arabidopsis thaliana BAC T19B17 from chromsome IV, near
                    19.3 cM, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    140243
                    LIB24-131-Q1-E1-D10
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2879811
 BLAST score
                    451
 E value
                    5.0e-45
                    93
 Match length
                    89
 % identity
 NCBI Description
                   (AJ223316) ribosomal protein L30 [Lupinus luteus]
                    140244
 Seq. No.
 Seq. ID
                    LIB24-131-Q1-E1-E10
 Method
                    BLASTX
 NCBI GI
                    g1351987
 BLAST score
                    687
E value
                    1.0e-72
 Match length
                    130
                    100
 % identity
 NCBI Description
                   ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING)
                    (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi 507946
                    (L29083) glutamine-dependent asparagine synthetase
                    [Arabidopsis thaliana]
 Seq. No. Seq. ID
                    140245
                    LIB24-131-Q1-E1-F12
 Method
                    BLASTX
 NCBI GI
                    g3402757
 BLAST score
                    282
 E value
                    2.0e-25
 Match length
                    64
 % identity
                    89
                    (AL031187) receptor-like serine/threonine protein kinase
 NCBI Description
                    ARK3 [Arabidopsis thaliana]
```

BLAST score

E value

51 5.0e-20



```
Method
                  BLASTN
NCBI GI
                   g2351070
BLAST score
                   63
E value
                   8.0e-27
                   67
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTH12, complete sequence [Arabidopsis thaliana]
                   140247
Seq. No.
                  LIB24-131-Q1-E1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4538945
BLAST score
                  236
                   7.0e-20
E value
Match length
                   66
                   67
% identity
                  (AL049483) putative thioredoxin [Arabidopsis thaliana]
NCBI Description
                   140248
Seq. No.
                  LIB24-132-Q1-E1-B9
Seq. ID
Method
                  BLASTX
                   g3600036
NCBI GI
BLAST score
                   343
E value
                   2.0e-32
Match length
                   83
                  84
% identity
                  (AF080119) contains similarity to protein kinase domains
NCBI Description
                   (Pfam: pkinase.hmm, score: 227.04) [Arabidopsis thaliana]
                   140249
Seq. No.
                   LIB24-132-Q1-E1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2275199
BLAST score
                   707
                   5.0e-75
E value
Match length
                   131
% identity
                   100
                  (AC002337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   140250
Seq. No.
                   LIB24-132-Q1-E1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1418331
BLAST score
                   278
E value
                   8.0e-25
Match length
                   111
                   50
% identity
NCBI Description
                   (X95909) receptor like protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   140251
Seq. ID
                   LIB24-132-Q1-E1-H4
Method
                   BLASTN
NCBI GI
                   g2772831
```



Match length 75
% identity 92
NCBI Description Arabidopsis thaliana minisatellite-like locus CMs9
Seq. No. 140252
Seq. ID LIB24-133-Q1-E1-B10

Method BLASTX
NCBI GI g1172872
BLAST score 575
E value 2.0e-59
Match length 109
% identity 100

NCBI Description CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A

precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_

(D13042) thiol protease [Arabidopsis thaliana]

>gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible
cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No. 140253

Seq. ID LIB24-133-Q1-E1-C5

Method BLASTX
NCBI GI g2924520
BLAST score 717
E value 4.0e-76
Match length 136
% identity 100

NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP)

[Arabidopsis thaliana]

Seq. No. 140254

Seq. ID LIB24-133-Q1-E1-D10

Method BLASTN
NCBI GI g2505873
BLAST score 176
E value 3.0e-94
Match length 421
% identity 98

NCBI Description Arabidopsis thaliana DNA, 40 kb surrounding ACS1 locus

Seq. No. 140255

Seq. ID LIB24-133-Q1-E1-D11

Method BLASTX
NCBI GI g2191142
BLAST score 724
E value 6.0e-77
Match length 139
% identity 32

NCBI Description (AF007269) A IG002N01.27 gene product [Arabidopsis

thaliana]

Seq. No. 140256

Seq. ID LIB24-133-Q1-E1-D6

Method BLASTX
NCBI GI g3046703
BLAST score 715
E value 6.0e-76



Match length % identity 100 (AL021749) protein kinase ADK1-like protein [Arabidopsis NCBI Description thaliana] 140257 Seq. No. Seq. ID LIB24-133-Q1-E1-D7 Method BLASTX g3776581 NCBI GI BLAST score 435 E value 4.0e-43 Match length 135

% identity 57

NCBI Description (AC005388) Similar to Beta integral membrane protein homolog gb U43629 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 140258

Seq. ID LIB24-133-Q1-E1-E1

Method BLASTN
NCBI GI g4469002
BLAST score 318
E value 1.0e-179
Match length 422
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15

(ESSA project)

Seq. No. 140259

Seq. ID LIB24-133-Q1-E1-E8

Method BLASTX
NCBI GI g1170711
BLAST score 98
E value 7.0e-04
Match length 78
% identity 86

NCBI Description SHAGGY RELATED PROTEIN KINASE ASK-ALPHA

>gi_541901_pir__S41596 protein kinase ASK-alpha (EC
2.7.1.-) - Arabidopsis thaliana >gi_460832_emb_CAA53181_
(X75432) shaggy related kinase [Arabidopsis thaliana]
>gi_1769889_emb_CAA48538_ (X68525) serine /threonine

protein kinase [Arabidopsis thaliana]

Seq. No. 140260

Seq. ID LIB24-133-Q1-E1-F2

Method BLASTX
NCBI GI g2462836
BLAST score 403
E value 2.0e-39
Match length 129
% identity 67

NCBI Description (AF000657) beta-glucanase [Arabidopsis thaliana]

Seq. No. 140261

Seq. ID LIB24-133-Q1-E1-F7

Method BLASTX NCBI GI g2213615 BLAST score 473



```
E value
                   1.0e-47
Match length
                   137
% identity
                   61
NCBI Description
                   (AC000103) F21J9.9 [Arabidopsis thaliana]
Seq. No.
                   140262
Seq. ID
                   LIB24-133-Q1-E1-G10
Method
                   BLASTX -
NCBI GI
                   g417060
BLAST score
                   568
E value
                   1.0e-58
Match length
                   128
% identity
                   82
NCBI Description
                   GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA
                   LIGASE) (GS) >gi_170637 (M94765) glutamine synthetase [Vigna aconitifolia] >gi_1094850_prf__2106409A Gln
                   synthetase [Vigna aconitifolia]
Seq. No.
                   140263
Seq. ID
                   LIB24-133-Q1-E1-H1
Method
                   BLASTN
NCBI GI
                   q3046851
BLAST score
                   382
E value
                   0.0e+00
Match length
                   382
% identity
                   100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MIJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   140264
Seq. ID
                   LIB24-134-Q1-E1-A7
Method
                   BLASTX
NCBI GI
                   g2244765
BLAST score
                   544
E value
                   7.0e-56
Match length
                   141
% identity
                   39
NCBI Description
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   140265
Seq. ID
                   LIB24-134-Q1-E1-B10
Method
                   BLASTX
NCBI GI
                   g3355480
BLAST score
                   227
                   9.0e-19
E value
Match length
                   76
% identity
NCBI Description
                   (AC004218) Medicago nodulin N21-like protein [Arabidopsis
                   thaliana]
```

Seq. No. 140266

Seq. ID LIB24-134-Q1-E1-B4

Method BLASTN NCBI GI g3281847 BLAST score 164 E value 2.0e-87 Match length 200



% identity Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 NCBI Description (ESSAII project) Seq. No. 140267 LIB24-134-Q1-E1-F7 Seq. ID Method BLASTX NCBI GI g3915169 BLAST score 163 3.0e-11 E value Match length 97 36 % identity NCBI Description PROBABLE TRNA (GUANOSINE-2'-O-)-METHYLTRANSFERASE (TRNA [GM18] METHYLTRANSFERASE) >gi 2983982 (AE000749) rRNA methylase SpoU [Aquifex aeolicus] Seq. No. 140268 Seq. ID LIB24-135-Q1-E1-A7 Method BLASTX NCBI GI g2245131 BLAST score 142 8.0e-09 E value Match length 114 % identity 33 NCBI Description (297344) hypothetical protein [Arabidopsis thaliana] Seq. No. 140269 Seq. ID LIB24-135-Q1-E1-B1 Method BLASTN NCBI GI q4204173 BLAST score 121 6.0e-62 E value 137 Match length % identity 97 Arabidopsis thaliana chromosome 1 BAC T2K10 sequence, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 140270 Seq. ID LIB24-135-Q1-E1-E1 Method BLASTX NCBI GI q3033400 BLAST score 469 E value 3.0e-47Match length 107 % identity 79 NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

140271 Seq. No.

Seq. ID LIB24-135-Q1-E1-F12

Method BLASTX NCBI GI q4056444 · BLAST score 167 E value 2.0e-22 Match length 92 % identity 68

NCBI Description (AC005990) Similar to OBP32pep protein gb U37698 from



Arabidopsis thaliana. [Arabidopsis thaliana]

```
Seq. No.
                  140272
Seq. ID
                  LIB24-135-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                   g2558962
BLAST score
                   206
                  2.0e-16
E value
                   43
Match length
                   98
% identity
                  (AF025667) histone H2B1 [Gossypium hirsutum]
NCBI Description
                   140273
Seq. No.
                   LIB24-135-Q1-E1-H12
Seq. ID
Method
                   BLASTN
                   g2833627
NCBI GI
BLAST score
                   77
                   8.0e-36
E value
                   105
Match length
                   93
% identity
                  Arabidopsis thaliana chromosome 1 BAC F1707 complete
NCBI Description
                   sequence [Arabidopsis thaliana]
                   140274
Seq. No.
                   LIB24-135-Q1-E1-H4
Seq. ID
Method
                   BLASTX
                   g2664200
NCBI GI
                   495
BLAST score
                   3.0e-50
E value
Match length
                   94
                   69
% identity
                  (AJ003216) GTL2 [Arabidopsis thaliana]
NCBI Description
                   140275
Seq. No.
                   LIB24-135-Q1-E1-H6
Seq. ID
                   BLASTN
Method
                   g2341023
NCBI GI
BLAST score
                   210
E value
                   1.0e-115
                   226
Match length
% identity
                   98
                   Sequence of BAC F19P19 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   140276
                   LIB24-136-Q1-E1-A12
Seq. ID
                   BLASTN
Method
                   g3980374
NCBI GI
BLAST score
                   74
                   2.0e-33
E value
Match length
                   146
% identity
                   Arabidopsis thaliana chromosome II BAC F16P2 genomic
NCBI Description
```

Seq. No. 140277

Seq. ID LIB24-136-Q1-E1-A3

17023

sequence, complete sequence [Arabidopsis thaliana]

% identity

92

```
Method
                   BLASTX
 NCBI GI
                   q2129569
 BLAST score
                   566
 E value
                   2.0e-58
 Match length
                   120
 % identity
                   90
 NCBI Description
                   cytosolic cyclophilin ROC3 - Arabidopsis thaliana
                   >gi_1305455 (U40399) cytosolic cyclophilin [Arabidopsis
                   thaliana] >gi_4581104_gb_AAD24594.1 AC005825 1 (AC005825)
                   cytosolic cyclophilin (ROC3) [Arabidopsis thaliana]
 Seq. No.
                   140278
 Seq. ID
                   LIB24-136-Q1-E1-C11
 Method
                   BLASTX
 NCBI GI
                   q2130442
 BLAST score
                   263
 E value
                   6.0e-23
Match length
                   138
 % identity .
                   41
NCBI protein SPAC8A4.01c - fission yeast
                   (Schizosaccharomyces pombe) (fragment)
                   >gi_1052534_emb_CAA91511 (Z66569) unknown
                   [Schizosaccharomyces pombe]
Seq. No.
                   140279
Seq. ID
                  LIB24-136-Q1-E1-D1
Method
                  BLASTN
NCBI GI
                  q4691223
BLAST score
                  276
E value
                  1.0e-154
Match length
                  309
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
                  (ESSA project)
Seq. No.
                  140280
Seq. ID
                  LIB24-136-Q1-E1-D12
Method
                  BLASTX
NCBI GI
                  g3881836
BLAST score
                  593
E value
                  1.0e-61
Match length
                  139
% identity
                  80
NCBI Description
                  (Z78019) Similarity to Yeast LPG22P protein (TR:G1151240);
                  cDNA EST EMBL: T00686 comes from this gene; cDNA EST
                  EMBL:C12415 comes from this gene; cDNA EST EMBL:C12728
                  comes from this gene; cDNA EST EMBL:C10626 comes from this
Seq. No.
                  140281
Seq. ID
                  LIB24-136-Q1-E1-E12
Method
                  BLASTX
NCBI GI
                  g1175012
BLAST score
                  591
E value
                  2.0e-61
Match length
                  126
```

17024

Method

NCBI GI

BLASTN

g3128143

```
NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN
                       B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane
                       protein TMP-B [Arabidopsis thaliana]
    Seq. No.
                       140282
    Seq. ID
                       LIB24-136-Q1-E1-F3
    Method
                       BLASTX
    NCBI GI
                       q3873677
    BLAST score
                       172
    E value
                       2.0e-12
    Match length
                       102
    % identity
                       33
                      (Z71178) Similarity with yeast hypothetical protein (Swiss
    NCBI Description
                       Prot accession number P43577) [Caenorhabditis elegans]
                       >gi_4115737_dbj BAA36497 (AB017628) acetyltransferase
                       [Caenorhabditis elegans]
    Seq. No.
                       140283
    Seq. ID
                      LIB24-136-Q1-E1-G11
Method
                      BLASTX
   NCBI GI
                      q2271485
   BLAST score
                      735
   E value
                      3.0e-78
   Match length
                      140
    % identity
                      100
                      (AF009647) arginine decarboxylase [Arabidopsis thaliana]
   NCBI Description
                      >gi_3096940_emb_CAA18850.1 (AL023094) arginine
                      decarboxylase SPE2 [Arabidopsis thaliana]
   Seq. No.
                      140284
   Seq. ID
                      LIB24-136-Q1-E1-G6
   Method
                      BLASTN
   NCBI GI
                      g16306
   BLAST score
                      49
   E value
                      2.0e-19
   Match length
                      70
   % identity
                      90
   NCBI Description A.thaliana genes encoding glycine-rich proteins
   Seq. No.
                      140285
   Seq. ID
                      LIB24-136-01-E1-H11
   Method
                      BLASTX
   NCBI GI
                      g2499611
   BLAST score
                      676
   E value
                      2.0e-71
   Match length
                      132
   % identity
                      99
   NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7)
                      (ATMPK7) >gi_629548_pir__S40473 mitogen-activated protein kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana
                      >gi_457406_dbj_BAA04870_ (D21843) MAP kinase [Arabidopsis
                      thaliana]
   Seq. No.
                      140286
   Seq. ID
                     LIB24-136-Q1-E1-H5
```

```
BLAST score
                    230
E value
                    1.0e-126
Match length
                    298
 % identity
                    98
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MTI20, complete sequence [Arabidopsis thaliana]
Seq. No.
                    140287
Seq. ID
                    LIB24-137-Q1-E1-E12
Method
                    BLASTN
NCBI GI
                    g3293582
BLAST score
                    317
E value
                    1.0e-178
Match length
                    377
% identity
                    95
NCBI Description Arabidopsis thaliana BAC T15F16
Seq. No.
                    140288
                   LIB24-137-Q1-E1-E3
Seq. ID
Method
               BLASTX
NCBI GI
                   g4193388
BLAST score
                   278
                   6.0e-25
E value
Match length
                   74
% identity
                   76
NCBI Description
                   (AF091455) translationally controlled tumor protein [Hevea
                   brasiliensis]
Seq. No.
                   140289
Seq. ID
                   LIB24-137-Q1-E1-H10
Method
                   BLASTX
NCBI GI
                   q4033468
BLAST score
                   102
E value
                   4.0e-04
Match length
                   109
% identity
                   33
NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP40
                   >gi_2582641_emb_CAA67800_ (X99437) splicing factor
[Arabidopsis thaliana] >gi_2980800_emb_CAA18176_ (AL022197)
                   splicing factor At-SRp40 [Arabidopsis thaliana]
Seq. No.
                   140290
Seq. ID
                   LIB25-001-Q1-E1-A9
Method
                   BLASTX
NCBI GI
                   q3033388
BLAST score
                   168
                   9.0e-12
E value
Match length
                   104
% identity
NCBI Description
                  (AC004238) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   140291
                   LIB25-001-Q1-E1-B11
Seq. ID
Method
                   BLASTN
NCBI GI
```

17026

g3763944

6.0e-39

82

BLAST score

E value

```
Match length
 % identity
                   100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23
                   (ESSAII project)
Seq. No.
                   140292
Seq. ID
                   LIB25-001-Q1-E1-C12
Method
                   BLASTN
NCBI GI
                   g2262097
BLAST score
                   180
E value
                   8.0e-97
Match length
                   284
% identity
NCBI Description Arabidopsis thaliana chromosome IV BAC T19F6 genomic
                   sequence, complete sequence
Seq. No.
                   140293
Seq. ID
                   LIB25-001-Q1-E2-B11
Method
                  BLASTN
NCBI GI
                   g3763944 ···
BLAST score
                   71
E value
                   2.0e-32
Match length
                   79
                   97
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23
                   (ESSAII project)
Seq. No.
                  140294
Seq. ID
                  LIB25-001-Q1-E2-C3
Method
                  BLASTX
NCBI GI
                  g2062170
BLAST score
                   427
E value
                  2.0e-43
Match length
                  97
% identity
                  86
NCBI Description (AC001645) unknown protein [Arabidopsis thaliana]
Seq. No.
                  140295
Seq. ID
                  LIB25-001-Q1-E2-D4
Method
                  BLASTX
NCBI GI
                  g499862
BLAST score
                  176
E value
                  1.0e-12
Match length
                  130
% identity
NCBI Description
                 (L33893) NADPH-cytochrome P-450 oxidoreductase [Sus scrofa]
Seq. No.
                  140296
Seq. ID
                  LIB25-001-Q1-E2-E1
Method
                  BLASTN
NCBI GI
                  g2760172
BLAST score
                  136
E value
                  1.0e-70
Match length
                  267
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

17027

MUB3, complete sequence [Arabidopsis thaliana]

, *

```
Seq. No.
                   140297
 Seq. ID
                   LIB25-001-Q1-E2-E6
 Method
                   BLASTN
NCBI GI
                   q2342673
BLAST score
                   120
                   7.0e-61
E value
Match length
                   320
 % identity
NCBI Description Sequence of BAC F7G19 from Arabidopsis thaliana chromosome
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   140298
Seq. ID
                   LIB25-001-Q1-E2-F11
Method
                   BLASTN
NCBI GI
                   q1483217
BLAST score
                   346
                   0.0e+00
E value
Match length
                   437
% identity ...
                   99
                                     1 1
NCBI Description A.thaliana gene induced upon wounding stress
Seq. No.
                   140299
Seq. ID
                   LIB25-001-Q1-E2-G1
Method
                   BLASTX
NCBI GI
                   q1170851
BLAST score
                   228
E value
                   4.0e-19
Match length
                   90
% identity
                   53
NCBI Description MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE
                   (MAN(9)-ALPHA-MANNOSIDASE) (ALPHA-MANNOSIDASE 1A)
                   >gi_1083410_pir__A54408 mannosyl-oligosaccharide
                   1,2-alpha-mannosidase (EC 3.2.1.113) - mouse >gi 474280
                   (U04299) mannosyl-oligosaccharide alpha-1,2-mannosidase
                   [Mus musculus]
Seq. No.
                  140300
Seq. ID
                  LIB25-001-Q1-E2-G10
Method
                  BLASTX
NCBI GI
                  q4680651
BLAST score
                  155
E value
                  3.0e-10
Match length
                  85
% identity
                  40
NCBI Description (AF132940) CGI-06 protein [Homo sapiens]
Seq. No.
                  140301
Seq. ID
                  LIB25-001-Q1-E2-G2
Method
                  BLASTN
NCBI GI
                  q2088638
BLAST score
                  308
E value
                  1.0e-173
Match length
                  380
% identity
                  94
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T28M21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```

Seq. No.

140307

```
Seq. No.
                     140302
  Seq. ID
                     LIB25-002-Q1-E1-A10
  Method
                     BLASTX
  NCBI GI
                     q3646451
  BLAST score
                     172
  E value
                     3.0e-12
  Match length
                     83
  % identity
                     48
  NCBI Description
                    (AL031603) mRNA cap methyltransferase [Schizosaccharomyces
                     pombe]
  Seq. No.
                     140303
  Seq. ID
                     LIB25-002-Q1-E1-B1
  Method
                     BLASTN
  NCBI GI
                     q4732167
  BLAST score
                     261
  E value
                     1.0e-145
  Match length
                     312
% identity
                     100
  NCBI Description Arabidopsis thaliana BAC F28D6
  Seq. No.
                    140304
  Seq. ID
                    LIB25-002-Q1-E1-B6
  Method
                    BLASTX
  NCBI GI
                    q3021277
  BLAST score
                     391
  E value
                    3.0e-38
  Match length
                    72
  % identity
                    35
                     (AL022347) protein kinase - like protein [Arabidopsis
  NCBI Description
                    thaliana]
  Seq. No.
                    140305
  Seq. ID
                    LIB25-002-Q1-E1-C10
  Method
                    BLASTX
  NCBI GI
                    g4127456
  BLAST score
                    447
  E value
                    2.0e-44
  Match length
                    91
  % identity
                    47
  NCBI Description
                    (AJ010818) Cpn21 protein [Arabidopsis thaliana]
  Seq. No.
                    140306
  Seq. ID
                    LIB25-002-Q1-E1-C3
  Method
                    BLASTX
  NCBI GI
                    g4587570
  BLAST score
                    352
  E value
                    2.0e-33
  Match length
                    105
  % identity
                    41
  NCBI Description
                    (AC006550) Strong similarity to gi_2244833 centromere
                    protein homolog from Arabidopsis thaliana chromosome 4
                    contig gb_Z97337. ESTs gb_T20765 and gb_AA586277 come from
                    this gene
```

% identity

```
Seq. ID
                   LIB25-002-Q1-E1-C4
Method
                   BLASTX
NCBI GI
                   g136636
BLAST score
                   475
E value
                   8.0e-48
Match length
                   87
% identity
                   100
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
                   LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                   >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 -
                   Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin
                   Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894 pdb 2AAK
                   Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                   >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis
                   thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
                   [Arabidopsis thaliana]
Seq. No.
                   140308
Seq. ID
                  LIB25-002-Q1-E1-C8
Method
                  BLASTN
NCBI GI
                  g2924733
BLAST score
                  164
E value
                   4.0e-87
Match length
                  402
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUF9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140309
Seq. ID
                  LIB25-002-Q1-E1-D1
Method
                  BLASTX
NCBI GI
                  g2052383
BLAST score
                  254
E value
                  7.0e-22
Match length
                  53
% identity
                  83
NCBI Description (U66345) calreticulin [Arabidopsis thaliana]
Seq. No.
                  140310
Seq. ID
                  LIB25-002-Q1-E1-E5
Method
                  BLASTN
NCBI GI
                  g3212102
BLAST score
                  131
E value
                  1.0e-67
Match length
                  211
% identity
                  100
NCBI Description Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  140311
Seq. ID
                  LIB25-002-Q1-E1-H3
Method
                  BLASTX
NCBI GI
                  g4432858
BLAST score
                  237
E value
                  5.0e-20
Match length
                  90
```

```
NCBI Description
                  (AC006300) putative disease resistance protein [Arabidopsis
                   thaliana]
Seq. No.
                   140312
Seq. ID
                   LIB25-002-Q1-E1-H6
Method
                  BLASTN
NCBI GI
                  q3193282
BLAST score
                   149
E value
                   3.0e-78
Match length
                   354
% identity
                   100
NCBI Description Arabidopsis thaliana BAC T14P8
Seq. No.
                  140313
Seq. ID
                  LIB25-003-Q1-E1-A12
Method
                  BLASTX
NCBI GI
                  q3355471
BLAST score
                  728
                  2.0e-77
E value
Match length
                 -143
% identity
                  99
NCBI Description
                  (AC004218) putative lysophospholipase [Arabidopsis
                  thaliana]
Seq. No.
                  140314
                  LIB25-003-Q1-E1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1488521
BLAST score
                  342
E value
                  3.0e-32
Match length
                  69
% identity
                  100
NCBI Description (X99938) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  140315
Seq. ID
                  LIB25-003-Q1-E1-E1
Method
                  BLASTX
NCBI GI
                  g1825727
BLAST score
                  450
E value
                  7.0e-45
Match length
                  138
                  59
% identity
NCBI Description (U88308) C32E8.5 gene product [Caenorhabditis elegans]
Seq. No.
                  140316
Seq. ID
                  LIB25-003-Q1-E1-E5
Method
                  BLASTX
```

NCBI GI q4508070 BLAST score 586 E value 8.0e-61 Match length 110 % identity 99

NCBI Description (AC005882) 24349 [Arabidopsis thaliana]

Seq. No. 140317

Seq. ID LIB25-003-Q1-E1-F1

Method BLASTX

BLAST score

103

```
NCBI GI
                      g1769905
   BLAST score
                      416
   E value
                      7.0e-41
   Match length
                      121
   % identity
                      67
   NCBI Description
                      (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                      [Arabidopsis thaliana]
   Seq. No.
                      140318
   Seq. ID
                      LIB25-003-Q1-E1-G4
   Method
                      BLASTN
   NCBI GI
                      g2351067
   BLAST score
                      322
   E value
                      0.0e+00
   Match length
                      387
   % identity
                      100
   NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                      MPO12, complete sequence [Arabidopsis thaliana]
Seq. No.
                      140319
   Seq. ID
                      LIB25-004-Q1-E1-B10
   Method
                      BLASTN
   NCBI GI
                      g4376087
                      276
   BLAST score
   E value
                      1.0e-154
   Match length
                      359
   % identity
                      100
   NCBI Description
                     Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                      fragment No
   Seq. No.
                      140320
   Seq. ID
                     LIB25-004-Q1-E1-C10
   Method
                     BLASTN
   NCBI GI
                     g3510343
   BLAST score
                      431
   E value
                      0.0e+00
   Match length
                      431
   % identity
                     100
   NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                     MJC20, complete sequence [Arabidopsis thaliana]
   Seq. No.
                     140321
   Seq. ID
                     LIB25-004-Q1-E1-C6
   Method
                     BLASTN
   NCBI GI
                     g3335331
   BLAST score
                     47
   E value
                     3.0e-18
   Match length
                     47
   % identity
                     100
   NCBI Description
                     Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
                     complete sequence [Arabidopsis thaliana]
   Seq. No.
                     140322
                     LIB25-004-Q1-E1-C9
   Seq. ID
  Method
                     BLASTN
  NCBI GI
                     q166645
```

E value

Match length

% identity

1.0e-38

85

89

```
E value
                   3.0e-51
Match length
                   107
% identity
                   99
NCBI Description
                  Arabidopsis thaliana light-harvesting chlorophyll
                   a/b-binding protein (Cab4) mRNA, complete cds
Seq. No.
                   140323
Seq. ID
                   LIB25-004-Q1-E1-D11
Method
                   BLASTX
NCBI GI
                   q2695931
BLAST score
                   282
E value
                   4.0e-25
Match length
                   74
% identity
                   70
NCBI Description
                  (AJ222779) hypothetical protein [Hordeum vulgare]
Seq. No.
                  140324
Seq. ID
                  LIB25-005-Q1-E1-B9
Method
                  BLASTN
NCBI GI
                  g3046851' `
BLAST score
                  126
E value
                  1.0e-64
Match length
                  290
% identity
                  91
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MIJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140325
Seq. ID
                  LIB25-005-Q1-E1-G12
Method
                  BLASTX
NCBI GI
                  q4455199
BLAST score
                  547
E value
                  2.0e-56
Match length
                  116
% identity
                  97
NCBI Description
                  (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  140326
Seq. ID
                  LIB25-006-Q1-E1-A4
Method
                  BLASTX
NCBI GI
                  g480907
BLAST score
                  390
E value
                  3.0e-38
Match length
                  81
% identity
                  95
NCBI Description
                  peroxidase (EC 1.11.1.7) - Arabidopsis thaliana
                  >gi_405611_emb_CAA50677_ (X71794) peroxidase [Arabidopsis
                  thaliana]
Seq. No.
                  140327
                  LIB25-006-Q1-E1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  396
```



NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 140328

Seq. ID LIB25-006-Q1-E1-C6

Method BLASTX
NCBI GI g4455336
BLAST score 430
E value 1.0e-42
Match length 86
% identity 98

NCBI Description (AL035525) pectinesterase-like protein [Arabidopsis

thaliana]

Seq. No. 140329

Seq. ID LIB25-006-Q1-E1-D1

Method BLASTN
NCBI GI g3985958
BLAST score 155
E value 4.0e-82
Match length 162
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MZN1, complete sequence [Arabidopsis thaliana]

Seq. No. 140330

Seq. ID LIB25-006-Q1-E1-D7

Method BLASTN
NCBI GI g3643588
BLAST score 164
E value 3.0e-87
Match length 302
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140331

Seq. ID LIB25-006-Q1-E1-E1

Method BLASTX
NCBI GI g1617274
BLAST score 392
E value 3.0e-38
Match length 96
% identity 71

NCBI Description (Z72152) AMP-binding protein [Brassica napus]

Seq. No. 140332

Seq. ID LIB25-006-Q1-E1-E10

Method BLASTN
NCBI GI g2961335
BLAST score 93
E value 3.0e-45
Match length 141
% identity 91

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20



```
(ESSAII project)
Seq. No.
                   140333
Seq. ID
                   LIB25-006-Q1-E1-E3
Method
                   BLASTN
NCBI GI
                   g2980787
BLAST score
                   141
E value
                   2.0e-73
Match length
                   275
% identity
                   95
                   Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2
NCBI Description
                   (ESSAII project)
Seq. No.
                   140334
Seq. ID
                   LIB25-006-01-E1-F5
Method
                   BLASTX
NCBI GI
                   g2257743
BLAST score
                   196
E value
                   3.0e-15
Match length
                   74
% identity
                   55
NCBI Description
                   (U62020) lysine-sensitive aspartate kinase [Arabidopsis
                   thaliana]
Seq. No.
                   140335
Seq. ID
                   LIB25-006-Q1-E1-G3
Method
                   BLASTX
NCBI GI
                   q4581132
BLAST score
                   381
E value
                   6.0e-37
Match length
                   74
% identity
                   99
NCBI Description
                  (AC005825) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   140336
Seq. ID
                   LIB25-006-Q1-E1-G6
Method
                   BLASTX
NCBI GI
                   q3415117
BLAST score
                   363
E value
                   1.0e-34
Match length
                   72
                   47
% identity
NCBI Description
                  (AF081203) villin 3 [Arabidopsis thaliana]
Seq. No.
                   140337
Seq. ID
                  LIB25-006-Q1-E2-A4
Method
                  BLASTN
NCBI GI
                  g3068702
BLAST score
                  193
E value
                  1.0e-105
Match length
                  193
% identity
                  100
```

NCBI Description Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), put



```
Seq. No.
                   140338
                  LIB25-006-Q1-E2-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3128137
BLAST score
                   58
E value
                   2.0e-24
Match length
                  130
% identity
                   86
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K9I9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140339
Seq. ID
                  LIB25-006-Q1-E2-F3
Method
                  BLASTX
NCBI GI
                  q3056592
BLAST score
                  607
E value
                  2.0e-63
Match length
                  118
% identity
                  98
NCBI Description (AC004255) T1F9.13 [Arabidopsis thaliana]
Seq. No.
                  140340
Seq. ID
                  LIB25-006-Q1-E2-F6
Method
                  BLASTX
NCBI GI
                  g1730674
BLAST score
                  211
E value
                  6.0e-17
Match length
                  96
% identity
                  43
NCBI Description
                  HYPOTHETICAL 62.7 KD PROTEIN IN SEC12-SSK2 INTERGENIC
                  REGION >gi_2132801_pir S63361 probable membrane protein
                  YNR030w - yeast (Saccharomyces cerevisiae)
                  >gi_1302525_emb_CAA96310_ (Z71645) ORF YNR030w
                  [Saccharomyces cerevisiae]
                  140341
Seq. No.
Seq. ID
                  LIB25-007-Q1-E1-A12
Method
                  BLASTN
NCBI GI
                  q4678315
BLAST score
                  142
E value
                  6.0e-74
Match length
                  388
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15
                  (ESSA project)
Seq. No.
                  140342
Seq. ID
                  LIB25-007-Q1-E1-A9
Method
                  BLASTN
NCBI GI
                  g4753195
BLAST score
                  370
```

E value 0.0e+00

Match length 370 % identity 100 NCBI Description

Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence



```
Seq. No.
                   140343
Seq. ID
                   LIB25-007-Q1-E1-B11
Method
                  BLASTN
NCBI GI
                  q3241922
BLAST score
                   126
E value
                  1.0e-64
Match length
                  281
% identity
                   93
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MLM24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140344
Seq. ID
                  LIB25-007-Q1-E1-B9
Method
                  BLASTX
                  q3510251
NCBI GI
BLAST score
                  221
E value
                  4.0e-18
Match length
                  78
% identity
                  51
NCBI Description
                 (AC005310) unknown protein [Arabidopsis thaliana]
Seq. No.
                  140345
Seq. ID
                  LIB25-007-Q1-E1-D1
Method
                  BLASTN
NCBI GI
                  g2351064
BLAST score
                  56
E value
                  3.0e-23
Match length
                  92
% identity
                  90
NCBI Description
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDJ22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140346
Seq. ID
                  LIB25-007-Q1-E1-D10
Method
                  BLASTX
NCBI GI
                  q1173018
BLAST score
                  206
E value
                  1.0e-16
Match length
                  68
% identity
                  62
                  60S RIBOSOMAL PROTEIN L2 >gi_1076399_pir__S54250 ribosomal
NCBI Description
                  protein L2 - Arabidopsis thaliana >gi 798818_emb CAA60445_
                  (X86765) 60S ribosomal protein L2 [Arabidopsis thaliana]
Seq. No.
                  140347
                  LIB25-007-Q1-E1-D11
                  BLASTX
                  g2497886
                  300
                  3.0e-27
```

Seq. ID

Method

NCBI GI BLAST score E value Match length 54 % identity 100

METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) NCBI Description

>gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis

thaliana]



```
Seq. No.
                  140348
Seq. ID
                  LIB25-007-Q1-E1-D12
Method
                  BLASTN
NCBI GI
                  q4262221
BLAST score
                  36
E value
                  1.0e-10
Match length
                  193
% identity
                  85
NCBI Description Arabidopsis thaliana chromosome II BAC F10A8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140349
Seq. ID
                  LIB25-007-Q1-E1-F6
                  BLASTN
Method
                  g4191771
NCBI GI
BLAST score
                  173
E value
                  1.0e-92
Match length
                  221
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC F3P11 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140350
Seq. ID
                  LIB25-007-Q1-E1-F8
Method
                  BLASTX
NCBI GI
                  g2947069
BLAST score
                  343
E value
                  2.0e-32
Match length
                  65
% identity
                  100
NCBI Description (AC002521) putative pectate lyase [Arabidopsis thaliana]
Seq. No.
                  140351
Seq. ID
                  LIB25-007-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                  q544075
BLAST score
                  371
E value
                  1.0e-35
Match length
                  87
% identity
                  45
NCBI Description COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)
                  (P102) >gi 486768 pir S35312 coatomer complex chain beta'
                  - bovine >gi_312732_emb_CAA51285_ (X72756) beta prime cop
                  [Bos taurus]
Seq. No.
                  140352
Seq. ID
                  LIB25-007-Q1-E1-H10
```

Method BLASTX NCBI GI g3882297 BLAST score 404 E value 2.0e-39 Match length 109 % identity 70

NCBI Description (AB018331) KIAA0788 protein [Homo sapiens]

Seq. No. 140353

Seq. ID LIB25-007-Q1-E1-H11



Method BLASTN
NCBI GI g3212846
BLAST score 233
E value 1.0e-128

E value 1.0e-1
Match length 254
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140354

Seq. ID LIB25-007-Q1-E1-H6

Method BLASTN
NCBI GI g2618602
BLAST score 115
E value 4.0e-58
Match length 247
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 140355

Seq. ID LIB25-007-Q1-E1-H7

Method BLASTN
NCBI GI g2351068
BLAST score 371
E value 0.0e+00
Match length 371
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRH10, complete sequence [Arabidopsis thaliana]

Seq. No. 140356

Seq. ID LIB25-008-Q1-E1-A2

Method BLASTX
NCBI GI 9728867
BLAST score 158
E value 1.0e-10
Match length 140
% identity 27

NCBI Description ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR

>gi_99694_pir__S21961 proline-rich protein APG -

Arabidopsis thaliana >gi_22599_emb_CAA42925_ (X60377) APG

[Arabidopsis thaliana]

Seq. No. 140357

Seq. ID LIB25-008-Q1-E1-C7

Method BLASTX
NCBI GI g2493133
BLAST score 186
E value 7.0e-14
Match length 75
% identity 51

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT)

>gi_2183244 (AF002134) Vma8p [Candida albicans]

Seq. No. 140358

Seq. ID LIB25-008-Q1-E1-E5

Seq. ID

Method

NCBI GI



```
Method
                   BLASTX
NCBI GI
                   q1416514
BLAST score
                   69
E value
                   6.0e-40
Match length
                   109
% identity
                   81
NCBI Description
                  (D63168) CTP:phosphocholine cytidylyltransferase [Brassica
                  napus]
                   140359
Seq. No.
Seq. ID
                  LIB25-008-Q1-E1-F3
Method
                  BLASTN
NCBI GI
                  g4193383
BLAST score
                  80
                  2.0e-37
E value
Match length
                  144
% identity
                  100
NCBI Description
                 Arabidopsis thaliana ribosomal protein S27 (ARS27A) gene,
                  complete cds
Seq. No.
                  140360
Seq. ID
                  LIB25-008-Q1-E1-G3
Method
                  BLASTN
NCBI GI
                  g4376087
BLAST score
                  100
E value
                  5.0e-49
Match length
                  301
% identity
                  93
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                  fragment No
Seq. No.
                  140361
Seq. ID
                  LIB25-008-Q1-E1-H3
Method
                  BLASTN
                  g4538918
NCBI GI
BLAST score
                  413
E value
                  0.0e+00
Match length
                  417
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20B18
                  (ESSA project)
Seq. No.
                  140362
Seq. ID
                  LIB25-009-Q1-E1-A1
Method
                  BLASTN
NCBI GI
                  g3046855
BLAST score
                  133
E value
                  1.0e-68
Match length
                  357
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSL1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140363
```

17040

LIB25-009-Q1-E1-A4

BLASTX

g3183491



BLAST score 242 E value 2.0e-20 Match length 129 % identity 38

NCBI Description HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III

>gi_1065510 (U40419) C27F2.7 gene product [Caenorhabditis

elegans]

Seq. No. 140364

Seq. ID LIB25-009-Q1-E1-D11

Method BLASTX
NCBI GI g3757516
BLAST score 433
E value 6.0e-43
Match length 121
% identity 74

NCBI Description (AC005167) putative TMV resistance protein [Arabidopsis

thaliana]

Seq. No. 140365

Seq. ID LIB25-009-Q1-E1-E1

Method BLASTX
NCBI GI g4098572
BLAST score 73
E value 1.2e+00
Match length 78
% identity 26

NCBI Description (U79569) no arches [Homo sapiens]

Seq. No. 140366

Seq. ID LIB25-009-Q1-E1-E3

Method BLASTN
NCBI GI g4589437
BLAST score 332
E value 0.0e+00
Match length 380
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MPN9, complete sequence

Seq. No. 140367

Seq. ID LIB25-009-Q1-E1-F5

Method BLASTN
NCBI GI g2244829
BLAST score 91
E value 5.0e-44
Match length 127
% identity 93

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 140368

Seq. ID LIB25-009-Q1-E1-G10

Method BLASTX
NCBI GI g729406
BLAST score 190
E value 2.0e-14



Match length % identity 59

ELONGATION FACTOR P (EF-P) >gi_421056_pir__S34443 NCBI Description

translation elongation factor EF-P - Escherichia coli >gi_433670_emb_CAA43851_ (X61676) elongation factor P
[Escherichia coli] >gi_536991 (U14003) elongation factor P
[Escherichia coli] >gi_1790590 (AE000487) elongation factor

P (EF-P) [Escherichia coli]

Seq. No. 140369

Seq. ID LIB25-009-Q1-E1-G5

Method BLASTX NCBI GI q2245138 BLAST score 223 E value 3.0e-18 Match length 85 % identity 45

NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.

140370 LIB25-009-Q1-E1-G6 Seq. ID

Method BLASTX NCBI GI q131398 BLAST score 533 E value 1.0e-54 Match length 123 % identity

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

> >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi 16447 emb CAA39441 (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 140371

Seq. ID LIB25-009-Q1-E1-H4

Method BLASTX NCBI GI g3822223 BLAST score 390 E value 5.0e-38 Match length 104 % identity 65

NCBI Description (AF077955) branched-chain alpha keto-acid dehydrogenase E1

alpha subunit [Arabidopsis thaliana]

Seq. No. 140372

Seq. ID LIB25-010-Q1-E1-A8

Method BLASTN NCBI GI g2924731 BLAST score 54 E value 5.0e-22 Match length 123 % identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

Match length

% identity NCBI Description 138



MSI17, complete sequence [Arabidopsis thaliana]

```
140373
Seq. No.
Seq. ID
                  LIB25-010-Q1-E1-B3
Method
                  BLASTN
NCBI GI
                  q1931636
BLAST score
                  63
E value
                  7.0e-27
Match length
                  196
% identity
                  89
NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence
Seq. No.
                  140374
Seq. ID
                  LIB25-010-Q1-E1-E12
Method
                  BLASTX
NCBI GI
                  g464707
BLAST score
                  727
E value
                  3.0e-77
Match length
                  141
                  99
% identity
NCBI Description
                 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal
                  protein S18.A - Arabidopsis thaliana
                  >gi_405613_emb CAA80684 (Z23165) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi 434343 emb CAA82273 (Z28701)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi_434345_emb CAA82274 (Z28702) S18 ribosomal protein
                  [Arabidopsis thaliana] >gi_434906 emb_CAA82275 (Z28962)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi 2505871 emb CAA72909_ (Y12227) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi 3287678 (AC003979) Match to
                  ribosomal S18 gene mRNA gb Z28701, DNA gb Z23165 from A.
                  thaliana. ESTs gb T21121, gb Z17755, gb R64776 and
                  gb R30430 come from this gene. [Arabidopsis thaliana]
                  >gi 4538910_emb CAB39647.1 (AL049482) S18.A ribosomal
                  protein [Arabidopsis thaliana]
Seq. No.
                  140375
Seq. ID
                  LIB25-010-Q1-E1-E8
Method
                  BLASTX
NCBI GI
                  q3024528
BLAST score
                  596
E value
                  6.0e-62
Match length
                  118
                  97
% identity
NCBI Description
                  RAS-RELATED PROTEIN RAB2BV >gi_974778 emb CAA89049
                  (Z49190) small G protein [Beta vulgaris]
Seq. No.
                  140376
Seq. ID
                  LIB25-010-Q1-E1-F6
Method
                  BLASTX
NCBI GI
                  q3860277
BLAST score
                  567
E value
                  1.0e-58
```

17043

(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604 (AC006232) putative





ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 140377 LIB25-010-Q1-E1-F8 Seq. ID Method BLASTX NCBI GI g2749752 BLAST score 147 E value 3.0e-09 Match length 133 % identity 37 NCBI Description (AL021086) /prediction=(method:; /match=(desc:; /match=(desc:; /match=(desc: [Drosophila melanogaster] Seq. No. 140378 Seq. ID LIB25-010-Q1-E1-G6 Method BLASTX NCBI GI q3152576 BLAST score 412 E value 2.0e-40 Match length 136 58 % identity NCBI Description (AC002986) Similar to liver-specific transport protein gb L27651 from Rattus norviegicus. [Arabidopsis thaliana] Seq. No. 140379 Seq. ID LIB25-011-Q1-E1-B1 Method BLASTX NCBI GI q2344896 BLAST score 135 E value 5.0e-08 Match length 110

% identity

NCBI Description (AC002388) hypothetical protein [Arabidopsis thaliana]

Seq. No. 140380

Seq. ID LIB25-011-Q1-E1-B10

Method BLASTN NCBI GI q2618605 BLAST score 363 E value 0.0e + 00Match length 394 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUK11, complete sequence [Arabidopsis thaliana]

Seq. No. 140381

Seq. ID LIB25-011-Q1-E1-B2

Method BLASTX NCBI GI g3549678 BLAST score 578 E value 8.0e-60 Match length 126 % identity 90

NCBI Description (AL031394) putative aspartate--tRNA ligase [Arabidopsis

thaliana]



```
Seq. No.
                  140382
Seq. ID
                  LIB25-011-Q1-E1-B8
Method
                  BLASTX
NCBI GI
                  g3337361
BLAST score
                  226
E value
                  2.0e-71
                  142
Match length
% identity
                  94
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]
Seq. No.
                  140383
Seq. ID
                  LIB25-011-Q1-E1-C7
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  25
E value
                  4.0e-04
Match length
                  36
% identity
                  60
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  140384
Seq. No.
                  LIB25-011-Q1-E1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1550740
BLAST score
                  748
E value
                  9.0e-80
Match length
                  144
% identity
                  99
NCBI Description (Y07961) GDP-associated inhibitor [Arabidopsis thaliana]
Seq. No.
                  140385
                  LIB25-011-Q1-E1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4235093
BLAST score
                  244
E value
                  1.0e-20
Match length
                  91
% identity
                  48
NCBI Description (AF108944) beta-xylosidase [Aspergillus niger]
                  140386
Seq. No.
Seq. ID
                  LIB25-011-Q1-E1-F6
Method
                  BLASTX
NCBI GI
                  q115767
BLAST score
                  594
E value
                  9.0e-62
Match length
                  114
% identity
                  99
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
```

Seq. No. 140387



```
Seq. ID
                  LIB25-011-Q1-E1-F7
Method
                  BLASTN
NCBI GI
                  q2760167
BLAST score
                  47
E value
                  1.0e-17
Match length
                  110
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCO15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140388
Seq. ID
                  LIB25-011-Q1-E1-F8
Method
                  BLASTX
                  q4186184
NCBI GI
BLAST score
                  235
E value
                  1.0e-19
Match length
                  91
% identity
                  48
NCBI Description (AF111168) unknown [Homo sapiens]
Seq. No.
                  140389
Seq. ID
                  LIB25-011-Q1-E1-G5
Method
                  BLASTX
NCBI GI
                  g2827713
BLAST score
                  722
E value
                  1.0e-76
Match length
                  143
% identity
                  100
NCBI Description
                  (AL021684) pyridoxal-phosphate-dependent aminotransferase -
                  like protein [Arabidopsis thaliana]
Seq. No.
                  140390
Seq. ID
                  LIB25-011-Q1-E1-G6
Method
                  BLASTX
NCBI GI
                  q4455273
BLAST score
                  431
E value
                  1.0e-42
Match length
                  122
% identity
                  75
                  (AL035527) subtilisin proteinase-like [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  140391
Seq. ID
                  LIB25-011-Q1-E1-H12
Method
                  BLASTX
NCBI GI
                  g3834325
BLAST score
                  526
E value
                  9.0e-54
Match length
                  104
% identity
                  100
NCBI Description
                  (AC005679) Strong similarity to gb AF067141 gamma-qlutamyl
```

hydrolase from Arabidopsis thaliana. ESTs gb R83955,

gb_T45062, gb_T22220, gb AA586207, gb AI099851 and gb_AI00672 come from this gene. [Arabidopsis thaliana]

Seq. No. 140392

Seq. ID LIB25-012-Q1-E1-A11



```
Method BLASTN
NCBI GI g3849811
BLAST score 193
E value 1.0e-104
Match length 214
% identity 97
NCBI Description Arabidopsis sequence, co
```

NCBI Description Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140393

 Seq. ID
 LIB25-012-Q1-E1-B1

 Method
 BLASTN

 NCBI GI
 g2529657

 BLAST score
 118

 E value
 6.0e-60

Match length 194 % identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140394

Seq. ID LIB25-012-Q1-E1-G2

Method BLASTN
NCBI GI g3859590
BLAST score 78
E value 7.0e-36
Match length 282
% identity 96

NCBI Description Arabidopsis thaliana BAC T15B16

Seq. No. 140395

Seq. ID LIB25-012-Q1-E1-G4

Method BLASTN
NCBI GI g3128138
BLAST score 234
E value 1.0e-129
Match length 234
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MFO20, complete sequence [Arabidopsis thaliana]

Seq. No. 140396

Seq. ID LIB25-012-Q1-E1-H10

Method BLASTX
NCBI GI g115783
BLAST score 483
E value 7.0e-49
Match length 91
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 140397

Seq. ID LIB25-012-Q1-E1-H8

Method BLASTN



NCBI GI g3868723 BLAST score 297 E value 1.0e-166 Match length 297 % identity 64

NCBI Description Arabidopsis thaliana chromosome V map 60.5 cM, complete

sequence [Arabidopsis thaliana]

Seq. No. 140398

Seq. ID LIB25-013-Q1-E1-B4

Method BLASTN
NCBI GI g2182287
BLAST score 228
E value 1.0e-125
Match length 228
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T7N9,

complete sequence [Arabidopsis thaliana]

Seq. No. 140399

Seq. ID LIB25-013-Q1-E1-C8

Method BLASTX
NCBI GI g115783
BLAST score 470
E value 3.0e-47
Match length 90
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 140400

Seq. ID LIB25-013-Q1-E1-F6

Method BLASTX
NCBI GI g2459435
BLAST score 569
E value 7.0e-59
Match length 120
% identity 86

NCBI Description (AC002332) putative serine carboxypeptidase [Arabidopsis

thaliana]

Seq. No. 140401

Seq. ID LIB25-013-Q1-E1-H6

Method BLASTN
NCBI GI g3849811
BLAST score 205
E value 1.0e-112
Match length 226
% identity 97

NCBI Description Arabidopsis thaliana chromosome I BAC T2P11 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140402

Seq. ID LIB25-013-Q1-E1-H9

Method BLASTX

```
NCBI GI
                   a4006913
BLAST score
                  476
E value
                  6.0e-48
Match length
                  100
% identity
                  95
NCBI Description
                  (Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  140403
Seq. ID
                  LIB25-014-Q1-E1-A5
Method
                  BLASTN
NCBI GI
                  g3869064
BLAST score
                  196
E value
                  1.0e-106
Match length
                  366
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K1013, complete sequence [Arabidopsis thaliana]
                  140404
Seq. No.
                  LIB25-014-Q1-E1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4704732
BLAST score
                  178
E value
                  6.0e-38
Match length
                  83
% identity
                  96
                  (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  140405
Seq. ID
                  LIB25-014-Q1-E1-C3
Method
                  BLASTX
NCBI GI
                  g4507081
BLAST score
                  165
E value
                  7.0e-12
Match length
                  78
% identity
                  40
NCBI Description
                  SWI/SNF related, matrix associated, actin dependent
                  regulator of chromatin, subfamily c, member 2 >gi_1549241
                  (U66616) SWI/SNF complex 170 KDa subunit [Homo sapiens]
Seq. No.
                  140406
Seq. ID
                  LIB25-014-Q1-E1-D10
Method
                  BLASTN
NCBI GI
                  g2264315
BLAST score
                  98
E value
                  3.0e-48
Match length
                  130
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRN17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140407
Seq. ID
                  LIB25-014-Q1-E1-E11
```

Method BLASTX NCBI GI g4587552 BLAST score 650 E value 2.0e-68



Match length 128 % identity 99

NCBI Description (AC006577) Strong similarity to gb_S77096 aldehyde

dehydrogenase homolog from Brassica napus and is a member of PF_00171 Aldehyde dehydrogenase family. ESTs gb_T46213,

gb_T4\(\bar{2}\)164, gb_T4\(\bar{3}\)682, gb_N9\(\bar{6}\)380, gb_T4\(\bar{2}\)973, gb

Seq. No. 140408

Seq. ID LIB25-014-Q1-E1-E5

Method BLASTN
NCBI GI g853718
BLAST score 150
E value 7.0e-79
Match length 229
% identity 100

NCBI Description A.thaliana mRNA for cytochrome P450

Seq. No. 140409

Seq. ID LIB25-014-Q1-E1-E7

Method BLASTX
NCBI GI g99696
BLAST score 439
E value 1.0e-43
Match length 110
% identity 81

NCBI Description glutamate--ammonia ligase (EC 6.3.1.2) precursor,

chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi 228453 prf_1804333A Gln

synthetase [Arabidopsis thaliana]

Seq. No. 140410

Seq. ID LIB25-014-Q1-E1-G11

Method BLASTX
NCBI GI g4038037
BLAST score 105
E value 2.0e-04
Match length 131
% identity 3

NCBI Description (AC005936) hypothetical protein [Arabidopsis thaliana]

Seq. No. 140411

Seq. ID LIB25-014-Q1-E1-H3

Method BLASTX
NCBI GI g1169422
BLAST score 306
E value 5.0e-28
Match length 72
% identity 85

NCBI Description DIHYDROFOLATE REDUCTASE 1 / THYMIDYLATE SYNTHASE 1

(DHFR-TS) >gi 289193 (L08593) dihydrofolate

reductase-thymidylate synthase [Arabidopsis thaliana]

Seq. No. 140412

Seq. ID LIB25-015-Q1-E1-D4

Method BLASTN



NCBI GI g4469002 BLAST score 321 E value 0.0e+00 Match length 321 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15

(ESSA project)

Seq. No. 140413

Seq. ID LIB25-015-Q1-E1-E9

Method BLASTN
NCBI GI g4159706
BLAST score 259
E value 1.0e-144
Match length 259
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGL6, complete sequence

Seq. No. 140414

Seq. ID LIB25-015-Q1-E1-F10

Method BLASTX
NCBI GI g4678949
BLAST score 544
E value 6.0e-56
Match length 111
% identity 62

NCBI Description (AL049711) dihydrolipoamide S-acetyltransferase precursor

[Arabidopsis thaliana]

Seq. No. 140415

Seq. ID LIB25-015-Q1-E1-F6

Method BLASTX
NCBI GI g1345592
BLAST score 568
E value 1.0e-58
Match length 115
% identity 100

NCBI Description 14-3-3-LIKE PROTEIN GF14 EPSILON >gi 1022778 (U36446) GF14

epsilon isoform [Arabidopsis thaliana]

Seq. No. 140416

Seq. ID LIB25-016-Q1-E1-C8

Method BLASTN
NCBI GI g3047074
BLAST score 170
E value 6.0e-91
Match length 238
% identity 98

NCBI Description Arabidopsis thaliana BAC F21E10

Seq. No. 140417

Seq. ID LIB25-016-Q1-E1-E10

Method BLASTX
NCBI GI g4337025
BLAST score 265
E value 3.0e-23



```
Match length
% identity
                  100
NCBI Description
                  (AF123253) AIM1 protein [Arabidopsis thaliana]
                  140418
Seq. No.
Seq. ID
                  LIB25-016-Q1-E1-F11
Method
                  BLASTX
NCBI GI
                  q113512
BLAST score
                  330
E value
                  9.0e-31
Match length
                  66
% identity
                  100
NCBI Description
                  FLORAL HOMEOTIC PROTEIN AGL2 >gi 81610 pir B39534 floral
                  homeotic protein AGL2 - Arabidopsis thaliana >gi_166591
                  (M55551) transcription factor [Arabidopsis thaliana]
                  140419
Seq. No.
Seq. ID
                  LIB25-016-Q1-E1-G7
Method
                  BLASTN
NCBI GI
                  g4159705
BLAST score
                  409
E value
                  0.0e+00
Match length
                  413
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGD8, complete sequence
Seq. No.
                  140420
Seq. ID
                  LIB25-016-Q1-E1-H4
Method
                  BLASTN
NCBI GI
                  g2828187
BLAST score
                  293
E value
                  1.0e-164
Match length
                  365
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21C13, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140421
Seq. ID
                  LIB25-016-Q1-E1-H8
Method
                  BLASTN
NCBI GI
                  g4490291
BLAST score
                  79
E value
                  6.0e-37
Match length
                  125
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5
                  (ESSA project)
```

Seq. No. 140422

Seq. ID LIB25-017-Q1-E1-A10

Method BLASTN
NCBI GI g3193311
BLAST score 392
E value 0.0e+00
Match length 396
% identity 94



NCBI Description Arabidopsis thaliana BAC F6N15

 Seq. No.
 140423

 Seq. ID
 LIB25-017-Q1-E1-A3

 Method
 BLASTN

Method BLASTN
NCBI GI g166787
BLAST score 112
E value 2.0e-56
Match length 147
% identity 99

NCBI Description A.thaliana chloroplast ATP synthase gamma subunit (atpC2)

gene, complete cds

Seq. No. 140424

Seq. ID LIB25-017-Q1-E1-A6

Method BLASTX
NCBI GI g4204258
BLAST score 439
E value 7.0e-44
Match length 91

% identity 89

NCBI Description (AC005223) 14409 [Arabidopsis thaliana]

Seq. No. 140425

Seq. ID LIB25-017-Q1-E1-A7

Method BLASTX
NCBI GI g3420054
BLAST score 311
E value 1.0e-28
Match length 136
% identity 62

NCBI Description (AC004680) unknown protein [Arabidopsis thaliana]

Seq. No. 140426

Seq. ID LIB25-017-Q1-E1-A9

Method BLASTN
NCBI GI g3406034
BLAST score 100
E value 3.0e-49
Match length 157
% identity 98

NCBI Description BAC F18A17 from chromosome V containing TINY at 60.5 cM,

complete sequence [Arabidopsis thaliana]

Seq. No. 140427

Seq. ID LIB25-017-Q1-E1-B11

Method BLASTN
NCBI GI g4468103
BLAST score 231
E value 1.0e-127
Match length 271
% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9

(ESSA project)

Seq. No. 140428

Seq. ID LIB25-017-Q1-E1-C5

E value

Match length

0.0e+00

333



```
Method
                  BLASTN
NCBI GI
                  q2275194
                  149
BLAST score
                  3.0e-78
E value
Match length
                  352
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T08I13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  140429
Seq. No.
                  LIB25-017-Q1-E1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3406034
BLAST score
                  91
                  1.0e-43
E value
Match length
                  292
                  100
% identity
                  BAC F18A17 from chromosome V containing TINY at 60.5 cM,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  140430
                  LIB25-017-Q1-E1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3004565
BLAST score
                  79
E value
                  2.0e-31
Match length
                  104
% identity
                  68
                  (AC003673) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  140431
Seq. No.
                  LIB25-017-Q1-E1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3184279
BLAST score
                  244
E value
                  5.0e-21
Match length
                  92
% identity
                  13
                  (AC004136) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  140432
                  LIB25-017-Q1-E1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244971
BLAST score
                  384
E value
                  3.0e-37
Match length
                  103
% identity
                  70
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  140433
Seq. ID
                  LIB25-017-Q1-E1-H5
Method
                  BLASTN
NCBI GI
                  g2191157
BLAST score
                  333
```



```
% identity
                  100
NCBI Description Arabidopsis thaliana BAC IG002P16
Seq. No.
                  140434
                  LIB25-018-Q1-E1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4588012
BLAST score
                  467
E value
                  7.0e-47
Match length
                  119
% identity
                  82
NCBI Description
                  (AF085717) putative callose synthase catalytic subunit
                  [Gossypium hirsutum]
Seq. No.
                  140435
Seq. ID
                  LIB25-018-Q1-E1-B2
Method
                  BLASTN
NCBI GI
                  q4220510
BLAST score
                  189
E value
                  1.0e-102
Match length
                  189
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
NCBI Description
                  (ESSAII project)
Seq. No.
                  140436
                  LIB25-018-Q1-E1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220510
BLAST score
                  286
E value
                  1.0e-160
Match length
                  384
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
                  (ESSAII project)
Seq. No.
                  140437
Seq. ID
                  LIB25-018-Q1-E1-E9
Method
                  BLASTX
NCBI GI
                  g3063698
BLAST score
                  322
E value
                  6.0e-30
Match length
                  109
% identity
                  58
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                  140438
                  LIB25-018-Q1-E1-F1
Seq. ID
Method
```

BLASTN NCBI GI g304114 BLAST score 156 E value 1.0e-82 Match length 164 % identity 99

NCBI Description Arabidopsis thaliana thioglucosidase mRNA, complete cds

Seq. No. 140439



Seq. ID LIB25-018-Q1-E1-F10

Method BLASTN
NCBI GI g4335744
BLAST score 73
E value 8.0e-33
Match length 197
% identity 84

NCBI Description Arabidopsis thaliana chromosome II BAC T4M8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140440

Seq. ID LIB25-018-Q1-E1-H3

Method BLASTX
NCBI GI 94586047
BLAST score 596
E value 6.0e-62
Match length 129
% identity 92

NCBI Description (AC007020) putative ferritin protein [Arabidopsis thaliana]

>gi_4588004_gb_AAD25945.1_AF085279_18 (AF085279)
hypothetical ferritin subunit [Arabidopsis thaliana]

Seq. No. 140441

Seq. ID LIB25-019-Q1-E1-A1

Method BLASTN
NCBI GI g3075383
BLAST score 206
E value 1.0e-112
Match length 319
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T1D16 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140442

Seq. ID LIB25-019-Q1-E1-A4

Method BLASTN
NCBI GI g3168605
BLAST score 176
E value 1.0e-94
Match length 176
% identity 100

NCBI Description Arabidopsis thaliana catalase 3 (CAT3) and catalase 1

(CAT1) genes, complete cds

Seq. No. 140443

Seq. ID LIB25-019-Q1-E1-A5

Method BLASTN
NCBI GI g2342673
BLAST score 387
E value 0.0e+00
Match length 394
% identity 100

NCBI Description Sequence of BAC F7G19 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 140444

Seq. ID LIB25-019-Q1-E1-B10



Method BLASTX
NCBI GI g3413717
BLAST score 613
E value 6.0e-64
Match length 117
% identity 100

NCBI Description (AC004747) unknown protein [Arabidopsis thaliana]

>gi_3643590 (AC005395) unknown protein [Arabidopsis

thaliana]

Seq. No. 140445

Seq. ID LIB25-019-Q1-E1-B7

Method BLASTN
NCBI GI g3608126
BLAST score 71
E value 2.0e-32
Match length 71
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T32F12 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140446

Seq. ID LIB25-019-Q1-E1-C6

Method BLASTN
NCBI GI g555975
BLAST score 107
E value 1.0e-53
Match length 107
% identity 100

NCBI Description Arabidopsis thaliana metallothionein-like protein (AtMT-K)

mRNA, complete cds

Seq. No. 140447

Seq. ID LIB25-019-Q1-E1-D9

Method BLASTX
NCBI GI g1172873
BLAST score 642
E value 2.0e-67
Match length 127
% identity 100

NCBI Description CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719

drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_

(D13043) thiol protease [Arabidopsis thaliana]

Seq. No. 140448

Seq. ID LIB25-019-Q1-E1-E5

Method BLASTX
NCBI GI g267069
BLAST score 631
E value 5.0e-66
Match length 117
% identity 100

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594

tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

% identity

NCBI Description

76

[Arabidopsis thaliana]



```
Seq. No.
                  140449
Seq. ID
                  LIB25-019-Q1-E1-E8
Method
                  BLASTX
NCBI GI
                  g549975
BLAST score
                  718
E value
                  3.0e-76
Match length
                  143
                  99
% identity
NCBI Description
                  (U12858) nucleosome assembly protein I-like protein;
                  similar to mouse nap I, PIR Accession Number JS0707
                  [Arabidopsis thaliana]
Seq. No.
                  140450
Seq. ID
                  LIB25-019-Q1-E1-F1
Method
                  BLASTN
NCBI GI
                  q3668073
BLAST score
                  235
E value
                  1.0e-129
Match length
                  259
                  97
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T4C15 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140451
Seq. ID
                  LIB25-019-Q1-E1-G11
Method
                  BLASTX
                  g4415907
NCBI GI
BLAST score
                  553
E value
                  6.0e-57
Match length
                  110
                  98
% identity
                  (AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana]
NCBI Description
                  >gi_4581159_gb_AAD24643.1 AC006919 21 (AC006919) putative
                  60S ribosomal protein L24 [Arabidopsis thaliana]
Seq. No.
                  140452
Seq. ID
                  LIB25-019-Q1-E1-G8
Method
                  BLASTN
NCBI GI
                  g2264313
BLAST score
                  210
E value
                  1.0e-115
Match length
                  210
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MOP10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140453
Seq. ID
                  LIB25-020-Q1-E1-A4
Method
                  BLASTX
NCBI GI
                  q1778015
BLAST score
                  237
                  2.0e-20
E value
Match length
                  59
```

17058

(U59508) osmotic stress-induced proline dehydrogenase



```
Seq. No.
                  140454
                  LIB25-020-Q1-E1-B3
Seq. ID
Method
                  BLASTX
                  q3860420
NCBI GI
                  168
BLAST score
E value
                  6.0e-12
                  70
Match length
% identity
                  44
                  (AJ011047) exo galactanase [Lupinus angustifolius]
NCBI Description
Seq. No.
                  140455
Seq. ID
                  LIB25-020-Q1-E1-C11
Method
                  BLASTN
NCBI GI
                  q4589434
                  376
BLAST score
                  0.0e + 00
E value
Match length
                  380
% identity
                  78
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNJ7, complete sequence
                  140456
Seq. No.
Seq. ID
                  LIB25-020-Q1-E1-D4
Method
                  BLASTN
NCBI GI
                  g2832667
BLAST score
                  51
E value
                  8.0e-20
Match length
                  51
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14
NCBI Description
                  (ESSAII project)
Seq. No.
                  140457
Seq. ID
                  LIB25-020-Q1-E1-D8
Method
                  BLASTN
NCBI GI
                  q4159705
BLAST score
                  201
E value
                  1.0e-109
Match length
                  305
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGD8, complete sequence
Seq. No.
                  140458
Seq. ID
                  LIB25-020-Q1-E1-E4
Method
                  BLASTN
NCBI GI
                  g3869074
BLAST score
                  419
                  0.0e + 00
E value
                  430
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MMI9, complete sequence [Arabidopsis thaliana]
```

17059

140459

LIB25-020-Q1-E1-E5

Seq. No. Seq. ID



```
Method
                  BLASTX
NCBI GI
                   q577301
BLAST score
                   200
E value
                   2.0e-15
                  121
Match length
                   40
% identity
                  (D42044) The ha3523 gene product is related to S.cerevisiae
NCBI Description
                  gene product located in chromosome III. [Homo sapiens]
                   140460
Seq. No.
Seq. ID
                  LIB25-020-Q1-E1-F6
Method
                  BLASTX
NCBI GI
                   q3805849
                   334
BLAST score
                   3.0e-31
E value
Match length
                   65
                   98
% identity
NCBI Description
                   (AL031986) cytoplasmatic aconitate hydratase (citrate
                  hydro-lyase) (aconitase) (EC 4.2.1.3) [Arabidopsis thaliana]
                  140461
Seq. No.
                  LIB25-020-Q1-E1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1871199
BLAST score
                   165
E value
                   2.0e-11
Match length
                  131
                  17
% identity
                  (U91318) pM5 (3' partial) [Homo sapiens]
NCBI Description
Seq. No.
                   140462
                  LIB25-020-Q1-E1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4567303
BLAST score
                   546
E value
                   4.0e-56
Match length
                   102
                   100
% identity
                  (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
                   140463
Seq. No.
Seq. ID
                   LIB25-020-Q1-E1-H5
Method
                   BLASTX
NCBI GI
                   q4826435
BLAST score
                   89
E value
                   1.8e-02
Match length
                   98
% identity
                   15
NCBI Description
                  (AL031447) dJ126A5.4 (KIAA0469) [Homo sapiens]
Seq. No.
                   140464
Seq. ID
                   LIB25-021-Q1-E1-A2
                   BLASTN
Method
NCBI GI
                   g4589434
BLAST score
```

17060

174

222

3.0e-93

E value

Match length



% identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence 140465 Seq. No. LIB25-021-Q1-E1-A5 Seq. ID Method BLASTX g2688544 NCBI GI BLAST score 216 E value 2.0e-17 Match length 108 % identity 38 NCBI Description (AE001163) 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein (thiJ) [Borrelia burgdorferi] Seq. No. 140466 Seq. ID LIB25-021-Q1-E1-C2 Method BLASTX NCBI GI q3549681 BLAST score 443 5.0e-44 E value Match length 123 % identity 78 NCBI Description (AL031394) male sterility 2-like protein [Arabidopsis thaliana] 140467 Seq. No. Seq. ID LIB25-021-Q1-E1-D3 Method BLASTX NCBI GI g16374 BLAST score 359 3.0e-34 E value Match length 69 % identity 100 NCBI Description (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana] Seq. No. 140468 Seq. ID LIB25-021-Q1-E1-E8 Method BLASTX NCBI GI g3805846 BLAST score 717 E value 4.0e-76 Match length 138 100 % identity (AL031986) DNA-directed RNA polymerase (EC 2.7.7.6) II NCBI Description largest chain [Arabidopsis thaliana]

Seq. No. 140469

Seq. ID LIB25-021-Q1-E1-F6

Method BLASTN NCBI GI q166589 BLAST score 104 E value 1.0e-51 Match length 216 % identity 88



```
NCBI Description
                  Arabidopsis thaliana transcription factor (AGL2) mRNA,
                  complete cds
                  140470
Seq. No.
Seq. ID
                  LIB25-021-Q1-E1-G1
Method
                  BLASTN
NCBI GI
                  g4220627
BLAST score
                  326
E value
                  0.0e + 00
Match length
                  366
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K20J1, complete sequence [Arabidopsis thaliana]
                  140471
Seq. No.
Seq. ID
                  LIB25-021-Q1-E1-G5
Method
                  BLASTN
NCBI GI
                  g3193282
BLAST score
                  252
E value
                  1.0e-140
Match length
                  300
                  100
% identity
NCBI Description Arabidopsis thaliana BAC T14P8
                  140472
Seq. No.
Seq. ID
                  LIB25-021-Q1-E1-H11
Method
                  BLASTX
NCBI GI
                  q2507587
BLAST score
                  284
E value
                  2.0e-25
Match length
                  57
% identity
                  88
NCBI Description
                  METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G)
                  >gi 1361998 pir S57861 metallothionein 2a - Arabidopsis
                  thaliana >gi_55\overline{59}76 (U15108) metallothionein-like protein
                   [Arabidopsis thaliana] >gi 1580892 prf 2116236A
                  metallothionein 1 [Arabidopsis thaliana]
                  140473
Seq. No.
Seq. ID
                  LIB25-021-Q1-E1-H9
Method
                  BLASTX
NCBI GI
                  g2244866
                  379
BLAST score
                  2.0e-36
E value
Match length
                  117
                  56
% identity
NCBI Description
                 (Z97337) hypothetical protein [Arabidopsis thaliana]
```

Seq. ID LIB25-022-Q1-E1-C8

Method BLASTN NCBI GI g3985957 BLAST score 222 1.0e-121 E value Match length 424 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:





MYN8, complete sequence [Arabidopsis thaliana]

Seq. No. 140475 LIB25-022-Q1-E1-D11 Seq. ID Method BLASTX NCBI GI g2443886 BLAST score 446 E value 2.0e-44 Match length 89 100 % identity NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana] Seq. No. 140476 Seq. ID LIB25-022-Q1-E1-D12 Method BLASTX g3157937 NCBI GI BLAST score 699 5.0e-74 E value Match length 138 % identity 99 NCBI Description (AC002131) Identical to aspartic proteinase cDNA gb_U51036 from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb AA728734, gb Seq. No. 140477 LIB25-022-Q1-E1-D9 Seq. ID Method BLASTX NCBI GI q1619956 BLAST score 434 6.0e-43 E value Match length 96 % identity 89 NCBI Description thaliana]

(U72151) voltage-gated chloride channel [Arabidopsis

140478 Seq. No.

LIB25-022-Q1-E1-E11 Seq. ID

Method BLASTX NCBI GI q4587514 BLAST score 282 E value 4.0e-25 Match length 54 % identity 100

(AC007060) Similar to WO8E3.3 gi_3880615 putative NCBI Description

GTP-binding protein from C. elegans cosmid gb Z92773. EST gb AA597331 comes from this gene. [Arabidopsis thaliana]

Seq. No. 140479

Seq. ID LIB25-022-Q1-E1-F11

Method BLASTN NCBI GI q4757395 BLAST score 66 E value 5.0e-29 Match length 136 % identity 92



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No. 140480

Seq. ID LIB25-022-Q1-E1-F9

Method BLASTN
NCBI GI g2494106
BLAST score 431
E value 0.0e+00
Match length 431
% identity 100

NCBI Description Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 140481

Seq. ID LIB25-023-Q1-E1-A11

Method BLASTN
NCBI GI g3763944
BLAST score 303
E value 1.0e-170
Match length 307
% identity 78

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23

(ESSAII project)

Seq. No. 140482

Seq. ID LIB25-023-Q1-E1-A4

Method BLASTN
NCBI GI g2275194
BLAST score 295
E value 1.0e-165
Match length 298
% identity 100

% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T08I13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.

No. 140483

Seq. ID LIB25-023-Q1-E1-B1

Method BLASTN
NCBI GI 94220468
BLAST score 154
E value 3.0e-81
Match length 286
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T8011 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140484

Seq. ID LIB25-023-Q1-E1-B2

Method BLASTX
NCBI GI g2462833
BLAST score 530
E value 2.0e-54
Match length 108
% identity 99

NCBI Description (AF000657) highly similar to froha and frohb, potential

frohc [Arabidopsis thaliana]



```
Seq. No.
                  140485
Seq. ID
                  LIB25-023-Q1-E1-B6
Method
                  BLASTX
NCBI GI
                  q2244750
                  581
BLAST score
E value
                  3.0e-60
Match length
                  124
% identity
                  89
                  (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
NCBI Description
                  >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                  [Arabidopsis thaliana]
Seq. No.
                  140486
                  LIB25-023-Q1-E1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2262115
BLAST score
                  521
E value
                  2.0e-53
Match length
                  97
                  99
% identity
NCBI Description
                  (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
                  140487
Seq. No.
Seq. ID
                  LIB25-023-Q1-E1-D9
Method
                  BLASTN
NCBI GI
                  g4454004
BLAST score
                  149
E value
                  4.0e-78
Match length
                  415
% identity
                  97
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6
                  (ESSAII project)
Seq. No.
                  140488
Seq. ID
                  LIB25-023-Q1-E1-E11
Method
                  BLASTN
NCBI GI
                  g2924733
BLAST score
                  22
E value
                  2.0e-02
                  336
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUF9, complete sequence [Arabidopsis thaliana]
```

Seq. ID LIB25-023-Q1-E1-E4

Method BLASTX
NCBI GI g4309698
BLAST score 601
E value 1.0e-62
Match length 115
% identity 97

NCBI Description (AC006266) putative glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 140490



LIB25-023-Q1-E1-F4 Seq. ID Method BLASTN NCBI GI q4455348 152 BLAST score 3.0e-80 E value Match length 230 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project) 140491 Seq. No. LIB25-023-Q1-E1-F6 Seq. ID Method BLASTX NCBI GI q2191175 538 BLAST score 3.0e-55 E value Match length 101 % identity 100 (AF007270) A IG002P16.24 gene product [Arabidopsis NCBI Description thaliana] 140492 Seq. No. LIB25-023-Q1-E1-H5 Seq. ID Method BLASTX NCBI GI q120675 BLAST score 518 E value 9.0e-53 Match length 134 % identity 76 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844 (X04301) GAPDH (aa 1-338) [Sinapis alba] Seq. No. 140493 Seq. ID LIB25-024-Q1-E1-B1 Method BLASTX NCBI GI q2129538 BLAST score 375 E value 3.0e-36 Match length 76 100 % identity NCBI Description AT103 protein - Arabidopsis thaliana >gi 1033195 (U38232) AT103 [Arabidopsis thaliana] 140494 Seq. No. Seq. ID LIB25-024-Q1-E1-B2 Method BLASTN NCBI GI q4455290 BLAST score 198 E value 1.0e-107

Match length 206 % identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5

(ESSAII project)



```
Seq. No.
                  140495
                  LIB25-024-Q1-E1-C3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4337186
BLAST score
                  24
                  1.0e-03
E value
Match length
                  348
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T28I24 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140496
                  LIB25-024-Q1-E1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3176694
BLAST score
                  112
E value
                  1.0e-56
Match length
                  112
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T14N5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140497
                  LIB25-024-Q1-E1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1199466
BLAST score
                  44
                  7.0e-16
E value
Match length
                  48
                  98
% identity
                  Arabidopsis thaliana CER1 mRNA for possible aldehyde
NCBI Description
                  decarbonylase, complete cds >gi 3717039 emb A63188.1 A63188
                  Sequence 2 from Patent EP0776973
                  140498
Seq. No.
                  LIB25-024-Q1-E1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1181530
BLAST score
                  145
E value
                  4.0e-76
Match length
                  193
% identity
                  94
NCBI Description Arabidopsis thaliana thionin (Thi2.1) mRNA, complete cds
Seq. No.
                  140499
Seq. ID
                  LIB25-025-Q1-E1-A12
Method
                  BLASTX
                  g4587550
                  648
```

NCBI GI BLAST score 5.0e-68 E value Match length 138 % identity

NCBI Description (AC006577) EST gb R64848 comes from this gene. [Arabidopsis

thaliana]

140500 Seq. No.

Seq. ID LIB25-025-Q1-E1-A4



Method BLASTX
NCBI GI g3582328
BLAST score 163
E value 3.0e-11
Match length 112
% identity 20

NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 140501

Seq. ID LIB25-026-Q1-E1-B8

Method BLASTN
NCBI GI g2564047
BLAST score 85
E value 6.0e-40
Match length 442
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJB21, complete sequence [Arabidopsis thaliana]

Seq. No. 140502

Seq. ID LIB25-026-Q1-E1-C3

Method BLASTN
NCBI GI g2351065
BLAST score 194
E value 1.0e-105
Match length 358
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MHF15, complete sequence [Arabidopsis thaliana]

Seq. No. 140503

Seq. ID LIB25-026-Q1-E1-F1

Method BLASTN
NCBI GI g2244901
BLAST score 301
E value 1.0e-169
Match length 389
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 140504

Seq. ID LIB25-026-Q1-E1-F7

Method BLASTN
NCBI GI g3869071
BLAST score 211
E value 1.0e-115
Match length 279
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MIL23, complete sequence [Arabidopsis thaliana]

Seq. No. 140505

Seq. ID LIB25-026-Q1-E1-G10

Method BLASTX
NCBI GI g4115918
BLAST score 175



8.0e-16 E value Match length 63 77 % identity (AF118222) similar to nascent polypeptide associated NCBI Description complex alpha chain [Arabidopsis thaliana] Seq. No. 140506 LIB25-026-Q1-E1-H6 Seq. ID Method BLASTX g2760330 NCBI GI BLAST score 354 E value 1.0e-33 Match length 83 % identity 80 NCBI Description (AC002130) F1N21.15 [Arabidopsis thaliana] Seq. No. 140507 Seq. ID LIB25-026-Q1-E1-H9 Method BLASTN NCBI GI g3402695 BLAST score 314 E value 1.0e-176 Match length 334 % identity 99 NCBI Description Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 140508 Seq. ID LIB25-027-Q1-E1-A1 Method BLASTX NCBI GI g1345595 BLAST score 316 9.0e-30 E value Match length 65 % identity 100 NCBI Description 14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1) >gi_1084332_pir__S53727 14-3-3-like protein (ATF1) -Arabidopsis thaliana >gi_953221 (U02565) 14-3-3-like protein 1 [Arabidopsis thaliana] >gi 1549404 (U68545) GF14 lambda [Arabidopsis thaliana] Seq. No. 140509 Seq. ID LIB25-027-Q1-E1-A8 Method BLASTX NCBI GI g1684913 BLAST score 133 E value 8.0e-08 Match length 101 % identity NCBI Description (U77888) receptor-like protein kinase [Ipomoea nil] Seq. No. 140510

Seq. ID LIB25-027-Q1-E1-C3

Method BLASTX NCBI GI g4249662 BLAST score 254 E value 5.0e-22



Match length 52 % identity 100

NCBI Description (AF089810) Altered Response to Gravity [Arabidopsis

thaliana]

Seq. No. 140511

Seq. ID LIB25-027-Q1-E1-E4

Method BLASTN
NCBI GI g4558521
BLAST score 158
E value 7.0e-84
Match length 182
% identity 97

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T10024,

complete sequence

Seq. No. 140512

Seq. ID LIB25-027-Q1-E1-E8

Method BLASTX
NCBI GI g1076291
BLAST score 202
E value 2.0e-54
Match length 110
% identity 100

NCBI Description amino acid transporter AAT1 - Arabidopsis thaliana

>gi_2911069 emb CAA17531.1 (AL021960) amino acid transport

protein AAT1 [Arabidopsis thaliana]

Seq. No. 140513

Seq. ID LIB25-027-Q1-E1-F2

Method BLASTX
NCBI GI g3738288
BLAST score 200
E value 4.0e-16
Match length 61
% identity 56

NCBI Description (AC005309) auxin-responsive GH3-like protein [Arabidopsis

thaliana]

Seq. No. 140514

Seq. ID LIB25-027-Q1-E1-F3

Method BLASTN
NCBI GI 94584519
BLAST score 292
E value 1.0e-163
Match length 312
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18

(ESSA project)

Seq. No. 140515

Seq. ID LIB25-027-Q1-E1-G2

Method BLASTX
NCBI GI g4539465
BLAST score 436
E value 1.0e-43
Match length 88



% identity 98

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 140516

Seq. ID LIB25-027-Q1-E1-H2

Method BLASTN
NCBI GI g4567300
BLAST score 275
E value 1.0e-153
Match length 291
% identity 99

NCBI Description Arabidopsis thaliana chromosome II P1 MHK10 genomic

sequence, complete sequence

Seq. No. 140517

Seq. ID LIB25-028-Q1-E1-A8

Method BLASTN
NCBI GI g313837
BLAST score 149
E value 2.0e-78
Match length 189
% identity 95

NCBI Description A.thaliana gene for hemC

Seq. No. 140518

Seq. ID LIB25-028-Q1-E1-C7

Method BLASTN
NCBI GI g4757413
BLAST score 231
E value 1.0e-127
Match length 312
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MXO21, complete sequence

Seq. No. 140519

Seq. ID LIB25-028-Q1-E1-H4

Method BLASTX
NCBI GI g4510395
BLAST score 573
E value 2.0e-59
Match length 107
% identity 100

NCBI Description (AC006587) putative beta-galactosidase precursor

[Arabidopsis thaliana]

Seq. No. 140520

Seq. ID LIB25-028-Q1-E1-H7

Method BLASTN
NCBI GI g3522932
BLAST score 168
E value 1.0e-89
Match length 260
% identity 92

NCBI Description Arabidopsis thaliana chromosome II BAC F14M4 genomic



```
Seq. No.
                  140521
                  LIB25-029-Q1-E1-A11
Seq. ID
Method
                  BLASTN
                  g4510323
NCBI GI
BLAST score
                  251
                  1.0e-139
E value
                  303
Match length
% identity
                  96
                  Arabidopsis thaliana BAC T7B11 from chromosome IV near 10
NCBI Description
                  cM, complete sequence
                  140522
Seq. No.
                  LIB25-029-Q1-E1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245004
BLAST score
                  391
                  7.0e-38
E value
Match length
                  143
                  55
% identity
                  (Z97341) similarity to membrane transport protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  140523
                  LIB25-029-Q1-E1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263519
BLAST score
                  420
E value
                  2.0e-41
Match length
                  86
                  94
% identity
NCBI Description
                   (ACO04044) small nuclear riboprotein Sm-D1 [Arabidopsis
                  thaliana]
                  140524
Seq. No.
Seq. ID
                  LIB25-029-Q1-E1-D5
Method
                  BLASTX
NCBI GI
                  g4263791
                  709
BLAST score
E value
                  3.0e-75
Match length
                  137
% identity
                  98
NCBI Description
                   (AC006068) putative receptor protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  140525
                  LIB25-029-Q1-E1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567305
BLAST score
                  704
                  1.0e-74
E value
Match length
                  128
```

% identity

NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana]

Seq. No.

140526 LIB25-029-Q1-E1-F1

99

Seq. ID LIB25-02

Method BLASTN



 NCBI GI
 g4544381

 BLAST score
 270

 E value
 1.0e-150

 Match length
 382

 % identity
 100

NCBI Description Arabidopsis thaliana chromosome II BAC F16F14 genomic

sequence, complete sequence

Seq. No. 140527

Seq. ID LIB25-029-Q1-E1-G12

Method BLASTN
NCBI GI g4589432
BLAST score 225
E value 1.0e-123
Match length 343
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MMJ24, complete sequence

Seq. No. 140528

Seq. ID LIB25-029-Q1-E1-G5

Method BLASTN
NCBI GI g3831448
BLAST score 178
E value 1.0e-95
Match length 245
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T32F6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140529

Seq. ID LIB25-029-Q1-E1-H7

Method BLASTN
NCBI GI g3241924
BLAST score 265
E value 1.0e-147
Match length 319
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNC6, complete sequence [Arabidopsis thaliana]

Seq. No. 140530

Seq. ID LIB25-029-Q1-E1-H9

Method BLASTX
NCBI GI g3850571
BLAST score 430
E value 2.0e-42
Match length 83
% identity 100

NCBI Description (AC005278) Similar to gb_U85207 snRNP core Sm protein

homolog Sm-X5 from Mus musculus. EST gb AA612141 comes

from this gene. [Arabidopsis thaliana]

Seq. No. 140531

Seq. ID LIB25-030-Q1-E1-D4

Method BLASTX NCBI GI g3335366



BLAST score E value 8.0e-17 101 Match length 40 % identity (AC003028) unknown protein [Arabidopsis thaliana] NCBI Description 140532 Seq. No. LIB25-030-Q1-E1-E2 Seq. ID Method BLASTN NCBI GI g4432811 BLAST score 43 E value 6.0e-15 Match length 79 % identity 89 Arabidopsis thaliana chromosome II BAC F16D14 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 140533 Seq. No. LIB25-031-Q1-E1-F6 Seq. ID BLASTN Method g4006885 NCBI GI BLAST score 62 9.0e-27 E value Match length 118 % identity 88 Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig NCBI Description fragment No 140534 Seq. No. LIB25-032-Q1-E1-C12 Seq. ID Method BLASTN NCBI GI g414339 BLAST score 37 E value 6.0e-12 Match length 85 % identity 86 NCBI Description A.thaliana rd19A gene for thiol protease, exon 1, exon 2 and exon Seq. No. 140535 Seq. ID LIB25-032-Q1-E1-F4 Method BLASTX NCBI GI g4633131 BLAST score 485 E value 4.0e-49 Match length 97 100 % identity

(AF110407) ATP sulfurylase precursor [Arabidopsis thaliana] NCBI Description

>gi 4803653 emb CAB42640.1 (AJ012586) sulfate

adenylyltransferase [Arabidopsis thaliana]

140536 Seq. No.

Seq. ID LIB25-032-Q1-E1-F6

Method BLASTX NCBI GI g2811292 BLAST score 289 4.0e-26 E value



```
Match length
 % identity
 NCBI Description
                    (AF043343) putative vegetative storage protein [Arabidopsis
 Seq. No.
                   140537
 Seq. ID
                   LIB25-032-Q1-E1-H6
 Method
                   BLASTX
 NCBI GI
                   q4455243
 BLAST score
                   523
 E value
                   2.0e-53
 Match length
                   117
 % identity
                   86
                   (AL035523) alpha-amylase-like protein [Arabidopsis
 NCBI Description
                   thaliana]
 Seq. No.
                   140538
 Seq. ID
                   LIB25-032-Q1-E1-H7
 Method
                   BLASTX
 NCBI GI
                   q461498
 BLAST score
                   507
                   1.0e-51
 E value
 Match length
                   112
 % identity
                   86
 NCBI Description ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
                   TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                    (ALAAT-2) >gi_320619_pir__S28429 alanine transaminase (EC
                   2.6.1.2) - proso millet >gi_296204 emb_CAA49199_ (X69421)
                   alanine aminotransferase [Panicum miliaceum]
 Seq. No.
                   140539
 Seq. ID
                   LIB25-033-Q1-E1-A2
 Method
                   BLASTX
 NCBI GI
                   g4206194
BLAST score
                   631
                    4.0e-66
 E value
 Match length
                   122
                   100
 % identity
                   (AF071527) GH3-like protein [Arabidopsis thaliana]
 NCBI Description
                   >gi_4262168_gb_AAD14468_ (AC005275) putative GH3-like
                   protein [Arabidopsis thaliana]
 Seq. No.
                   140540
 Seq. ID
                   LIB25-033-Q1-E1-B5
 Method
                   BLASTX
 NCBI GI
                   q400515
 BLAST score
                   164
 E value
                   1.0e-11
 Match length
                   57
                   54
 % identity
 NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE B8 SUBUNIT (COMPLEX I-B8)
                    (CI-B8) >gi 346540 pir S28249 NADH dehydrogenase
                    (ubiquinone) (EC 1.6.5.3) chain CI-B8 - bovine
```

taurus]

>gi_246_emb_CAA44904 (X63219) NADH dehydrogenase [Bos



```
LIB25-033-Q1-E1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2618683
BLAST score
                  184
                  2.0e-99
E value
Match length
                  184
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T32G6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  140542
Seq. No.
Seq. ID
                  LIB25-033-Q1-E1-B9
Method
                  BLASTX
                  g3135254
NCBI GI
BLAST score
                  285
E value
                  5.0e-26
Match length
                  62
% identity
                  87
NCBI Description
                  (AC003058) hypothetical protein [Arabidopsis thaliana]
                  140543
Seq. No.
                  LIB25-033-Q1-E1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2832689
BLAST score
                  158
E value
                  6.0e - 84
Match length
                  158
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21
NCBI Description
                  (ESSAII project)
Seq. No.
                  140544
Seq. ID
                  LIB25-033-Q1-E1-G4
Method
                  BLASTN
NCBI GI
                  g3080430
BLAST score
                  223
E value
                  1.0e-122
Match length
                  454
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19
                  (ESSAII project)
Seq. No.
                  140545
Seq. ID
                  LIB25-033-Q1-E1-G7
Method
                  BLASTX
NCBI GI
                  q2281631
BLAST score
                  446
E value
                  2.0e-44
Match length
                  86
% identity
                  100
                  (AF003096) AP2 domain containing protein RAP2.3
NCBI Description
                  [Arabidopsis thaliana]
```

Seq. ID LIB25-033-Q1-E1-G8

Method BLASTN NCBI GI g4519193

E value Match length



```
BLAST score
E value
                  3.0e-84
Match length
                  304
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDC11, complete sequence
Seq. No.
                  140547
Seq. ID
                  LIB25-033-Q1-E1-H4
Method
                  BLASTN
NCBI GI
                  q4249393
BLAST score
                  335
E value
                  0.0e+00
Match length
                  335
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC T9J23 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140548
Seq. ID
                  LIB25-034-Q1-E1-D3
Method
                  BLASTN
                  q2760168
NCBI GI
BLAST score
                  155
E value
                  7.0e-82
Match length
                  313
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MEE6, complete sequence [Arabidopsis thaliana]
                  140549
Seq. No.
Seq. ID
                  LIB25-034-Q1-E1-H6
Method
                  BLASTX
NCBI GI
                  q509810
BLAST score
                  294
E value
                  1.0e-26
Match length
                  59
% identity
                  100
NCBI Description
                 (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]
Seq. No.
                  140550
Seq. ID
                  LIB25-035-Q1-E1-B3
Method
                  BLASTN
NCBI GI
                  g1946354
BLAST score
                  204
E value
                  1.0e-111
Match length
                  299
% identity
                  97
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T06B20 genomic
                  sequence, complete sequence
Seq. No.
                  140551
Seq. ID
                  LIB25-035-Q1-E1-C6
Method
                  BLASTX
NCBI GI
                  g3643192
BLAST score
                  478
```

17077

4.0e-48



```
% identity
                  (AF087435) unknown [Arabidopsis thaliana]
NCBI Description
                  140552
Seq. No.
Seq. ID
                  LIB25-035-Q1-E1-E4
Method
                  BLASTX
NCBI GI
                  g4587527
BLAST score
                  447
                  1.0e-44
E value
Match length
                  103
% identity
                  85
NCBI Description
                  (AC007060) Strong similarity to F19I3.2 gi 3033375 putative
                  berberine bridge enzyme from Arabidopsis thaliana BAC
                  gb AC004238
                  140553
Seq. No.
Seq. ID
                  LIB25-035-Q1-E1-F12
Method
                  BLASTN
NCBI GI
                  q1184276
BLAST score
                  45
                  4.0e-16
E value
Match length
                  279
                  85
% identity
NCBI Description
                  Brassica napus (clone Sta 39-4) arabinogalactan protein
                  mRNA, complete cds
Seq. No.
                  140554
                  LIB25-035-Q1-E1-F7
Seq. ID
Method
                  BLASTN
                  g450879
NCBI GI
BLAST score
                  102
E value
                  2.0e-50
Match length
                  146
% identity
                  75
NCBI Description A.thaliana hsc70-1 gene
Seq. No.
                  140555
Seq. ID
                  LIB25-035-Q1-E1-G11
Method
                  BLASTN
NCBI GI
                  q3046847
BLAST score
                  66
E value
                  5.0e-29
Match length
                  134
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:
NCBI Description
                  K11J9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140556
```

Seq. ID LIB25-035-Q1-E1-H4

Method BLASTN
NCBI GI g4159710
BLAST score 194
E value 1.0e-105
Match length 258
% identity 48

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSD23, complete sequence

Parks.



```
Seq. No.
                   140557
```

LIB25-036-Q1-E1-A3 Seq. ID

Method BLASTN NCBI GI g2618599 BLAST score 262 E value 1.0e-145 Match length 456 100 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBD2, complete sequence [Arabidopsis thaliana]

Seq. No. 140558

Seq. ID LIB25-036-Q1-E1-B10

Method BLASTX NCBI GI q3036805 BLAST score 290 E value 1.0e-26 Match length 57 95 % identity

NCBI Description (AL022373) thaumatin-like protein [Arabidopsis thaliana]

140559 Seq. No.

Seq. ID LIB25-036-Q1-E1-B11

Method BLASTX NCBI GI g3249083 BLAST score 174 E value 2.0e-12 Match length 73 % identity 45

NCBI Description (AC004473) Contains similarity to heat shock transcription

factor homolog gb 2244754 from A. thaliana chromosome 4

contig gb Z97335. [Arabidopsis thaliana]

Seq. No. 140560

Seq. ID LIB25-036-Q1-E1-B3

Method BLASTX NCBI GI g3914117 BLAST score 631 E value 5.0e-66 Match length 147 % identity

NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE II PRECURSOR (NDK II) (NDP

KINASE II) >gi 3093480 (AF017640) nucleoside diphosphate

kinase type 2 [Arabidopsis thaliana]

140561

Seq. No. Seq. ID LIB25-036-Q1-E1-B4

Method BLASTX NCBI GI g1617013 BLAST score 284 E value 2.0e-25 Match length 56 % identity 100

NCBI Description (Y07745) histone H2B like protein [Arabidopsis thaliana]

Seq. No. 140562

BLAST score

E value

444

0.0e + 00



```
Seq. ID
                  LIB25-036-Q1-E1-B6
Method
                  BLASTX
NCBI GI
                  q4469024
BLAST score
                  479
                  1.0e-48
E value
Match length
                  93
% identity
                  99
                  (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  140563
Seq. ID
                  LIB25-036-Q1-E1-C1
Method
                  BLASTX
NCBI GI
                  q4539383
BLAST score
                  684
E value
                  3.0e-72
Match length
                  141
% identity
NCBI Description
                  (AL035526) putative protein (fragment) [Arabidopsis
                  thaliana]
Seq. No.
                  140564
                  LIB25-036-Q1-E1-C2
Seq. ID
Method
                  BLASTX
                  g4538961
NCBI GI
BLAST score
                  620
                  8.0e-65
E value
Match length
                  127
% identity
                  100
NCBI Description
                  (AL049488) isoleucine-tRNA ligase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  140565
Seq. ID
                  LIB25-036-Q1-E1-C6
Method
                  BLASTX
NCBI GI
                  q3386606
BLAST score
                  163
E value
                  4.0e-11
Match length
                  46
% identity
                  70
NCBI Description (AC004665) putative beta-amylase [Arabidopsis thaliana]
                  140566
Seq. No.
Seq. ID
                  LIB25-036-Q1-E1-E3
Method
                  BLASTN
NCBI GI
                  g3158375
BLAST score
                  132
E value
                  3.0e-68
Match length
                  132
                  100
% identity
NCBI Description Arabidopsis thaliana SEN5 mRNA, partial cds
                  140567
Seq. No.
Seq. ID
                  LIB25-036-Q1-E1-E7
Method
                  BLASTN
NCBI GI
                  g4432829
```



Match length 448 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140568

Seq. ID LIB25-036-Q1-E1-E8

Method BLASTX
NCBI GI g2851455
BLAST score 356
E value 9.0e-34
Match length 84
% identity 86

NCBI Description DYNAMIN-LIKE PROTEIN >gi 2267213 (L36939) dynamin-like GTP

binding protein [Arabidopsis thaliana]

Seq. No. 140569

Seq. ID LIB25-036-Q1-E1-F5

Method BLASTN
NCBI GI g3659491
BLAST score 138
E value 5.0e-72
Match length 138
% identity 50

NCBI Description Sequence of BAC T22H22 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 140570

Seq. ID LIB25-036-Q1-E1-F8

Method BLASTX
NCBI GI g1854445
BLAST score 544
E value 8.0e-56
Match length 131
% identity 77

NCBI Description (D83971) CPRD14 protein [Vigna unguiculata]

Seq. No. 140571

Seq. ID LIB25-036-Q1-E1-H8

Method BLASTX
NCBI GI g1350680
BLAST score 529
E value 4.0e-54
Match length 128
% identity 98

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 140572

Seq. ID LIB25-037-Q1-E1-A3

Method BLASTX
NCBI GI g2905643
BLAST score 325
E value 4.0e-30
Match length 125
% identity 53

NCBI Description (AF045244) ribitol kinase [Klebsiella pneumoniae]



Seq. ID LIB25-037-Q1-E1-A4

Method BLASTX
NCBI GI g1170660
BLAST score 623
E value 4.0e-65
Match length 123
% identity 100

NCBI Description MEVALONATE KINASE (MK) >gi_541880 pir_S42088 mevalonate

kinase (EC 2.7.1.36) - Arabidopsis thaliana

>gi_456614_emb_CAA54820_ (X77793) mevalonate kinase

[Arabidopsis thaliana]

Seq. No. 140574

Seq. ID LIB25-037-Q1-E1-A7

Method BLASTN
NCBI GI g2696018
BLAST score 310
E value 1.0e-174
Match length 442
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXC9, complete sequence [Arabidopsis thaliana]

Seq. No. 140575

Seq. ID LIB25-037-Q1-E1-B10

Method BLASTX
NCBI GI g1168530
BLAST score 489
E value 2.0e-49
Match length 96
% identity 99

NCBI Description SERINE/THREONINE-PROTEIN KINASE ASK2 >gi_99748_pir__S24586

probable serine/threonine-specific protein kinase (EC

2.7.1.-) (clone ASK2) - Arabidopsis thaliana >gi_16443_emb_CAA78106_ (Z12120) protein kinase

[Arabidopsis thaliana]

Seq. No. 140576

Seq. ID LIB25-037-Q1-E1-B8

Method BLASTX
NCBI GI g1181531
BLAST score 606
E value 4.0e-63
Match length 124
% identity 91

NCBI Description (L41244) thionin [Arabidopsis thaliana]

>gi_1586833 prf 2204399A thionin [Arabidopsis thaliana]

Seq. No. 140577

Seq. ID LIB25-037-Q1-E1-C11

Method BLASTN
NCBI GI g1244741
BLAST score 256
E value 1.0e-142
Match length 256
% identity 100



NCBI Description Arabidopsis thaliana nuclear ribosomal ITS-1, 5.8S

ribosomal RNA, and ITS-2. >gi_1245679_gb_U52185_ASU52185 Arabidopsis suecica nuclear ribosomal ITS-1, 5.8S ribosomal

RNA, and ITS-2

Seq. No. 140578

Seq. ID LIB25-037-Q1-E1-D4

Method BLASTX
NCBI GI g3250677
BLAST score 735
E value 3.0e-78
Match length 143
% identity 100

NCBI Description (AL024486) putative Fe(II) transport protein [Arabidopsis

thaliana]

Seq. No. 140579

Seq. ID LIB25-037-Q1-E1-D5

Method BLASTX
NCBI GI g3063453
BLAST score 373
E value 9.0e-36
Match length 139
% identity 54

NCBI Description (AC003981) F22013.15 [Arabidopsis thaliana]

Seq. No. 140580

Seq. ID LIB25-037-Q1-E1-E2

Method BLASTN
NCBI GI g4159708
BLAST score 165
E value 1.0e-87
Match length 425
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MKP6, complete sequence

Seq. No. 140581

Seq. ID LIB25-037-Q1-E1-E4

Method BLASTX
NCBI GI g3914024
BLAST score 209
E value 1.0e-16
Match length 59
% identity 63

NCBI Description (R)-MANDELONITRILE LYASE ISOFORM 2 PRECURSOR

(HYDROXYNITRILE LYASE 2) ((R)-OXYNITRILASE 2) >gi_2773274

(AF040078) (R)-(+)-mandelonitrile lyase isoform MDL2 precursor [Prunus serotina] >gi 2773276 (AF040079)

(R)-(+)-mandelonitrile lyase isoform MDL2 precursor [Prunus

serotina]

Seq. No. 140582

Seq. ID LIB25-037-Q1-E1-E7

Method BLASTX NCBI GI g4263704 BLAST score 238



E value 6.0e-20 Match length 80 % identity 50

NCBI Description (AC006223) putative sugar starvation-induced protein

[Arabidopsis thaliana]

Seq. No. 140583

Seq. ID LIB25-037-Q1-E1-G1

Method BLASTN
NCBI GI g4263813
BLAST score 368
E value 0.0e+00
Match length 425
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC T13P21 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140584

Seq. ID LIB25-037-Q1-E1-G4

Method BLASTX
NCBI GI 94220474
BLAST score 509
E value 9.0e-52
Match length 144
% identity 71

NCBI Description (AC006069) putative myosin heavy chain [Arabidopsis

thaliana]

Seq. No. 140585

Seq. ID LIB25-037-Q1-E1-H1

Method BLASTX
NCBI GI 94587542
BLAST score 562
E value 6.0e-58
Match length 146
% identity 75

NCBI Description (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase

with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No. 140586

Seq. ID LIB25-037-Q1-E1-H2

Method BLASTN
NCBI GI g3402695
BLAST score 60
E value 5.0e-25
Match length 124
% identity 87

NCBI Description Arabidopsis thaliana chromosome II BAC T3K9 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140587

Seq. ID LIB25-037-Q1-E1-H6

Method BLASTN
NCBI GI g2351070
BLAST score 192
E value 1.0e-104



Match length % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH12, complete sequence [Arabidopsis thaliana]

140588 Seq. No.

Seq. ID LIB25-038-Q1-E1-A4

Method BLASTX NCBI GI g2129538 BLAST score 357 E value 5.0e-34 Match length 69 % identity 100

NCBI Description AT103 protein - Arabidopsis thaliana >gi 1033195 (U38232)

AT103 [Arabidopsis thaliana]

140589 Seq. No.

Seq. ID LIB25-038-Q1-E1-A9

Method BLASTN NCBI GI g4510360 BLAST score 348 E value 0.0e+00Match length 407 % identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic

sequence, complete sequence

Seq. No. 140590

Seq. ID LIB25-038-Q1-E1-B10

Method BLASTX NCBI GI g2465923 192 BLAST score E value 1.0e-14 Match length 143 % identity 38

NCBI Description (AF024648) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

Seq. No. Seq. ID 140591

LIB25-038-Q1-E1-F10

Method BLASTN NCBI GI q2264314 BLAST score 345 E value 0.0e + 00Match length 349 100 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MQK4, complete sequence [Arabidopsis thaliana]

Seq. No. 140592

Seq. ID LIB25-038-Q1-E1-F11

Method BLASTX NCBI GI q585084 BLAST score 290 E value 4.0e-26 Match length 70 % identity 79



NCBI Description ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)

>gi_543383_pir__S40780 translation elongation factor G,

mitochondrial - rat >gi_310102 (L14684) elongation factor G

[Rattus norvegicus]

Seq. No. 140593

Seq. ID LIB25-038-Q1-E1-F5

Method BLASTX
NCBI GI g3242710
BLAST score 460
E value 5.0e-46
Match length 94
% identity 95

NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No. 140594

Seq. ID LIB25-038-Q1-E1-F8

Method BLASTN
NCBI GI g2160132
BLAST score 214
E value 1.0e-117
Match length 214
% identity 100

NCBI Description Sequence of BAC F19K23 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 140595

Seq. ID LIB25-038-Q1-E1-H1

Method BLASTN
NCBI GI g2739359
BLAST score 92
E value 2.0e-44
Match length 191
% identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC T9J22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140596

Seq. ID LIB25-038-Q1-E1-H11

Method BLASTN
NCBI GI g3059018
BLAST score 86
E value 3.0e-41
Match length 86
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12

(ESSAII project)

Seq. No. 140597

Seq. ID LIB25-038-Q1-E1-H6

Method BLASTX
NCBI GI g3608155
BLAST score 295
E value 5.0e-27
Match length 61
% identity 92

NCBI Description (ACQ05314) putative RNA helicase [Arabidopsis thaliana]

```
Seq. No.
                   140598
 Seq. ID
                   LIB25-038-Q1-E1-H7
 Method
                   BLASTN
 NCBI GI
                   g4662609
 BLAST score
                   179
 E value
                   3.0e-96
Match length
                   274
 % identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5,
                   complete sequence
 Seq. No.
                   140599
 Seq. ID
                   LIB25-038-Q1-E1-H9
Method
                   BLASTX
NCBI GI
                   g3334124
BLAST score
                   650
E value
                   3.0e-68
Match length
                   134
% identity
                   99
NCBI Description ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
                   (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                   >gi_1655482_dbj_BAA13600_ (D88375) delta subunit of
                   mitochondrial F1-ATPase [Arabidopsis thaliana]
Seq. No.
                   140600
Seq. ID
                   LIB25-039-Q1-E1-B1
Method
                   BLASTX
NCBI GI
                   g4490316
BLAST score
                   318
E value
                   2.0e-29
Match length
                   97
% identity
NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana]
Seq. No.
                   140601
Seq. ID
                   LIB25-039-Q1-E1-B7
Method
                   BLASTX
NCBI GI
                   q399091
BLAST score
                   415
E value
                   1.0e-40
Match length
                   118
% identity
                   74
NCBI Description
                 PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP
                   (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)
                   (H+-PPASE) >gi_282878_pir__A38230 inorganic pyrophosphatase
                   (EC 3.6.1.1), \overline{\text{H+-translocating pyrophosphate-energized -}}
                  Arabidopsis thaliana >gi_166634 (M81892) vacuolar
                  H+-phosphatase [Arabidopsis thaliana]
Seq. No.
                  140602
Seq. ID
                  LIB25-039-Q1-E1-C10
Method
                  BLASTN
NCBI GI
                  q2618683
BLAST score
                  151
```

17087

. . .

E value

Match length

2.0e-79

362 💢



% identity NCBI Description Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana] 140603 Seq. No. Seq. ID LIB25-039-Q1-E1-C6 Method BLASTX NCBI GI q3169172 BLAST score 327 E value 2.0e-30 Match length 76 % identity 82 NCBI Description (AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445214 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana] Seq. No. 140604 LIB25-039-Q1-E1-D4 Seq. ID Method BLASTN NCBI GI g4490291 BLAST score 232 E value 1.0e-127 Match length 392 % identity 100 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project) Seq. No. 140605 Seq. ID LIB25-039-Q1-E1-D5 Method BLASTX NCBI GI q4581141 BLAST score 307 E value 5.0e-28 Match length 134 % identity 56 NCBI Description (AC006919) unknown protein [Arabidopsis thaliana] Seq. No. 140606 Seq. ID LIB25-039-01-E1-D9 Method BLASTX NCBI GI q2961373 BLAST score 274 E value 2.0e-24 Match length 112 % identity 54 NCBI Description (AL022141) putative disease resistance protein [Arabidopsis thaliana]

Seq. No. 140607

Seq. ID LIB25-039-Q1-E1-E11

Method BLASTN NCBI GI q4220629 BLAST score 236 1.0e-130 E value Match length 342 96 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

% identity

94

fragment No



K24F5, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  140608
                  LIB25-039-Q1-E1-E2
Seq. ID
                  BLASTX
Method
                  g2829899
NCBI GI
BLAST score
                  741
                  6.0e-79
E value
Match length
                  145
                  100
% identity
                  (AC002311) similar to ripening-induced protein,
NCBI Description
                  gp_AJ001449_2465015 and major#latex protein,
                  gp_X91961_1107495 [Arabidopsis thaliana]
                  140609
Seq. No.
                  LIB25-039-Q1-E1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4567259
BLAST score
                  119
E value
                  3.0e-60
                  420
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F3K23 genomic
                  sequence, complete sequence
Seq. No.
                  140610
                  LIB25-039-Q1-E1-G5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3269280
                  306
BLAST score
E value
                  1.0e-172
Match length
                  403
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, Pl clone M4I22
                  (ESSAII project)
Seq. No.
                  140611
Seq. ID
                  LIB25-040-Q1-E1-A5
Method
                  BLASTN
NCBI GI
                  q4733952
BLAST score
                  183
E value
                  2.0e-98
                                     . .
Match length
                  368
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome I BAC F23H11 genomic
                  sequence, complete sequence
Seq. No.
                  140612
Seq. ID
                  LIB25-040-Q1-E1-B11
Method
                  BLASTN
NCBI GI
                  q2244901
BLAST score
                  106
                  5.0e-53
E value
Match length
                  142
```

17089

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig



```
Seq. No.
                  140613
Seq. ID
                  LIB25-040-Q1-E1-C6
Method
                  BLASTN
NCBI GI
                  g2494106
                  355
BLAST score
E value
                  0.0e + 00
Match length
                  355
% identity
                  100
                  Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  140614
                  LIB25-040-Q1-E1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3292816
BLAST score
                  202
E value
                  6.0e-16
Match length
                  62
% identity
                  77
                  (AL031018) putative fizzy-related protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  140615
Seq. ID
                  LIB25-040-Q1-E1-G12
Method
                  BLASTN
NCBI GI
                  g2262097
BLAST score
                  283
E value
                  1.0e-158
                  390
Match length
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome IV BAC T19F6 genomic
                  sequence, complete sequence
                  140616
Seq. No.
Seq. ID
                  LIB25-040-Q1-E1-G9
Method
                  BLASTN
NCBI GI
                  q3868723
BLAST score
                  112
                  3.0e-56
E value
Match length
                  295
% identity
                  96
NCBI Description Arabidopsis thaliana chromosome V map 60.5 cM, complete
                  sequence [Arabidopsis thaliana]
Seq. No.
                  140617
Seq. ID
                  LIB25-041-Q1-E1-A10
Method
                  BLASTX
                  g4115381
NCBI GI
BLAST score
                  633
                  2.0e-66
E value
Match length
                  120
% identity
                  99
```

NCBI Description

Seq. ID LIB25-041-Q1-E1-B10

17090

(AC005967) putative limonene cyclase [Arabidopsis thaliana]



```
Method
                  BLASTX
NCBI GI
                  q4678930
BLAST score
                  381
E value
                  3.0e-37
Match length
                  77
                  96
% identity
NCBI Description
                  (AL049711) serine-type carboxypeptidase like protein
                   [Arabidopsis thaliana]
Seq. No.
                  140619
Seq. ID
                  LIB25-041-Q1-E1-B4
Method
                  BLASTX
NCBI GI
                  q4508074
BLAST score
                  386
E value
                  2.0e-37
Match length
                  136
% identity
                  60
NCBI Description
                  (AC005882) 45341 [Arabidopsis thaliana]
Seq. No.
                  140620
                  LIB25-041-Q1-E1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1871173
BLAST score
                  219
E value
                  1.0e-120
Match length
                  219
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T06D20 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  140621
Seq. ID
                  LIB25-041-Q1-E1-C8
Method
                  BLASTX
NCBI GI
                  g2947059
BLAST score
                  560
E value
                  1.0e-57
Match length
                  114
                  90
% identity
NCBI Description
                  (AC002521) similar to myb transforming protein [Arabidopsis
                  thalianal
Seq. No.
                  140622
Seq. ID
                  LIB25-041-Q1-E1-D11
Method
                  BLASTN
NCBI GI
                  q4589432
BLAST score
                  386
E value
                  0.0e + 00
Match length
                  394
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MMJ24, complete sequence
```

Seq. ID LIB25-041-Q1-E1-E12

Method BLASTX
NCBI GI g2642433
BLAST score 319



```
1.0e-29
E value
Match length
                  75
% identity
                  (AC002391) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  140624
Seq. No.
                  LIB25-041-Q1-E1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539419
BLAST score
                  466
E value
                  1.0e-46
Match length
                  113
% identity
                  84
                  (AL049171) putative ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
                  140625
Seq. No.
                  LIB25-041-Q1-E1-F3
Seq. ID
Method
                  BLASTN
                  g4159705
NCBI GI
BLAST score
                  174
                  5.0e-93
E value
Match length
                  423
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGD8, complete sequence
                  140626
Seq. No.
Seq. ID
                  LIB25-041-Q1-E1-F4
Method
                  BLASTN
NCBI GI
                  g2264307
                  133
BLAST score
E value
                  1.0e-68
                  384
Match length
% identity
                  93
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MED24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140627
                  LIB25-041-Q1-E1-F5
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2760168
BLAST score
                  41
E value
                  1.0e-13
Match length
                  198
% identity
                  84
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MEE6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140628
```

 Seq. No.
 140628

 Seq. ID
 LIB25-041-Q1-E1-F6

 Method
 BLASTX

NCBI GI g4490737
BLAST score 307
E value 5.0e-28
Match length 119



% identity 55
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 140629

Seq. ID LIB25-041-Q1-E1-G3

Method BLASTX
NCBI GI g3395756
BLAST score 609
E value 2.0e-67
Match length 128
% identity 96

NCBI Description (U76297) plantacyanin [Arabidopsis thaliana] >gi 3461812

(AC004138) putative basic blue protein [Arabidopsis

thaliana]

Seq. No. 140630

Seq. ID LIB25-041-Q1-E1-G7

Method BLASTN
NCBI GI g2264306
BLAST score 168
E value 2.0e-89
Match length 320
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBK5, complete sequence [Arabidopsis thaliana]

Seq. No. 140631

Seq. ID LIB25-041-Q1-E1-H2

Method BLASTX
NCBI GI g127041
BLAST score 252
E value 7.0e-22
Match length 46
% identity 98

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_81647_pir__JN0131 methionine adenosyltransferase (EC
2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077)
S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No. 140632

Seq. ID LIB25-042-Q1-E1-A12

Method BLASTX
NCBI GI g4314365
BLAST score 425
E value 6.0e-42
Match length 99
% identity 80

NCBI Description (AC006340) putative copia-like retrotransposon Hopscotch

[Arabidopsis thaliana]

Seq. No. 140633

Seq. ID LIB25-042-Q1-E1-A5

Method BLASTX
NCBI GI g3779021
BLAST score 598
E value 3.0e-62



```
Match length
% identity
                  100
                  (AC005171) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
                  140634
Seq. No.
Seq. ID
                  LIB25-042-Q1-E1-A7
Method
                  BLASTX
                  g1168609
NCBI GI
BLAST score
                  403
E value
                  2.0e-39
Match length
                  89
% identity
                  83
NCBI Description
                 AUXIN-RESISTANCE PROTEIN AXR1 >gi 479664 pir S35071
                  auxin-resistance protein AXR1 - Arabidopsis Thaliana
                  >gi_304104 (L13922) ubiquitin-activating enzyme E1
                  [Arabidopsis thaliana] >gi 2388579 (AC000098) Match to
                  Arabidopsis AXR1 (gb ATHAXR1122). [Arabidopsis thaliana]
                  >gi 448755 prf 1917337A ubiquitin-activating enzyme E1
                  [Arabidopsis thaliana]
                  140635
Seq. No.
Seq. ID
                  LIB25-042-Q1-E1-A9
Method
                  BLASTX
NCBI GI
                  q1732572
BLAST score
                  129
E value
                  3.0e-31
Match length
                  107
% identity
                  66
NCBI Description (U72154) beta-glucosidase [Brassica nigra]
Seq. No.
                  140636
Seq. ID
                  LIB25-042-Q1-E1-C2
Method
                  BLASTX
NCBI GI
                  q1350548
BLAST score
                  266
E value
                  3.0e-23
Match length
                  99
% identity
                  49
NCBI Description (L47609) heat shock-like protein [Picea glauca]
Seq. No.
                  140637
Seq. ID
                  LIB25-042-Q1-E1-G7
Method
                  BLASTX
NCBI GI
                  g2827160
BLAST score
                  170
E value
                  5.0e-12
Match length
                  106
% identity
NCBI Description (AF032667) rexo70 [Rattus norvegicus]
```

Seq. ID LIB25-043-Q1-E1-B11

140638

Method BLASTX NCBI GI g2832695 BLAST score 734 E value 4.0e-78



Match length 147 % identity 100

NCBI Description (AL021713) putative protein [Arabidopsis thaliana]

Seq. No. 140639

Seq. ID LIB25-043-Q1-E1-C9

Method BLASTX
NCBI GI g1345973
BLAST score 559
E value 1.0e-57
Match length 120
% identity 85

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 140640

Seq. ID LIB25-043-Q1-E1-D7

Method BLASTN
NCBI GI g2924731
BLAST score 352
E value 0.0e+00
Match length 432
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSI17, complete sequence [Arabidopsis thaliana]

Seq. No. 140641

Seq. ID LIB25-043-Q1-E1-D9

Method BLASTX
NCBI GI g625977
BLAST score 620
E value 9.0e-65
Match length 120
% identity 100

NCBI Description p40 protein homolog - Arabidopsis thaliana >gi 402904

(U01955) laminin receptor-like protein [Arabidopsis

thaliana]

Seq. No. 140642

Seq. ID LIB25-043-Q1-E1-E11

Method BLASTX
NCBI GI g3915826
BLAST score 597
E value 5.0e-62
Match length 138
% identity 81

NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 140643

Seq. ID LIB25-043-Q1-E1-H9



Method BLASTX
NCBI GI g115783
BLAST score 557
E value 2.0e-57
Match length 105
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 140644

Seq. ID LIB25-044-Q1-E1-A3

Method BLASTX
NCBI GI g4567235
BLAST score 552
E value 7.0e-57
Match length 129
% identity 82

NCBI Description (AC007119) putative phosphatidylinositol/phophatidylcholine

transfer protein [Arabidopsis thaliana]

Seq. No. 140645

Seq. ID LIB25-044-Q1-E1-B10

Method BLASTX
NCBI GI g2407802
BLAST score 217
E value 1.0e-17
Match length 52
% identity 85

NCBI Description (Y12576) histone H2B [Arabidopsis thaliana]

Seq. No. 140646

Seq. ID LIB25-044-Q1-E1-B11

Method BLASTX
NCBI GI g3695023
BLAST score 632
E value 4.0e-66
Match length 140
% identity 89

NCBI Description (AF055850) unknown [Arabidopsis thaliana]

Seq. No. 140647

Seq. ID LIB25-044-Q1-E1-B2

Method BLASTX
NCBI GI g4006851
BLAST score 250
E value 5.0e-22
Match length 57
% identity 81

NCBI Description (Z99707) cytochrome P450-like protein [Arabidopsis

thaliana]

Seq. No. 140648

Seq. ID LIB25-044-Q1-E1-B8

Method BLASTX NCBI GI g3299896



```
BLAST score
E value
                  3.0e-37
Match length
                  145
                  55
% identity
                 (AF020390) beta-galactosidase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  140649
Seq. ID
                  LIB25-044-Q1-E1-C10
Method
                  BLASTX
                  g2760325
NCBI GI
BLAST score
                  472
E value
                  2.0e-47
Match length
                  146
% identity
                  72
NCBI Description (AC002130) F1N21.10 [Arabidopsis thaliana]
                  140650
Seq. No.
Seq. ID
                  LIB25-044-Q1-E1-C4
Method
                  BLASTN
NCBI GI
                  g3510339
BLAST score
                  176
                  2.0e-94
E value
Match length
                  290
% identity
                  97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K3K7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140651
                  LIB25-044-Q1-E1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1146165
BLAST score
                  328
E value
                  2.0e-30
Match length
                  62
% identity
                  100
NCBI Description
                  (L47479) urophorphyrin III methylase [Arabidopsis thaliana]
Seq. No.
                  140652
                  LIB25-044-Q1-E1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2245048
                  600
BLAST score
                  2.0e-62
E value
Match length
                  136
% identity
                  18
NCBI Description
                  (Z97342) resistance gene homolog [Arabidopsis thaliana]
                  140653
Seq. No.
Seq. ID
                  LIB25-044-Q1-E1-F12
Method
                  BLASTN
NCBI GI
                  g3212846
BLAST score
                  31
E value
                  2.0e-08
Match length
                  80
```

17097

Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

95

% identity

NCBI Description

Seq. No.

Seq. ID

140659

LIB25-045-Q1-E1-C5



```
140654
Seq. No.
Seq. ID
                  LIB25-044-Q1-E1-G6
Method
                  BLASTX
                  g1103318
NCBI GI
BLAST score
                  292
E value
                  2.0e-26
Match length
                  61
                  95
% identity
NCBI Description
                  (X78818) casein kinase I [Arabidopsis thaliana]
                  >gi 2244791 emb CAB10213.1 (Z97336) casein kinase I
                  [Arabidopsis thaliana]
Seq. No.
                  140655
                  LIB25-044-Q1-E1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2580440
BLAST score
                  231
E value
                  4.0e-19
Match length
                  59
                  73
% identity
NCBI Description
                  (D87261) PCF2 [Oryza sativa]
                  140656
Seq. No.
Seq. ID
                  LIB25-045-Q1-E1-A10
Method
                  BLASTN
NCBI GI
                  g431257
BLAST score
                  438
                  0.0e + 00
E value
Match length
                  438
% identity
                  100
NCBI Description Arabidopsis thaliana lipoxygenase (Lox2) mRNA, complete cds
                  140657
Seq. No.
                  LIB25-045-Q1-E1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2677828
BLAST score
                  401
                  4.0e-39
E value
Match length
                  103
% identity
                  73
NCBI Description
                  (U93166) cysteine protease [Prunus armeniaca]
Seq. No.
                  140658
Seq. ID
                  LIB25-045-Q1-E1-A5
Method
                  BLASTX
NCBI GI
                  g3142294
BLAST score
                  737
E value
                  2.0e-78
Match length
                  147
% identity
                  99
                  (AC002411) Strong similarity to initiation factor eIF-2,
NCBI Description
                  gb U37354 from S. pombe. ESTs gb T41979, gb N37284 and
```

17098

gb N37529 come from this gene. [Arabidopsis thaliana]



Method BLASTX
NCBI GI g2746341
BLAST score 406
E value 1.0e-39
Match length 84
% identity 85

NCBI Description (AF037590) ATA27 [Arabidopsis thaliana]

Seq. No. 140660

Seq. ID LIB25-045-Q1-E1-C8

Method BLASTX
NCBI GI g99752
BLAST score 604
E value 7.0e-63
Match length 146
% identity 82

NCBI Description protochlorophyllide reductase (EC 1.3.1.33) precursor -

Arabidopsis thaliana

Seq. No. 140661

Seq. ID LIB25-045-Q1-E1-D10

Method BLASTN
NCBI GI g4581138
BLAST score 395
E value 0.0e+00
Match length 399
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F1011 genomic

sequence, complete sequence

Seq. No. 140662

Seq. ID LIB25-045-Q1-E1-D5

Method BLASTX
NCBI GI g461753
BLAST score 251
E value 2.0e-21
Match length 53
% identity 94

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

PRECURSOR >gi_419773_pir__S31164 ATP-dependent ClpB

proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi 169128 (L09547) nuclear encoded precursor

to chloroplast protein [Pisum sativum]

Seq. No. 140663

Seq. ID LIB25-045-Q1-E1-D6

Method BLASTN
NCBI GI g3193282
BLAST score 190
E value 1.0e-102
Match length 414
% identity 100

NCBI Description Arabidopsis thaliana BAC T14P8

Seq. No. 140664

Seq. ID LIB25-045-Q1-E1-D7

Method BLASTX



NCBI GI q2781354 BLAST score 648 E value 5.0e-68 Match length 122

99 % identity

(AC003113) F2401.10 [Arabidopsis thaliana] NCBI Description

140665 Seq. No.

LIB25-045-Q1-E1-G10 Seq. ID

Method BLASTN NCBI GI g2351065 BLAST score 32 3.0e-09 E value Match length 56

% identity 86

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MHF15, complete sequence [Arabidopsis thaliana]

Seq. No. 140666

Seq. ID LIB25-045-Q1-E1-G6

Method BLASTN NCBI GI g3763944 BLAST score 216 E value 1.0e-118 Match length 442 % identity 100

Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 NCBI Description

(ESSAII project)

140667 Seq. No.

LIB25-045-Q1-E1-G9 Seq. ID

Method BLASTN NCBI GI q2828184 BLAST score 264 E value 1.0e-147 Match length 300 % identity 99

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MSN9, complete sequence [Arabidopsis thaliana]

Seq. No. 140668

Seq. ID LIB25-046-Q1-E1-D5

Method BLASTX NCBI GI g3738287 BLAST score 384 E value 2.0e-37 Match length 84 % identity 89

(ACO05309) glutathione s-transferase, GST6 [Arabidopsis NCBI Description

thaliana]

140669 Seq. No.

Seq. ID LIB25-046-Q1-E1-E6

Method BLASTN NCBI GI g3367567 148 BLAST score E value 2.0e-77



Match length 449 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20

(ESSAII project)

Seq. No. 140670

Seq. ID LIB25-047-Q1-E1-C1

Method BLASTN
NCBI GI g4249393
BLAST score 173
E value 2.0e-92
Match length 416
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T9J23 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140671

Seq. ID LIB25-047-Q1-E1-C6^s

Method BLASTX
NCBI GI g3738327
BLAST score 417
E value 6.0e-41
Match length 113
% identity 73

NCBI Description (AC005170) putative serine carboxypeptidase [Arabidopsis

thaliana]

Seq. No. 140672

Seq. ID LIB25-047-Q1-E1-D9

Method BLASTX
NCBI GI g2129604
BLAST score 521
E value 3.0e-53
Match length 100
% identity 100

NCBI Description GTP-binding protein 1 - Arabidopsis thaliana

>gi_2129607_pir__S71584 GTP-binding protein ATBG1 -

Arabidopsis thaliana >gi_1184981 (U46924) ATGB1

[Arabidopsis thaliana]

Seq. No. 140673

Seq. ID LIB25-047-Q1-E1-E5

Method BLASTN
NCBI GI g4490734
BLAST score 158
E value 1.0e-83
Match length 265
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA

project)

Seq. No. 140674

Seq. ID LIB25-047-Q1-E1-F8

Method BLASTN
NCBI GI g3540210
BLAST score 64
E value 3.0e-28



Match length 68 % identity 99

NCBI Description Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140675

Seq. ID LIB25-047-Q1-E1-G9

Method BLASTX
NCBI GI g3075394
BLAST score 593
E value 1.0e-61
Match length 117
% identity 99

NCBI Description (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead

protein [Arabidopsis thaliana]

Seq. No. 140676

Seq. ID LIB25-048-Q1-E1-B10

Method BLASTX
NCBI GI g1480078
BLAST score 473
E value 1.0e-47
Match length 95
% identity 99

NCBI Description (X99696) shaggy-like protein kinase iota [Arabidopsis

thaliana] >gi_2444277_gb_AAB71545.1_ (AF019927)

GSK3/shaggy-like protein kinase [Arabidopsis thaliana]

Seq. No. 140677

Seq. ID LIB25-048-Q1-E1-C6

Method BLASTX
NCBI GI g3193296
BLAST score 659
E value 3.0e-69
Match length 131
% identity 92

NCBI Description (AF069298) similar to pectinesterase [Arabidopsis thaliana]

Seq. No. 140678

Seq. ID LIB25-048-Q1-E1-F7

Method BLASTN
NCBI GI g3668172
BLAST score 109
E value 6.0e-55
Match length 109
% identity 100

NCBI Description Arabidopsis thaliana vsp1 gene for vegetative storage

protein, complete cds

Seq. No. 140679

Seq. ID LIB25-048-Q1-E1-F9

Method BLASTN
NCBI GI g3641835
BLAST score 54
E value 2.0e-22
Match length 58

Match length

NCBI Description

% identity

106

100

thaliana]



% identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project) Seq. No. 140680 Seq. ID LIB25-048-Q1-E1-G3 Method BLASTX NCBI GI g1550740 BLAST score 411 E value 1.0e-40 Match length 78 % identity 100 NCBI Description (Y07961) GDP-associated inhibitor [Arabidopsis thaliana] Seq. No. 140681 Seq. ID LIB25-048-Q1-E1-H7 Method BLASTN NCBI GI g4753645 BLAST score 171 E value 3.0e-91 Match length 321 % identity 100 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18 (ESSA project) Seq. No. 140682 Seq. ID LIB25-049-Q1-E1-A2 Method BLASTX NCBI GI g3004557 BLAST score 678 E value 2.0e-71 Match length 150 % identity 91 (AC003673) plasma membrane proton pump H+ ATPase, PMA1 NCBI Description [Arabidopsis thaliana] Seq. No. 140683 Seq. ID LIB25-049-Q1-E1-B10 Method BLASTN NCBI GI g4580744 BLAST score 171 E value 1.0e-91 Match length 175 99 % identity NCBI Description Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence Seq. No. 140684 Seq. ID LIB25-049-Q1-E1-C4 Method BLASTX NCBI GI g3355480 BLAST score 539 E value 2.0e-55

(AC004218) Medicago nodulin N21-like protein [Arabidopsis

```
Seq. No.
                  140685
Seq. ID
                  LIB25-049-Q1-E1-F12
Method
                  BLASTN
NCBI GI
                  q3241926
                  317
BLAST score
E value
                  1.0e-178
Match length
                  452
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSG15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140686
                  LIB25-049-Q1-E1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2351064
BLAST score
                  330
E value
                  0.0e+00
Match length
                  409
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDJ22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140687
                  LIB25-049-Q1-E1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587600
BLAST score
                  346
E value
                  4.0e-35
Match length
                  80
% identity
                  91
                  (AC006951) putative translation initiation factor EIF-1A
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  140688
Seq. ID
                  LIB25-049-Q1-E1-H2
Method
                  BLASTN
NCBI GI
                  q4006815
BLAST score
                  416
E value
                  0.0e + 00
Match length
                  423
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC T6P5 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  140689
Seq. No.
Seq. ID
                  LIB25-050-Q1-E1-A4
Method
                  BLASTX
NCBI GI
                  g4539389
BLAST score
                  286
E value
                  8.0e-26
```

Match length 58 100 % identity

NCBI Description (AL035526) putative protein kinase [Arabidopsis thaliana]

Seq. No. 140690

Seq. ID LIB25-050-Q1-E1-D11



Method BLASTX
NCBI GI g1199967
BLAST score 215
E value 2.0e-17
Match length 42
% identity 100
NCBI Description (X95689) histone H4 [Allium cepa]

Seq. No. 140691

Seq. ID LIB25-050-Q1-E1-D12

Method BLASTX
NCBI GI g2506496
BLAST score 688
E value 1.0e-72
Match length 132
% identity 100

NCBI Description GLUTATHIONE S-TRANSFERASE ERD11 (CLASS PHI) >gi_1890156_emb_CAA72413_ (Y11727) gluthatione

S-transferase [Arabidopsis thaliana]

Seq. No. 140692

Seq. ID LIB25-050-Q1-E1-D2

Method BLASTX
NCBI GI g445612
BLAST score 309
E value 1.0e-28
Match length 77
% identity 78

NCBI Description ribosomal protein S19 [Solanum tuberosum]

Seq. No. 140693

Seq. ID LIB25-050-Q1-E1-E1

Method BLASTX
NCBI GI g3980404
BLAST score 477
E value 4.0e-48
Match length 95
% identity 100

NCBI Description (AC004561) putative tropinone reductase [Arabidopsis

thaliana]

Seq. No. 140694

Seq. ID LIB25-050-Q1-E1-G12

Method BLASTX
NCBI GI g3668173
BLAST score 612
E value 8.0e-64
Match length 132
% identity 92

NCBI Description (AB006777) vegetative storage protein [Arabidopsis

thaliana]

Seq. No. 140695

Seq. ID LIB25-051-Q1-E1-B1

Method BLASTX NCBI GI g1762150 BLAST score 161

E value



```
E value
                  1.0e-11
Match length
                  35
                  83
% identity
                  (U49919) lupeol synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  140696
Seq. ID
                  LIB25-051-Q1-E1-C8
Method
                  BLASTN
NCBI GI
                  g3510337
BLAST score
                  348
E value
                  0.0e+00
Match length
                  456
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19E20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140697
                  LIB25-051-Q1-E1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2833627
BLAST score
                  175
E value
                  6.0e-94
Match length
                  175
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome 1 BAC F1707 complete
                  sequence [Arabidopsis thaliana]
Seq. No.
                  140698
Seq. ID
                  LIB25-052-Q1-E1-A8
Method
                  BLASTX
NCBI GI
                  g2583123
BLAST score
                  499
                  1.0e-50
E value
Match length
                  127
% identity
                  74
NCBI Description
                  (AC002387) putative nucleotide sugar epimerase [Arabidopsis
                  thaliana]
Seq. No.
                  140699
Seq. ID
                  LIB25-052-Q1-E1-B6
Method
                  BLASTN
NCBI GI
                  g3766106
BLAST score
                  140
E value
                  3.0e-73
Match length
                  164
% identity
                  98
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F9K20 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No. Seq. ID
                  140700
                  LIB25-052-Q1-E1-C4
Method
                  BLASTX
NCBI GI
                  g3785991
BLAST score
                  488
```

Match length 124 % identity 87

4.0e-54





(AC005560) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 140701

NCBI Description

Seq. ID LIB25-052-Q1-E1-F9

Method BLASTX
NCBI GI g2129640
BLAST score 420
E value 2.0e-41
Match length 84
% identity 100

NCBI Description magnesium chelatase chain - Arabidopsis thaliana

>gi 1154627 emb CAA92802 (Z68495) magnesium chelatase

subunit [Arabidopsis thaliana]

Seq. No. 140702

Seq. ID LIB25-052-Q1-E1-G7

Method BLASTN
NCBI GI g2245031
BLAST score 429
E value 0.0e+00
Match length 435
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 140703

Seq. ID LIB25-052-Q1-E1-G8

Method BLASTN
NCBI GI 94415928
BLAST score 373
E value 0.0e+00
Match length 377
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F13A10 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140704

Seq. ID LIB25-053-Q1-E1-A6

Method BLASTN
NCBI GI g16500
BLAST score 122
E value 1.0e-62
Match length 122
% identity 100

NCBI Description A.thaliana rp19 gene for chloroplast ribosomal protein CL9

Seq. No. 140705

Seq. ID LIB25-053-Q1-E1-A8

Method BLASTN
NCBI GI g2245031
BLAST score 41
E value 3.0e-14
Match length 144
% identity 95

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NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No



```
140706
Seq. No.
Seq. ID
                  LIB25-053-Q1-E1-B11
Method
                  BLASTN
NCBI GI
                  q4154284
BLAST score
                  117
E value
                  1.0e-59
Match length
                  138
                  95
% identity
                  Arabidopsis thaliana germin-like protein 1 (GLP1) gene,
NCBI Description
                  complete cds
Seq. No.
                  140707
Seq. ID
                  LIB25-053-Q1-E1-C10
Method
                  BLASTX
NCBI GI
                  a115783
BLAST score
                  607
                  3.0e-63
E value
Match length
                  115
% identity
                  99
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  140708
                  LIB25-053-Q1-E1-C11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2264319
BLAST score
                  33
E value
                  7.0e-09
Match length
                  49
                  92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXA21, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140709
Seq. ID
                  LIB25-053-Q1-E1-D8
Method
                  BLASTN
NCBI GI
                  q4558521
BLAST score
                  286
E value
                  1.0e-160
Match length
                  286
% identity
                  100
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T10024,
                  complete sequence
Seq. No.
                  140710
Seq. ID
                  LIB25-053-Q1-E1-E10
Method
                  BLASTX
NCBI GI
                  g4538963
```

Method BLASTX
NCBI GI g4538963
BLAST score 539
E value 3.0e-55
Match length 132
% identity 62

NCBI Description (ALO49488) chlorophyll a/b-binding protein-like

[Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129_1

(AF134129) Lhcb5 protein [Arabidopsis thaliana]

NCBI Description

140716

Seq. No.



```
Seq. No.
                   140711
Seq. ID
                   LIB25-053-Q1-E1-E2
Method
                   BLASTX
NCBI GI
                   q2642446
BLAST score
                   607
E value
                   2.0e-63
Match length
                   115
% identity
                   100
NCBI Description
                   (AC002391) similar to auxin-responsive GH3 protein
                   [Arabidopsis thaliana]
Seq. No.
                   140712
Seq. ID
                  LIB25-053-Q1-E1-E9
Method
                   BLASTX
NCBI GI
                   q2160158
BLAST score
                   496
E value
                   3.0e-50
Match length
                   115
% identity
                   83
NCBI Description
                  (AC000132) Similar to elongation factor 1-gamma
                   (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   140713
                  LIB25-053-Q1-E1-G5
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4589438
BLAST score
                   253
E value
                   1.0e-140
Match length
                   257
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQJ2, complete sequence
Seq. No.
                   140714
Seq. ID
                  LIB25-053-Q1-E1-H7
Method
                  BLASTN
NCBI GI
                   q3860242
BLAST score
                   207
E value
                   1.0e-113
Match length
                   211
% identity
                   100
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T13M11 genomic
                  sequence, complete sequence
Seq. No.
                   140715
Seq. ID
                  LIB25-054-Q1-E1-C9
Method
                  BLASTX
NCBI GI
                   g4006875
BLAST score
                   397
                  7.0e-39
E value
Match length
                  95
% identity
                  86
```

17109

(Z99707) putative protein [Arabidopsis thaliana]



```
LIB25-054-Q1-E1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                  a4584531
BLAST score
                  128
                  6.0e-66
E value
Match length
                  214
% identity
                  95
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8
NCBI Description
                  (ESSA project)
Seq. No.
                  140717
Seq. ID
                  LIB25-054-Q1-E1-D8
Method
                  BLASTN
NCBI GI
                  q2618683
BLAST score
                  86
                  3.0e-41
E value
Match length
                  94
% identity
                  98
NCBI Description Arabidopsis thaliana chromosome II BAC T32G6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  140718
Seq. No.
                  LIB25-054-Q1-E1-G5
Seq. ID
Method
                  BLASTX
                  g2194125
NCBI GI
BLAST score
                  352
E value
                  1.0e-33
Match length
                  85
% identity
                  82
NCBI Description
                  (AC002062) ESTs gb R30459, gb N38441 come from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  140719
Seq. ID
                  LIB25-055-P1-E1-A12
Method
                  BLASTN
NCBI GI
                  q4733968
BLAST score
                  423
E value
                  0.0e + 00
Match length
                  427
% identity
                  Arabidopsis thaliana chromosome II BAC F12P23 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  140720
Seq. ID
                  LIB25-055-P1-E1-B12
Method
                  BLASTX
NCBI GI
                  g133448
BLAST score
                  327
E value
                  1.0e-30
Match length
                  74
% identity
```

NCBI Description DNA-DIRECTED RNA POLYMERASE BETA" CHAIN

>gi_81503_pir_ A29959 DNA-directed RNA polymerase (EC
2.7.7.6) beta'' chain - spinach chloroplast >gi_295122

(M55297) RNA polymerase [Spinacia oleracea]

Seq. No. 140721



Seq. ID LIB25-055-P1-E1-E7 Method BLASTX NCBI GI g2501296 BLAST score 173 2.0e-12 E value Match length 44 % identity 73 DNA GYRASE SUBUNIT B >gi 1652801 dbj BAA17720 (D90908) DNA NCBI Description gyrase B subunit [Synechocystis sp.] Seq. No. 140722 Seq. ID LIB25-055-P1-E1-F8 Method BLASTN NCBI GI q3449331 BLAST score 233 E value 1.0e-128 Match length 233 % identity 100 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MNC17, complete sequence [Arabidopsis thaliana] Seq. No. 140723 Seq. ID LIB25-055-P1-E1-H4 Method BLASTN NCBI GI q4755185 BLAST score 268 E value 1.0e-149 Match length 524 % identity 100 NCBI Description Arabidopsis thaliana chromosome II BAC F5G3 genomic sequence, complete sequence Seq. No. 140724 Seq. ID LIB25-056-Q1-E1-B11 Method BLASTX g1175013 NCBI GI BLAST score 458 7.0e-46 E value Match length 103 % identity 87 PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi 629542 pir S44084 NCBI Description plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana] Seq. No. 140725

Seq. ID LIB25-056-Q1-E1-C8

Method BLASTN NCBI GI q4678258 135 BLAST score 5.0e-70 E value 207 Match length 95 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F617

(ESSA project)

Seq. No. 140726



Seq. ID LIB25-056-Q1-E1-E11 Method BLASTX NCBI GI a166708 BLAST score 200 4.0e-16 E value Match length 49 % identity 86 NCBI Description (M64118) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] 140727

 Seq. No.
 140727

 Seq. ID
 LIB25-056-Q1-E1-H5

 Method
 BLASTN

 NCBI GI
 g2477521

 BLAST score
 248

 E value
 1.0e-137

 Match length
 271

 % identity
 100

NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

 Seq. No.
 140728

 Seq. ID
 LIB25-057-Q1-E1-D4

 Method
 BLASTX

 NCBI GI
 g2119848

 BLAST score
 446

 E. value
 2.0e-44

BLAST score 446
E value 2.0e-44
Match length 87
% identity 97
NCBI Description chlorop

ICBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459)
photosystem II type I chlorophyll a /b binding protein
[Arabidopsis thaliana] >gi_3128229 (AC004077) putative
photosystem II type I chlorophyll a/b binding protein

photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]

Seq. No. 140729

Seq. ID LIB25-057-Q1-E1-D6

Method BLASTX
NCBI GI g430947
BLAST score 587
E value 5.0e-61
Match length 108
% identity 100

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 140730

Seq. ID LIB25-057-Q1-E1-E3

Method BLASTX
NCBI GI g1617013
BLAST score 288
E value 6.0e-26
Match length 57
% identity 100



NCBI Description (Y07745) histone H2B like protein [Arabidopsis thaliana]

Seq. No. 140731

Seq. ID LIB25-057-Q1-E1-F7

Method BLASTN NCBI GI g3540210

BLAST score 70

E value 2.0e-31
Match length 98
% identity 93

NCBI Description Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140732

Seq. ID LIB25-058-P1-E1-A7

Method BLASTX
NCBI GI g3776005
BLAST score 370
E value 2.0e-35
Match length 87
% identity 85

NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No. 140733

Seq. ID LIB25-058-P1-E1-F11

Method BLASTX
NCBI GI g2244859
BLAST score 205
E value 3.0e-16
Match length 63
% identity 70

NCBI Description (297337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 140734

Seq. ID LIB25-058-P1-E1-F2

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 140735

Seq. ID LIB25-058-P1-E1-H10

Method BLASTN
NCBI GI g3228389
BLAST score 114
E value 2.0e-57
Match length 301
% identity 97

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17L21,

complete sequence [Arabidopsis thaliana]

Seq. No. 140736

Seq. ID LIB25-058-P1-E1-H8

Method BLASTN



```
NCBI GI
                   g3449325
                   374
BLAST score
                   0.0e+00
E value
                   401
Match length
% identity
                   89
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K16H17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   140737
Seq. ID
                   LIB25-059-Q1-E1-B1
Method
                   BLASTN
NCBI GI
                   q972918
BLAST score
                   156
E value
                   1.0e-82
Match length
                   184
% identity
                   96
NCBI Description Arabidopsis thaliana IAA8 (IAA8) gene complete cds
Seq. No.
                   140738
Seq. ID
                   LIB25-059-Q1-E1-C10
Method
                   BLASTX
NCBI GI
                   g1703091
BLAST score
                   609
E value
                   1.0e-63
Match length
                   120
% identity
                   100
NCBI Description ACYL CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR (ACP)
                   (NADH-UBIQUINONE OXIDOREDUCTASE 9.6 KD SUBUNIT) (MTACP-1)
                   >gi 903689 (L23574) acyl carrier protein precursor
                   [Arabidopsis thaliana] >gi_3341682 (AC003672) acyl carrier
                   protein [Arabidopsis thaliana]
Seq. No.
                   140739
Seq. ID
                   LIB25-059-Q1-E1-C11
Method
                   BLASTN
NCBI GI
                   g2584827
BLAST score
                   350
                   0.0e + 00
E value
Match length
                   370
                   99
% identity
NCBI Description
                   Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   140740
Seq. ID
                   LIB25-059-Q1-E1-D11
Method
                   BLASTX
NCBI GI
                   g3096935
BLAST score
                   199
E value
                   2.0e-15
                   69
Match length
                   59
% identity
NCBI Description
                  (AL023094) putative protein [Arabidopsis thaliana]
```

Seq. No. 140741

Seq. ID LIB25-059-Q1-E1-D9

Method BLASTX NCBI GI g1353052



BLAST score 171 E value 4.0e-12 Match length 65 % identity 42

NCBI Description HYPOTHETICAL 35.6 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION

>gi_1077867_pir__S55201 hypothetical protein YJR013w yeast (Saccharomyces cerevisiae) >gi_854586_emb_CAA60935_

(X87611) ORF YJR83.11 [Saccharomyces cerevisiae] >gi_1015644_emb_CAA89537_ (Z49513) ORF YJR013w

[Saccharomyces cerevisiae]

Seq. No. 140742

Seq. ID LIB25-059-Q1-E1-G10

Method BLASTN
NCBI GI g3785992
BLAST score 124
E value 3.0e-63
Match length 398
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T6A23 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140743

Seq. ID LIB25-059-Q1-E1-G12

Method BLASTN
NCBI GI g4510338
BLAST score 216
E value 1.0e-118
Match length 340
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F2H17 genomic

sequence, complete sequence

Seq. No. 140744

Seq. ID LIB25-059-Q1-E1-H2

Method BLASTN
NCBI GI g3985955
BLAST score 65
E value 1.0e-28
Match length 128
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTH16, complete sequence [Arabidopsis thaliana]

Seq. No. 140745

Seq. ID LIB25-060-Q1-E1-C1

Method BLASTN
NCBI GI g2182289
BLAST score 302
E value 1.0e-169
Match length 318
% identity 99

NCBI Description Arabidopsis thaliana chromosome I BAC F11P17 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140746

Seq. ID LIB25-060-Q1-E1-D1



Method BLASTN
NCBI GI g3668073
BLAST score 100
E value 3.0e-49
Match length 180
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC T4C15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140747

Seq. ID LIB25-060-Q1-E1-D11

Method BLASTN
NCBI GI g4468103
BLAST score 349
E value 0.0e+00
Match length 389
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9

(ESSA project)

Seq. No. 140748

Seq. ID LIB25-060-Q1-E1-D9

Method BLASTX
NCBI GI g3348077
BLAST score 141
E value 1.0e-08
Match length 83
% identity 39

NCBI Description (AF078080) isochorismate synthase [Arabidopsis thaliana]

Seq. No. 140749

Seq. ID LIB25-060-Q1-E1-F8

Method BLASTN
NCBI GI g4038029
BLAST score 250
E value 1.0e-138
Match length 250
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F504 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140750

Seq. ID LIB25-061-Q1-E1-C8

Method BLASTN
NCBI GI g3241927
BLAST score 298
E value 1.0e-167
Match length 358
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTE17, complete sequence [Arabidopsis thaliana]

Seq. No. 140751

Seq. ID LIB25-061-Q1-E1-D12

Method BLASTN
NCBI GI g3249094
BLAST score 143



4.0e-75 E value 143 Match length % identity 100 Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 140752 Seq. ID LIB25-061-Q1-E1-E2 Method BLASTX . g4704732 NCBI GI BLAST score 592 E value 2.0e-61 Match length 133 % identity 87 NCBI Description (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana] Seq. No. 140753 Seq. ID LIB25-061-Q1-E1-E4 Method BLASTN NCBI GI g4163996 BLAST score 202 E value 1.0e-110 Match length 229

% identity 96 NCBI Description Arabidopsis thaliana alpha-xylosidase precursor (XYL1) mRNA, partial cds

Seq. No. 140754 Seq. ID LIB25-061-Q1-E1-E5 Method BLASTX NCBI GI g4584346 BLAST score 265 4.0e-23

E value Match length 87 % identity 57

NCBI Description (AC007127) unknown protein [Arabidopsis thaliana]

Seq. No. 140755

Seq. ID LIB25-061-Q1-E1-F4

Method BLASTX NCBI GI g2244977 BLAST score 617 2.0e-64 E value Match length 133 91 % identity

NCBI Description (Z97340) cysteine proteinase [Arabidopsis thaliana]

Seq. No. 140756

Seq. ID LIB25-061-Q1-E1-F8

Method BLASTN NCBI GI g3309085 BLAST score 53 E value 2.0e-21 Match length 138 % identity 98

NCBI Description Arabidopsis thaliana calcineurin B-like protein 3 (CBL3)

mRNA, complete cds

```
Seq. No.
                  140757
Seq. ID
                  LIB25-061-Q1-E1-G2
Method
                  BLASTX
NCBI GI
                  q3929649
                  601
BLAST score
E value
                  1.0e-62
Match length
                  122
                  100
% identity
                   (AJ131205) mitochondrial NAD-dependent malate dehydrogenase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  140758
                  LIB25-061-Q1-E1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2656031
BLAST score
                  189
E value
                  1.0e-102
                  189
Match length
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
Seq. No.
                  140759
Seq. ID
                  LIB25-061-Q1-E1-H8
Method
                  BLASTX
NCBI GI
                  q4115387
                  497
BLAST score
E value
                  2.0e-50
Match length
                  98
                  99
% identity
NCBI Description
                  (AC005967) putative NADP-dependent
                  glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                  thaliana]
                  140760
Seq. No.
Seq. ID
                  LIB25-062-Q1-E1-B2
Method
                  BLASTN
NCBI GI
                  q3738275
                  160
BLAST score
E value
                   1.0e-84
                  376
Match length
% identity
                   98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F17A22 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140761
Seq. ID
                  LIB25-062-Q1-E1-C1
Method
                  BLASTX
                  g136636
NCBI GI
BLAST score
                   315
E value
                  5.0e-29
Match length
                  60
% identity
                  100
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
NCBI Description
```

>gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

Method

NCBI GI

E value

BLAST score

BLASTX

640

g4455323

4.0e-67



Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

```
140762
   Seq. No.
Seq. ID
                   LIB25-062-Q1-E1-C10
   Method
                      BLASTN
                      g2760168
   NCBI GI
    BLAST score
                      40
                      3.0e-13
    E value
    Match length
                      68
    % identity
                      90
                      Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
    NCBI Description
                      MEE6, complete sequence [Arabidopsis thaliana]
    Seq. No.
                      140763
    Seq. ID
                      LIB25-062-Q1-E1-C2
    Method
                      BLASTN
                      g4185128
    NCBI GI
    BLAST score
                      174
                      4.0e-93
    E value
    Match length
                      369
                      100
    % identity
    NCBI Description Arabidopsis thaliana chromosome II P1 MSF3 genomic
                      sequence, complete sequence [Arabidopsis thaliana]
    Seq. No.
                      140764
                      LIB25-062-Q1-E1-C3
    Seq. ID
    Method
                      BLASTX
    NCBI GI
                      g3021506
    BLAST score
                      270
    E value
                      9.0e-24
    Match length
                      98
                      57
    % identity
                      (X96727) isocitrate dehydrogenase (NAD+) [Nicotiana
    NCBI Description
                      tabacum]
                      140765
    Seq. No.
    Seq. ID
                      LIB25-062-Q1-E1-C4
    Method
                      BLASTX
    NCBI GI
                      g4586248
    BLAST score
                      617
    E value
                      2.0e-64
    Match length
                      127
    % identity
    NCBI Description
                      (AL049640) growth factor like protein [Arabidopsis
                      thaliana]
    Seq. No.
                      140766
    Seq. ID
                      LIB25-062-Q1-E1-D4
```

17119.



Match length 130 % identity 100 NCBI Description (AL035525) aminopeptidase-like protein [Arabidopsis thaliana] Seq. No. Seq. ID

140767 LIB25-062-Q1-E1-D8

Method BLASTN NCBI GI q1149572 BLAST score 364 E value 0.0e + 00Match length 364 % identity 100

A.thaliana rpl21 mRNA for chloroplast ribosomal large NCBI Description

subunit protein L21

140768 Seq. No.

Seq. ID LIB25-062-Q1-E1-E3

Method BLASTN NCBI GI q4263694 BLAST score 227 E value 1.0e-124 Match length 383 % identity 100

Arabidopsis thaliana chromosome II BAC F22D22 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140769

Seq. ID LIB25-062-Q1-E1-F8

Method BLASTN NCBI GI g2245031 BLAST score 299 E value 1.0e-167 Match length 394 % identity 98

Arabidopsis thaliana DNA chromosome 4, ESSA I contig NCBI Description

fragment No

Seq. No. 140770

Seq. ID LIB25-062-Q1-E1-H1

Method BLASTN NCBI GI g4733952 BLAST score 156 E value 2.0e-82 Match length 156 % identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F23H11 genomic

sequence, complete sequence

Seq. No. 140771

Seq. ID LIB25-062-Q1-E1-H2

Method BLASTX NCBI GI g2191137 BLAST score 643 E value 2.0e-67 Match length 123 % identity 100

Match length

% identity

363

100



```
NCBI Description
                   (AF007269) similar to the GDSL family of lipolytic enzymes
                   [Arabidopsis thaliana]
                  140772
Seq. No.
                  LIB25-062-Q1-E1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1212812
BLAST score
                  98
E value
                   9.0e-10
                · <sup>/</sup> 33
Match length
% identity
                  88
NCBI Description (X95875) seed imbibition protein [Cicer arietinum]
                  140773
Seq. No.
Seq. ID
                  LIB25-062-Q1-E1-H5
Method
                  BLASTX
                  g4539333
NCBI GI
BLAST score
                  319
                  2.0e-29
E value
Match length
                  119
% identity
                   58
NCBI Description
                  (AL035539) putative amino acid transport protein
                   [Arabidopsis thaliana]
Seq. No.
                  140774
Seq. ID
                  LIB25-063-Q1-E1-F11
Method
                  BLASTX
NCBI GI
                  g3668173
BLAST score
                   629
E value
                  7.0e-66
Match length
                  132
% identity
                   93
                  (AB006777) vegetative storage protein [Arabidopsis
NCBI Description
                  thaliana]
                  140775
Seq. No.
                  LIB25-063-Q1-E1-H9
Seq. ID
Method
                  BLASTN
                  g4678705
NCBI GI
BLAST score
                  254
E value
                   1.0e-141
Match length
                   350
% identity
                   97
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
                   (ESSA project)
Seq. No.
                  140776
Seq. ID
                  LIB25-064-Q1-E1-B6
Method
                  BLASTN
NCBI GI
                   g2351062
BLAST score
                   226
E value
                   1.0e-124
```

17121

MAH20, complete sequence [Arabidopsis thaliana]

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



```
Seq. No.
Seq. ID
                  LIB25-064-Q1-E1-C6
Method
                  BLASTX
NCBI GI
                  q4586109
BLAST score
                  207
E value
                  2.0e-16
Match length
                  46
                  78
% identity
                  (AL049638) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  140778
Seq. ID
                  LIB25-064-Q1-E1-E5
Method
                  BLASTN
NCBI GI
                  q2564049
BLAST score
                  132
                  5.0e-68
E value
Match length
                  261
% identity
                  86
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MLE2, complete sequence [Arabidopsis thaliana]
                  140779
Seq. No.
                  LIB25-064-Q1-E1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2282473
BLAST score
                  332
                  4.0e-31
E value
Match length
                  119
% identity
                   50
                  (AB005911) xanthine dehydrogenase [Bombyx mori]
NCBI Description
                  140780
Seq. No.
Seq. ID
                  LIB25-065-Q1-E1-A4
Method
                  BLASTN
NCBI GI
                  q3241925
BLAST score
                   116
E value
                   2.0e-58
Match length
                   370
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MOK9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140781
Seq. ID
                  LIB25-065-Q1-E1-B11
Method
                  BLASTN
NCBI GI
                  g4757407
BLAST score
                  65
E value
                  1.0e-28
Match length
                  81
% identity
                  95
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQD19, complete sequence
```

Seq. No. 140782

Seq. ID LIB25-065-Q1-E1-C6

Method BLASTX NCBI GI g4406820



BLAST score 468
E value 6.0e-47
Match length 89
% identity 100

NCBI Description (AC006201) putative ras superfamily member [Arabidopsis

thaliana]

Seq. No. 140783

Seq. ID $\pm IB25-065-Q1-E1-D5$.

Method BLASTN
NCBI GI g4539378
BLAST score 284
E value 1.0e-158
Match length 412
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21

(ESSA project)

Seq. No. 140784

Seq. ID LIB25-065-Q1-E1-G10

Method BLASTX
NCBI GI g4544390
BLAST score 600
E value 2.0e-62
Match length 137
% identity 88

NCBI Description (AC007047) hypothetical protein [Arabidopsis thaliana]

Seq. No. 140785

Seq. ID LIB25-065-Q1-E1-G11

Method BLASTN
NCBI GI g3128143
BLAST score 168
E value 1.0e-89
Match length 226
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTI20, complete sequence [Arabidopsis thaliana] .

Seq. No. 140786

Seq. ID LIB25-065-Q1-E1-G3

Method BLASTN
NCBI GI g2827038
BLAST score 190
E value 1.0e-102
Match length 360
% identity 100

NCBI Description Arabidopsis thaliana chloroplast processing enzyme (CPE)

gene, complete cds

Seq. No. 140787

Seq. ID LIB25-065-Q1-E1-H8

Method BLASTN
NCBI GI g2564044
BLAST score 119
E value 3.0e-60
Match length 246



% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19P17, complete sequence [Arabidopsis thaliana]

Seq. No. 140788

Seq. ID LIB25-066-Q1-E1-B12

Method BLASTX NCBI GI g2618691 BLAST score 292 E value 1.0e-26

Match length 87 % identity 69

NCBI Description (AC002510) putative chloroplast envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 140789

Seq. ID LIB25-066-Q1-E1-C8

Method BLASTX
NCBI GI g3024434
BLAST score 455
E value 2.0e-45
Match length 111
% identity 84

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING

PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj BAA22951

(D88663) Tat binding protein 1 [Brassica rapa]

Seq. No. 140790

Seq. ID LIB25-066-Q1-E1-C9

Method BLASTN
NCBI GI g2494106
BLAST score 121
E value 6.0e-62
Match length 121
% identity 100

NCBI Description Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 140791

Seq. ID LIB25-066-Q1-E1-D3

Method BLASTN
NCBI GI g3449325
BLAST score 103
E value 4.0e-51
Match length 163
% identity 91

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K16H17, complete sequence [Arabidopsis thaliana]

Seq. No. 140792

Seq. ID LIB25-066-Q1-E1-D6

Method BLASTX
NCBI GI g1172977
BLAST score 625
E value 2.0e-65
Match length 132
% identity 95



```
NCBI Description
                  60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
                  ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.
                  140793
Seq. ID
                  LIB25-066-Q1-E1-D8
Method
                  BLASTX
NCBI GI
                  q4185505
BLAST score
                  443
E value
                  5.0e-44
Match length
                  109
% identity
                  79
NCBI Description
                  (AF101038) nonspecific lipid-transfer protein precursor
                  [Brassica napus]
                  140794
Seq. No.
Seq. ID
                  LIB25-066-Q1-E1-E11
Method
                  BLASTX
NCBI GI
                  q1769905
BLAST score
                  437
E value
                  2.0e-43
Match length
                  123
% identity
                  69
NCBI Description
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                  [Arabidopsis thaliana]
Seq. No.
                  140795
Seq. ID
                  LIB25-066-Q1-E1-E3
Method
                  BLASTN
NCBI GI
                  g2494106
BLAST score
                  213
E value
                  1.0e-116
Match length
                  213
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  140796
Seq. ID
                  LIB25-066-Q1-E1-E5
Method
                  BLASTX
NCBI GI
                  q4567265
BLAST score
                  496
E value
                  3.0e-50
Match length
                  96
% identity
                  100
NCBI Description (AC006841) putative kinesin protein [Arabidopsis thaliana]
                  140797
Seq. No.
Seq. ID
                  LIB25-066-Q1-E1-F4
                  BLASTN
Method
                  g4263694
```

Method BLASTN
NCBI GI 94263694
BLAST score 88
E value 3.0e-42
Match length 132
% identity 92

NCBI Description Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                  140798
Seq. ID
                  LIB25-066-Q1-E1-F8
Method
                  BLASTX
NCBI GI
                  g3135252
BLAST score
                  479
E value
                  3.0e-48
Match length
                  113
% identity
                  41
NCBI Description
                  (AC003058) hypothetical protein [Arabidopsis thaliana]
                  >gi_3176720 (AC002392) hypothetical protein [Arabidopsis
                  thaliana]
Seq. No.
                  140799
Seq. ID
                  LIB25-066-Q1-E1-F9
Method
                  BLASTX
NCBI GI
                  q2506788
BLAST score
                  168
E value
                  8.0e-12
Match length
                  81
                  37
% identity
                  GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (RAB
NCBI Description
                  GERANYLGERANYLTRANSFERASE BETA SUBUNIT) (RAB
                  GERANYL-GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG
                  TRANSFERASE) (RAB GGTASE) >gi_1332508_emb_CAA66638
                   (X98001) geranylgeranyl transferase II [Homo sapiens]
Seq. No.
                  140800
Seq. ID
                  LIB25-066-Q1-E1-H2
Method
                  BLASTX
NCBI GI
                  g4008010
BLAST score
                  174
E value
                  7.0e-13
Match length
                  78
% identity
                  51
NCBI Description
                  (AF084036) receptor-like protein kinase [Arabidopsis
                  thaliana]
                  140801
Seq. No.
Seq. ID
                  LIB25-066-Q1-E1-H6
Method
                  BLASTX
NCBI GI
                  g2129918
BLAST score
                  146
E value
                  2.0e-09
Match length
                  95
                  42
% identity
                  BPF-1 protein - parsley >gi 396197 emb_CAA48413_ (X68337)
NCBI Description
                  BPF-1 [Petroselinum crispum] >gi 441310 emb CAA44518
                   (X62653) BPF-1 [Petroselinum crispum]
                  140802
Seq. No.
Seq. ID
                  LIB25-067-Q1-E1-A1
```

Method BLASTN
NCBI GI 94691223
BLAST score 186
E value 1.0e-100
Match length 341
% identity 99



NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No. 140803
Seq. ID LIB25-067-Q1-E1-A3
Method BLASTN

Method BLASTN
NCBI GI g4165340
BLAST score 380
E value 0.0e+00
Match length 380
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140804

Seq. ID LIB25-067-Q1-E1-A4

Method BLASTX
NCBI GI g2494130
BLAST score 530
E value 3.0e-54
Match length 102
% identity 99

NCBI Description (AC002376) Contains similarity to Glycine SRC2

(gb_AB000130). [Arabidopsis thaliana]

Seq. No. 140805

Seq. ID LIB25-067-Q1-E1-C2

Method BLASTX
NCBI GI g4262147
BLAST score 316
E value 3.0e-29
Match length 124
% identity 52

NCBI Description (AC005275) putative homolog of transport inhibitor response

1 [Arabidopsis thaliana]

Seq. No. 140806

Seq. ID LIB25-067-Q1-E1-C9

Method BLASTX
NCBI GI g2578818
BLAST score 169
E value 6.0e-12
Match length 116
% identity 36

NCBI Description (AB000121) TBPIP [Mus musculus]

Seq. No. 140807

Seq. ID LIB25-067-Q1-E1-E11

Method BLASTX
NCBI GI g2980770
BLAST score 183
E value 1.0e-13
Match length 132
% identity 59

NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 140808



```
Seq. ID
                  LIB25-067-Q1-E1-E3
Method
                  BLASTX
NCBI GI
                  q3005601
BLAST score
                  124
E value
                  1.0e-06
Match length
                  127
% identity
                  14
NCBI Description
                  (AF052433) katanin p80 subunit [Strongylocentrotus
                  purpuratus]
Seq. No.
                  140809
Seq. ID
                  LIB25-067-Q1-E1-E7
Method
                  BLASTX
NCBI GI
                  q2632061
BLAST score
                  565
E value
                  2.0e-58
Match length
                  106
% identity
                  100
                  (AJ002597) membrane-associated salt-inducible protein like
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  140810
Seq. ID
                  LIB25-067-Q1-E1-F5
Method
                  BLASTN
NCBI GI
                  q4587641
BLAST score
                  401
E value
                  0.0e + 00
Match length
                  401
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F20D21 genomic
                  sequence, complete sequence
Seq. No.
                  140811
Seq. ID
                  LIB25-067-Q1-E1-G7
Method
                  BLASTX
NCBI GI
                  q4539330
BLAST score
                  695
E value
                  1.0e-73
                  133
Match length
                  100
% identity
                  (AL035679) putative receptor-like protein kinase (fragment)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  140812
Seq. ID
                  LIB25-067-Q1-E1-H2
                  BLASTN
Method
NCBI GI
                  g4580454
BLAST score
                  389
                  0.0e + 00
E value
Match length
                  389
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC T2G17 genomic
```

sequence, complete sequence

Seq. No. 140813

Seq. ID LIB25-067-Q1-E1-H3

Method BLASTN



```
q3319339
NCBI GI
BLAST score
                  386
                  0.0e+00
E value
Match length
                  386
                  100
% identity
NCBI Description Arabidopsis thaliana BAC F9D12
Seq. No.
                  140814
                  LIB25-067-Q1-E1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3287270
BLAST score
                  471
E value
                  2.0e-47
Match length
                  128
% identity
                  74
NCBI Description
                  (Y09533) involved in starch metabalism [Solanum tuberosum]
                  140815
Seq. No.
Seq. ID
                  LIB25-067-Q1-E1-H7
Method
                  BLASTX
NCBI GI
                  g2129742
BLAST score
                  228
E value
                  4.0e-19
Match length
                  48
% identity
                  83
NCBI Description
                  stress-induced protein OZI1 precursor - Arabidopsis
                  thaliana >gi_790583 (U20347) mRNA corresponding to this
                  gene accumulates in response to ozone stress and pathogen
                   (bacterial) infection; putative pathogenesis-related
                  protein [Arabidopsis thaliana] >gi 2252869 (AF013294) No
                  definition line found [Arabidopsis thaliana]
                  140816
Seq. No.
Seq. ID
                  LIB25-068-Q1-E1-C10
Method
                  BLASTX
NCBI GI
                  g2760084
BLAST score
                  252
E value
                  1.0e-21
Match length
                  70
% identity
                  42
NCBI Description
                  (Y16045) leucine-rich repeat protein [Arabidopsis thaliana]
Seq. No.
                  140817
Seq. ID
                  LIB25-068-Q1-E1-C7
Method
                  BLASTN
NCBI GI
                  g3241920
BLAST score
                  289
E value
                  1.0e-161
Match length
                  394
% identity
                  91
```

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MAE1, complete sequence [Arabidopsis thaliana]

Seq. No. 140818

LIB25-068-Q1-E1-C8 Seq. ID

Method BLASTN NCBI GI g468770



```
BLAST score
                  146
E value
                  9.0e-77
Match length
                  165
% identity
                  66
NCBI Description
                  A.thaliana genes for chloroplast ribosomal protein L12 and
                  tRNA-Pro
Seq. No.
                  140819
Seq. ID
                  LIB25-068-Q1-E1-D11
Method
                  BLASTN
NCBI GI
                  g4757392
BLAST score
                  32
E value
                  1.0e-08
Match length
                  92
% identity
                  84
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                  K14A17, complete sequence
Seq. No.
                  140820
Seq. ID
                  LIB25-068-Q1-E1-D3
Method
                  BLASTN
NCBI GI
                  g3789706
BLAST score
                  179
E value
                  5.0e-96
Match length
                  404
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F15K9 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  140821
Seq. ID
                  LIB25-068-Q1-E1-D5
Method
                  BLASTX
NCBI GI
                  g4454018
BLAST score
                  685
                  2.0e-72
E value
Match length
                  134
% identity
                  100
NCBI Description
                  (AL035396) SRG1-like protein [Arabidopsis thaliana]
Seq. No.
                  140822
Seq. ID
                  LIB25-068-Q1-E1-E5
Method
                  BLASTN
NCBI GI
                  g2827698
BLAST score
                  244
E value
                  1.0e-135
Match length
                  413
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 5, BAC clone F6H11
                  (ESSAII project)
```

Seq. No.

Seq. ID

LIB25-068-Q1-E1-E8

140823

Method BLASTX NCBI GI q1169278 BLAST score 190 E value 6.0e-15 Match length 51



% identity 76

NCBI Description DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14

protein [Arabidopsis thaliana]

Seq. No. 140824

Seq. ID LIB25-068-Q1-E1-F6

Method BLASTN NCBI GI g4589444

BLAST score 81

E value 1.0e-37 Match length 96 % identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWF20, complete sequence

Seq. No. 140825

Seq. ID LIB25-068-Q1-E1-H7

Method BLASTN
NCBI GI g437313
BLAST score 167
E value 3.0e-89
Match length 167
% identity 54

NCBI Description Arabidopsis thaliana DNA sequence with repeats

Seq. No. 140826

Seq. ID LIB25-069-Q1-E1-A3

Method BLASTX
NCBI GI g2493144
BLAST score 331
E value 3.0e-31
Match length 82
% identity 52

NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE

16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132

H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi 926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis

thaliana]

Seq. No. 140827

Seq. ID LIB25-069-Q1-E1-B12

Method BLASTN
NCBI GI g4572664
BLAST score 301
E value 1.0e-169
Match length 411
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F25P17 genomic

sequence, complete sequence

Seq. No. 140828

Seq. ID LIB25-069-Q1-E1-B5

Method BLASTN
NCBI GI g3869074
BLAST score 61
E value 4.0e-26



Match length 130 % identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MMI9, complete sequence [Arabidopsis thaliana]

Seq. No. 140829

Seq. ID LIB25-069-Q1-E1-C10

Method BLASTX
NCBI GI g4512651
BLAST score 285
E value 2.0e-25
Match length 123
% identity 44

NCBI Description (AC007048) putative tyrosine transaminase [Arabidopsis

thaliana]

Seq. No. 140830

Seq. ID LIB25-069-Q1-E1-C12

Method BLASTX
NCBI GI g4544427
BLAST score 438
E value 2.0e-43
Match length 109
% identity 74

NCBI Description (AC006955) putative ferredoxin-thioredoxin reductase

[Arabidopsis thaliana]

Seq. No. 140831

Seq. ID LIB25-069-Q1-E1-D4

Method BLASTX
NCBI GI g4490341
BLAST score 416
E value 3.0e-41
Match length 83
% identity 92

NCBI Description (AL035656) putative protein [Arabidopsis thaliana]

Seq. No. 140832

Seq. ID LIB25-069-Q1-E1-E9

Method BLASTN
NCBI GI g2264311
BLAST score 247
E value 1.0e-136
Match length 303
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MLN1, complete sequence [Arabidopsis thaliana]

Seq. No. 140833

Seq. ID LIB25-069-Q1-E1-F3

Method BLASTX
NCBI GI g4206122
BLAST score 414
E value 1.0e-40
Match length 141
% identity 59

NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum

% identity

NCBI Description

90



crystallinum]

```
Seq. No.
                  140834
Seq. ID
                  LIB25-069-Q1-E1-F4
Method
                  BLASTX
NCBI GI
                  g1076663
BLAST score
                  579
                  5.0e-60
E value
Match length
                  129
                  87
% identity
NCBI Description
                  H+-transporting ATPase (EC 3.6.1.35) (clone PHA2) - potato
                  >gi_435001_emb_CAA54045 (X76535) H(+)-transporting ATPase
                  [Solanum tuberosum]
Seq. No.
                  140835
Seq. ID
                  LIB25-069-Q1-E1-F6
Method
                  BLASTN
NCBI GI
                  q2618603
BLAST score
                  33
                  2.0e-09
E value
Match length
                  97
% identity
                  84
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSL3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140836
Seq. ID
                  LIB25-069-Q1-E1-G11
Method
                  BLASTN
NCBI GI
                  q881520
BLAST score
                  108
E value
                  6.0e-54
Match length
                  219
% identity
                  88
NCBI Description
                  Arabidopsis thaliana hexokinase 1 (AtHXK1) mRNA, complete
                  cds
Seq. No.
                  140837
Seq. ID
                  LIB25-069-Q1-E1-G2
Method
                  BLASTX
NCBI GI
                  g4580473
BLAST score
                  472
E value
                  2.0e-47
Match length
                  104
% identity
                  92
NCBI Description
                  (AC006081) putative pathogenesis-related protein; similar
                  to PR-1 [Arabidopsis thaliana]
Seq. No.
                  140838
                  LIB25-069-Q1-E1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4510360
BLAST score
                  172
E value
                  5.0e-92
Match length
                  284
```

17133

sequence, complete sequence

Arabidopsis thaliana chromosome II BAC F11F19 genomic



```
140839
Seq. No.
Seq. ID
                  LIB25-069-Q1-E1-H6
Method
                  BLASTX
NCBI GI
                  g4539343
                  313
BLAST score
                  9.0e-29
E value
                  106
Match length
% identity
                  58
                 (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                  140840
Seq. No.
                  LIB25-070-Q1-E1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4539309
BLAST score
                  85
                  2.0e-40
E value
Match length
                  121
% identity
                  93
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22
                  (ESSA project)
Seq. No.
                  140841
                  LIB25-070-Q1-E1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4589419
BLAST score
                  360
E value
                  0.0e + 00
Match length
                  360
                  100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K2I5, complete sequence
                  140842
Seq. No.
                  LIB25-070-Q1-E1-B4
Seq. ID
Method
                  BLASTX
                  g2459417
NCBI GI
BLAST score
                  378
E value
                  2.0e-36
Match length
                  85
% identity
                  84
NCBI Description
                  (AC002332) putative pre-mRNA splicing factor PRP19
                   [Arabidopsis thaliana]
                  140843
Seq. No.
                  LIB25-070-Q1-E1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g457715
BLAST score
                  301
E value
                  1.0e-169
Match length
                  377
% identity
                  100
NCBI Description A.thaliana CXc750 gene
```

Seq. No. 140844

Seq. ID LIB25-070-Q1-E1-D3

Method BLASTX



NCBI GI g136636 BLAST score 375 E value 4.0e-36 Match length 68 % identity 100

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 -

Arabidopsis thaliana >gi_442594 pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894 pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 140845

Seq. ID LIB25-070-Q1-E1-F7

Method BLASTN
NCBI GI g4680765
BLAST score 327
E value 0.0e+00
Match length 361
% identity 100

NCBI Description Arabidopsis thaliana BAC F14I23 from chromosome V near 69

cM, complete sequence

Seq. No. 140846

Seq. ID LIB25-071-Q1-E1-A10

Method BLASTN
NCBI GI g4467131
BLAST score 168
E value 1.0e-89
Match length 235
% identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13

(ESSA project)

Seq. No. 140847

Seq. ID LIB25-071-Q1-E1-B12

Method BLASTX
NCBI GI g544424
BLAST score 204
E value 5.0e-16
Match length 39
% identity 97

NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir S30147

glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
>gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding

protein [Arabidopsis thaliana]

>gi_4567224 gb AAD23639.1 AC007119 5 (AC007119)

glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No. 140848

Seq. ID LIB25-071-Q1-E1-B3

Method BLASTX NCBI GI q2341034

```
BLAST score
E value
                  1.0e-40
Match length
                  87
% identity
                  97
NCBI Description
                  (AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.
                  140849
Seq. ID
                  LIB25-071-Q1-E1-C6
Method
                  BLASTX
NCBI GI
                  g2275202
BLAST score
                  353
E value
                  1.0e-33
Match length
                  67
% identity
                  100
NCBI Description
                  (AC002337) acyl-CoA synthetase isolog [Arabidopsis
                  thaliana]
Seq. No.
                  140850
Seq. ID
                  LIB25-071-Q1-E1-D1
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
```

E value 9.0e-11 Match length 36

% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

140851 Seq. No. Seq. ID LIB25-071-Q1-E1-D12 Method BLASTN NCBI GI q4531433 BLAST score 72

2.0e-32 E value Match length 165 % identity 93

Arabidopsis thaliana chromosome II P1 MFL8 genomic NCBI Description

sequence, complete sequence

140852 Seq. No.

LIB25-071-Q1-E1-E12 Seq. ID

Method BLASTN NCBI GI q3449315 BLAST score 220 E value 1.0e-120 Match length 368 % identity 99

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K23L20, complete sequence [Arabidopsis thaliana]

140853 Seq. No.

LIB25-071-Q1-E1-E7 Seq. ID

Method BLASTN NCBI GI q4490291 BLAST score 325 0.0e+00E value Match length 359 % identity 99



NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No. 140854

Seq. ID LIB25-071-Q1-E1-H6

Method BLASTX
NCBI GI g2244783
BLAST score 393
E value 2.0e-38
Match length 102
% identity 82

NCBI Description (297335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 140855

Seq. ID LIB25-073-Q1-E1-A11

Method BLASTN
NCBI GI g4589438
BLAST score 313
E value 1.0e-176
Match length 317
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQJ2, complete sequence

Seq. No. 140856

Seq. ID LIB25-073-Q1-E1-C10

Method BLASTX
NCBI GI g3461845
BLAST score 408
E value 6.0e-40
Match length 107
% identity 75

NCBI Description (AC005315) hypothetical protein [Arabidopsis thaliana]

Seq. No. 140857

Seq. ID LIB25-073-Q1-E1-D4

Method BLASTX
NCBI GI g1814401
BLAST score 549
E value 2.0e-56
Match length 136
% identity 79

NCBI Description (U84888) phosphoglucomutase [Mesembryanthemum crystallinum]

Seq. No. 140858

Seq. ID LIB25-073-Q1-E1-E11

Method BLASTX
NCBI GI g2262098
BLAST score 704
E value 1.0e-74
Match length 136
% identity 100

NCBI Description (AC002343) HSP90 isolog [Arabidopsis thaliana]

Seq. No. 140859

Seq. ID LIB25-073-Q1-E1-F2

Method BLASTN



NCBI GI g4519193 BLAST score 170 E value 1.0e-90 Match length 424 % identity 46

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC11, complete sequence

Seq. No. 140860

Seq. ID LIB25-073-Q1-E1-H6

Method BLASTN
NCBI GI g2980757
BLAST score 130
E value 5.0e-67
Match length 130
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18

(ESSAII project)

Seq. No. 140861

Seq. ID LIB25-074-Q1-E1-B12

Method BLASTX
NCBI GI g2499607
BLAST score 499
E value 1.0e-50
Match length 96
% identity 98

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 3 (MAP KINASE 3)

(ATMPK3) >gi_629544_pir__S40469 mitogen-activated protein

kinase 3 (EC 2.7.1.-) - Arabidopsis thaliana

>gi 457398 dbj BAA04866 (D21839) MAP kinase [Arabidopsis

thaliana]

Seq. No. 140862

Seq. ID LIB25-074-Q1-E1-C9

Method BLASTX
NCBI GI g1702986
BLAST score 187
E value 1.0e-14
Match length 47
% identity 83

NCBI Description 14-3-3-LIKE PROTEIN GF14 CHI >gi 1255987 (U09377) GF14chi

isoform [Arabidopsis thaliana] >gi_1256534 (L09112) GF14

chi chain [Arabidopsis thaliana]

Seq. No. 140863

Seq. ID LIB25-074-Q1-E1-G10

Method BLASTN
NCBI GI g1931636
BLAST score 341
E value 0.0e+00
Match length 353
% identity 99

NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No. 140864

Seq. ID LIB25-074-Q1-E1-G3



Method BLASTX
NCBI GI g4056425
BLAST score 171
E value 3.0e-12
Match length 45
% identity 71

NCBI Description (AC005322) ESTs gb_H36249, gb_AA59732 and gb_AA651219 come

from this gene. [Arabidopsis thaliana]

Seq. No. 140865

Seq. ID LIB25-075-Q1-E1-A2

Method BLASTN
NCBI GI g2281081
BLAST score 181
E value 2.0e-97
Match length 237
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F18019 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140866

Seq. ID LIB25-075-Q1-E1-A5

Method BLASTN
NCBI GI g2760169
BLAST score 140
E value 5.0e-73
Match length 241
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MFB13, complete sequence [Arabidopsis thaliana]

Seq. No. 140867

Seq. ID LIB25-075-Q1-E1-A6

Method BLASTN
NCBI GI g4262221
BLAST score 186
E value 1.0e-100
Match length 252
% identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140868

Seq. ID LIB25-075-Q1-E1-B6

Method BLASTN
NCBI GI g2264310
BLAST score 252
E value 1.0e-140
Match length 252
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MKP11, complete sequence [Arabidopsis thaliana]

Seq. No. 140869

Seq. ID LIB25-075-Q1-E1-C3

Method BLASTN NCBI GI q2358139



BLAST score 202 E value 1.0e-110 Match length 266 % identity 99

NCBI Description Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete

sequence [Arabidopsis thaliana]

Seq. No. 140870

Seq. ID LIB25-075-Q1-E1-C6

Method BLASTX
NCBI GI g1362007
BLAST score 423
E value 4.0e-42
Match length 79
% identity 100

NCBI Description thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana

>gi_871992_emb_CAA55787_ (X79195) thioglucosidase

[Arabidopsis thaliana]

Seq. No. 140871

Seq. ID LIB25-075-Q1-E1-D1

Method BLASTX
NCBI GI g2832685
BLAST score 381
E value 4.0e-37
Match length 87
% identity 87

NCBI Description (AL021712) putative protein [Arabidopsis thaliana]

Seq. No. 140872

Seq. ID LIB25-075-Q1-E1-D2

Method BLASTX
NCBI GI g4586108
BLAST score 328
E value 6.0e-31
Match length 82
% identity 84

NCBI Description (AL049638) putative transport protein [Arabidopsis

thaliana]

Seq. No. 140873

Seq. ID LIB25-075-Q1-E1-E1

Method BLASTX
NCBI GI g1076442
BLAST score 60
E value 9.0e-15
Match length 57
% identity 72

NCBI Description beta-glucosidase (EC 3.2.1.21) - rape

>gi 757740 emb CAA57913 (X82577) beta-glucosidase

[Brassica napus]

Seq. No. 140874

Seq. ID LIB25-075-Q1-E1-E5

Method BLASTN
NCBI GI g3047100
BLAST score 197



E value 1.0e-107 Match length 256 % identity 98

NCBI Description Arabidopsis thaliana BAC F6N23

Seq. No. 140875

Seq. ID LIB25-075-Q1-E1-F3

Method BLASTN
NCBI GI g2828185
BLAST score 148
E value 9.0e-78
Match length 265
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUD21, complete sequence [Arabidopsis thaliana]

Seq. No. 140876

Seq. ID LIB25-075-Q1-E1-G1

Method BLASTN
NCBI GI g2564044
BLAST score 140
E value 5.0e-73
Match length 267
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19P17, complete sequence [Arabidopsis thaliana]

Seq. No. 140877

Seq. ID LIB25-075-Q1-E1-G2

Method BLASTX
NCBI GI g416758
BLAST score 150
E value 5.0e-10
Match length 69
% identity 48

NCBI Description SERINE CARBOXYPEPTIDASE PRECURSOR >gi 166674 (M81130)

carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis

thaliana]

Seq. No. 140878

Seq. ID LIB25-075-Q1-E1-G3

Method BLASTX
NCBI GI g2454182
BLAST score 403
E value 1.0e-39
Match length 86
% identity 88

NCBI Description (U80185) pyruvate dehydrogenase El alpha subunit

[Arabidopsis thaliana]

Seq. No. 140879

Seq. ID LIB25-076-Q1-E1-A10

Method BLASTN
NCBI GI g2760165
BLAST score 318
E value 1.0e-179



Match length 360 % identity 66

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

MAC9, complete sequence [Arabidopsis thaliana]

Seq. No. 140880

Seq. ID LIB25-076-Q1-E1-B5

Method BLASTX
NCBI GI g2506443
BLAST score 135
E value 4.0e-43
Match length 119
% identity 78

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,

CHLOROPLAST >gi 2117520 pir JQ1285

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi 166704 (M64117) glyceraldehyde

3-phosphate dehydrogenase [Arabidopsis thaliana]

>gi_1402885_emb_CAA66816_ (X98130)

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) [Arabidopsis thaliana]

Seq. No. 140881

Seq. ID LIB25-076-Q1-E1-C11

Method BLASTX
NCBI GI g4415907
BLAST score 583
E value 2.0e-60
Match length 115
% identity 99

NCBI Description (AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana]

>qi 4581159 qb AAD24643.1 AC006919 21 (AC006919) putative

60S ribosomal protein L24 [Arabidopsis thaliana]

Seq. No. 140882

Seq. ID LIB25-076-Q1-E1-E12

Method BLASTN
NCBI GI 94309719
BLAST score 130
E value 2.0e-67
Match length 130
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T30D6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140883

Seq. ID LIB25-076-Q1-E1-E8

Method BLASTX
NCBI GI g3152940
BLAST score 201
E value 9.0e-16
Match length 88
% identity 49

NCBI Description (AF065483) sorting nexin 1 [Homo sapiens]

Seq. No. 140884



Seq. ID LIB25-076-Q1-E1-H11

Method BLASTN
NCBI GI g2392894
BLAST score 125
E value 5.0e-64
Match length 125
% identity 100

NCBI Description Arabidopsis thaliana brassinosteroid insensitive 1 (BRI1)

gene, complete cds

Seq. No. 140885

Seq. ID LIB25-077-Q1-E1-B12

Method BLASTN
NCBI GI g4159704
BLAST score 405
E value 0.0e+00
Match length 405
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MCB17, complete sequence

Seq. No. 140886

Seq. ID LIB25-077-Q1-E1-B5

Method BLASTN
NCBI GI g4185120
BLAST score 33
E value 5.0e-09
Match length 352
% identity 81

NCBI Description Arabidopsis thaliana chromosome 1 BAC F5F19 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 140887

Seq. ID LIB25-077-Q1-E1-C11

Method BLASTN
NCBI GI g4662609
BLAST score 76
E value 1.0e-34
Match length 247
% identity 83

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5,

complete sequence

Seq. No. 140888

Seq. ID LIB25-077-Q1-E1-C8

Method BLASTN
NCBI GI g4589421
BLAST score 351
E value 0.0e+00
Match length 359
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K5K13, complete sequence

Seq. No. 140889

Seq. ID LIB25-077-Q1-E1-D9

Method BLASTX



NCBI GI q1708236 BLAST score 506 2.0e-51 E value Match length 99 100 % identity

HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) NCBI Description

(3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)

>qi 2129617 pir JC4567 hydroxymethylglutaryl-CoA synthase

(EC 4.1.3.5) - Arabidopsis thaliana

>gi_1143390_emb_CAA58763_ (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]

>gi 1586548 prf 2204245A hydroxy methylglutaryl CoA

synthase [Arabidopsis thaliana]

Seq. No. 140890

Seq. ID LIB25-077-Q1-E1-E4

Method BLASTN g4325340 NCBI GI BLAST score 165 E value 6.0e-88 Match length 222 100 % identity

NCBI Description Arabidopsis thaliana BAC T1J1

140891 Seq. No.

Seq. ID LIB25-077-Q1-E1-F1

Method BLASTX NCBI GI g1438881 BLAST score 279 E value 7.0e-25 Match length 79 % identity 63

NCBI Description (U43839) GmCK2p [Glycine max]

140892 Seq. No.

LIB25-078-Q1-E1-B7 Seq. ID

Method BLASTX NCBI GI g4063734 BLAST score 563 E value 4.0e-58 Match length 123 % identity 88

NCBI Description (AC006259) putative P450 [Arabidopsis thaliana]

140893 Seq. No.

Seq. ID LIB25-078-Q1-E1-C2

Method BLASTN g2749918 NCBI GI BLAST score 135 E value 5.0e-70 Match length 193 % identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F316 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140894

Seq. ID LIB25-078-Q1-E1-C8



Method BLASTN
NCBI GI g3241926
BLAST score 140
E value 8.0e-73
Match length 388
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSG15, complete sequence [Arabidopsis thaliana]

Seq. No. 140895

Seq. ID LIB25-078-Q1-E1-D9

Method BLASTN
NCBI GI g1465734
BLAST score 335
E value 0.0e+00
Match length 335
% identity 100

NCBI Description Arabidopsis thaliana violaxanthin de-epoxidase precursor

(AVDE1) mRNA, complete cds

Seq. No. 140896

Seq. ID LIB25-078-Q1-E1-G6

Method BLASTX
NCBI GI g1363492
BLAST score 206
E value 3.0e-16
Match length 43
% identity 88

NCBI Description outer envelope membrane protein OEP75 precursor - garden

pea >gi_576507 (L36858) outer membrane protein [Pisum sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

Seq. No. 140897

Seq. ID LIB25-078-Q1-E1-G7

Method BLASTN
NCBI GI g1313927
BLAST score 45
E value 4.0e-16
Match length 146
% identity 82

NCBI Description B.oleracea mRNA for IFA binding protein (sp10)

Seq. No. 140898

Seq. ID LIB25-079-Q1-E1-A7

Method BLASTN
NCBI GI g4519191
BLAST score 97
E value 2.0e-47
Match length 166
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9P8, complete sequence

Seq. No. 140899

Seq. ID LIB25-079-Q1-E1-B12

Method BLASTN



NCBI GI g2281081
BLAST score 177
E value 6.0e-95
Match length 329
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F18019 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140900

Seq. ID LIB25-079-Q1-E1-B3

Method BLASTX
NCBI GI g584892
BLAST score 188
E value 1.0e-14
Match length 52
% identity 54

NCBI Description SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)

>gi_629805_pir__S43516 serine carboxypeptidase I - rice >gi_409580_dbj_BAA04510_ (D17586) serine carboxypeptidase I

[Oryza sativa]

Seq. No. 140901

Seq. ID LIB25-079-Q1-E1-B4

Method BLASTN
NCBI GI g1905774
BLAST score 191
E value 1.0e-103
Match length 202
% identity 99

NCBI Description A.thaliana mRNA for protein kinase

Seq. No. 140902

Seq. ID LIB25-079-Q1-E1-B6

Method BLASTX
NCBI GI g2738996
BLAST score 174
E value 4.0e-13
Match length 66
% identity 58

NCBI Description (AF022457) CYP97B2p [Glycine max]

Seq. No. 140903

Seq. ID LIB25-079-Q1-E1-C2

Method BLASTN
NCBI GI g4309683
BLAST score 77

E value 2.0e-35 Match length 177 % identity 86

NCBI Description Arabidopsis thaliana chromosome 1 BAC T31J12 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 140904

Seq. ID LIB25-079-Q1-E1-C3

Method BLASTN
NCBI GI g2264309
BLAST score 174



```
2.0e-93
E value
Match length
                  182
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MJJ3, complete sequence [Arabidopsis thaliana]
                  140905
Seq. No.
                  LIB25-079-Q1-E1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4191771
BLAST score
                  118
E value
                  6.0e-60
Match length
                  219
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F3P11 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  140906
Seq. No.
                  LIB25-079-Q1-E1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3522932
BLAST score
                  83
                  4.0e-39
E value
Match length
                  151
% identity
                  51
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F14M4 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140907
                  LIB25-079-Q1-E1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3046851
BLAST score
                  214
                  1.0e-117
E value
Match length
                  214
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MIJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140908
                  LIB25-079-Q1-E1-D5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4539309
BLAST score
                  174
E value
                  2.0e-93
Match length
                  201
% identity
                  96
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22
                  (ESSA project)
```

Seq. No. 140909

Seq. ID LIB25-079-Q1-E1-D6

Method BLASTN
NCBI GI g3193282
BLAST score 210
E value 1.0e-115
Match length 210

Match length

% identity

196

99

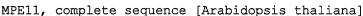


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% identity
NCBI Description
                  Arabidopsis thaliana BAC T14P8
Seq. No.
                  140910
Seq. ID
                  LIB25-079-Q1-E1-D7
Method
                  BLASTN
NCBI GI
                  q4559319
BLAST score
                  105
E value
                  3.0e-52
Match length
                  194
% identity
                  96
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F14N22 genomic
                  sequence, complete sequence
Seq. No.
                  140911
Seq. ID
                  LIB25-079-Q1-E1-E3
Method
                  BLASTN
NCBI GI
                  q992705
BLAST score
                  66
E value
                  5.0e-29
Match length
                  86
% identity
                  94
NCBI Description
                  Arabidopsis ubiquitin conjugating enzyme E2 (UBC13) gene,
                  complete cds
Seq. No.
                  140912
Seq. ID
                  LIB25-079-Q1-E1-E8
Method
                  BLASTX
NCBI GI
                  g256963
BLAST score
                  180
E value
                  8.0e-14
Match length
                  68
% identity
                  63
NCBI Description
                  (S45910) glyceraldehyde-3-phosphate-dehydrogenase subunit
                  GapA {N-terminal} [Arabidopsis thaliana, Peptide
                  Chloroplast Partial, 68 aa] [Arabidopsis thaliana]
Seq. No.
                  140913
Seq. ID
                  LIB25-079-Q1-E1-F12
Method
                  BLASTX
                  g2129623
NCBI GI
BLAST score
                  473
E value
                  1.0e-47
Match length
                  106
                  86
% identity
NCBI Description
                  immunophilin FKBP15-2 - Arabidopsis thaliana >gi 1272408
                  (U52047) immunophilin [Arabidopsis thaliana]
                  140914
Seq. No.
Seq. ID
                  LIB25-079-Q1-E1-F5
Method
                  BLASTN
NCBI GI
                  q4220640
BLAST score
                  188
E value
                  1.0e-101
```

17148

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:





Seq. No. 140915 Seq. ID LIB25-079-Q1-E1-F6 Method BLASTX NCBI GI q2499542 BLAST score 246 E value 2.0e-21 Match length 68 % identity 71 NCBI Description IRON(III) - ZINC(II) PURPLE ACID PHOSPHATASE PRECURSOR (PAP) >gi 1218042 (U48448) secreted purple acid phosphatase precursor [Arabidopsis thaliana] Seq. No. 140916 Seq. ID LIB25-079-Q1-E1-F7 Method BLASTN NCBI GI q3985958 BLAST score 203 E value 1.0e-110 Match length 203 % identity 100 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MZN1, complete sequence [Arabidopsis thaliana] Seq. No. 140917 Seq. ID LIB25-079-Q1-E1-G3 Method BLASTN NCBI GI q2979540 BLAST score 101 E value 8.0e-50 Match length 140 % identity 100 Arabidopsis thaliana chromosome II BAC F17K2 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 140918 LIB25-079-Q1-E1-G7 Seq. ID Method BLASTN NCBI GI g3985955 BLAST score 211 E value 1.0e-115 Match length 211 % identity 100 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MTH16, complete sequence [Arabidopsis thaliana] 140919 Seq. No.

Seq. ID LIB25-079-Q1-E1-H1

Method BLASTN
NCBI GI g4510360
BLAST score 203
E value 1.0e-110
Match length 203
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic

sequence, complete sequence



Seq. No. 140920 Seq. ID LIB25-079-Q1-E1-H8 Method BLASTX NCBI GI q3122673 BLAST score 331 E value 2.0e-31 Match length 62 100 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No. 140921

Seq. ID LIB25-079-Q1-E1-H9

Method BLASTX
NCBI GI g3273751
BLAST score 556
E value 2.0e-57
Match length 108
% identity 99

NCBI Description (AF061518) manganese superoxide dismutase [Arabidopsis

thaliana]

Seq. No. 140922

Seq. ID LIB25-080-Q1-E1-A6

Method BLASTX
NCBI GI g1170503
BLAST score 578
E value 5.0e-60
Match length 114
% identity 100

NCBI Description EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)

>gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1

[Arabidopsis thaliana]

Seq. No. 140923

Seq. ID LIB25-080-Q1-E1-A9

Method BLASTN
NCBI GI g2935341
BLAST score 150
E value 8.0e-79
Match length 310
% identity 100

NCBI Description Arabidopsis thaliana steroid 22-alpha-hydroxylase (DWF4)

gene, complete cds

Seq. No. 140924

Seq. ID LIB25-080-Q1-E1-B12

Method BLASTX
NCBI GI g132102
BLAST score 585
E value 8.0e-61
Match length 108
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR



(RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir_RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_(X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No. 140925 Seq. ID LIB25-080-Q1-E1-C4 Method BLASTX NCBI GI q4512655 BLAST score 516 E value 1.0e-52 Match length 94 100 % identity

NCBI Description (AC007048) putative protein phosphatase 2C [Arabidopsis

thaliana]

Seq. No. 140926

Seq. ID LIB25-080-Q1-E1-D4

Method BLASTN
NCBI GI g2623294
BLAST score 152
E value 5.0e-80
Match length 330
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC T20B5 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140927

Seq. ID LIB25-080-Q1-E1-D7

Method BLASTN
NCBI GI g2827698
BLAST score 118
E value 9.0e-60
Match length 329
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 5, BAC clone F6H11

(ESSAII project)

Seq. No. 140928

Seq. ID LIB25-080-Q1-E1-E10

Method BLASTX
NCBI GI g1335862
BLAST score 579
E value 4.0e-60
Match length 117
% identity 93

NCBI Description (U42608) clathrin heavy chain [Glycine max]

Seq. No. 140929

Seq. ID LIB25-080-Q1-E1-G1

Method BLASTX
NCBI GI g282865
BLAST score 472
E value 1.0e-47
Match length 97
% identity 91



NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana

>gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
protein [Arabidopsis thaliana] >gi_166644 (M85150)
chlorophyll a/b-binding protein [Arabidopsis thaliana]
>gi 4678304 emb CAB41095.1 (AL049655) chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 140930

Seq. ID LIB25-080-Q1-E1-G11

Method BLASTX
NCBI GI 94539314
BLAST score 410
E value 3.0e-40
Match length 117
% identity 81

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 140931

Seq. ID LIB25-080-Q1-E1-G12

Method BLASTX
NCBI GI g2760332
BLAST score 328
E value 1.0e-30
Match length 72
% identity 96

NCBI Description (AC002130) F1N21.17 [Arabidopsis thaliana]

Seq. No. 140932

Seq. ID LIB25-080-Q1-E1-H4

Method BLASTX
NCBI GI g2088652
BLAST score 584
E value 1.0e-60
Match length 115
% identity 97

NCBI Description (AF002109) 26S proteasome regulatory subunit S12 isolog

[Arabidopsis thaliana] >gi_2351376 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis

thaliana]

Seq. No. 140933

Seq. ID LIB25-080-Q1-E1-H6

Method BLASTN
NCBI GI g3193282
BLAST score 190
E value 1.0e-102
Match length 267
% identity 100

NCBI Description Arabidopsis thaliana BAC T14P8

Seq. No. 140934

Seq. ID LIB25-080-Q1-E1-H9

Method BLASTX
NCBI GI g3668175
BLAST score 521
E value 3.0e-53
Match length 111

% identity

100



```
% identity
  NCBI Description
                    (AB006778) vegetative storage protein [Arabidopsis
                    thaliana]
  Seq. No.
                    140935
                    LIB25-081-Q1-E1-A9
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q2829894
BLAST score
                    293
E value
                    1.0e-26
 Match length
                    88
  % identity
                    73
                    (AC002311) Unknown protein [Arabidopsis thaliana]
 NCBI Description
  Seq. No.
                    140936
  Seq. ID
                    LIB25-081-Q1-E1-B10
  Method
                    BLASTX
 NCBI GI
                    g886116
 BLAST score
                    537
 E value
                    4.0e-55
 Match length
                    105
  % identity
                    100
  NCBI Description
                    (U27609) TCH4 protein [Arabidopsis thaliana] >gi 2952473
                    (AF051338) xyloglucan endotransglycosylase related protein
                    [Arabidopsis thaliana]
  Seq. No.
                    140937
  Seq. ID
                    LIB25-081-Q1-E1-D4
 Method
                    BLASTN
 NCBI GI
                    g4580365
 BLAST score
                    265
                    1.0e-147
 E value
 Match length
                    354
                    100
  % identity
 NCBI Description Arabidopsis thaliana chromosome I BAC F3F20 genomic
                    sequence, complete sequence
                    140938
  Seq. No.
                    LIB25-081-Q1-E1-D7
  Seq. ID
  Method
                    BLASTN
                    g4263694
  NCBI GI
 BLAST score
                    110
 E value
                    6.0e-55
 Match length
                    370
  % identity
                    100
  NCBI Description
                   Arabidopsis thaliana chromosome II BAC F22D22 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
                    140939
  Seq. No.
                    LIB25-081-Q1-E1-D8
  Seq. ID
 Method
                    BLASTX
                    g3075394
 NCBI GI
 BLAST score
                    639
                    4.0e-67
 E value
 Match length
                    127
```

17153

NCBI Description (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis



thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No. 140940

Seq. ID LIB25-081-Q1-E1-E10

Method BLASTN
NCBI GI g3869062
BLAST score 141
E value 2.0e-73
Match length 350
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K11I1, complete sequence [Arabidopsis thaliana]

Seq. No. 140941

Seq. ID LIB25-081-Q1-E1-E12

Method BLASTX
NCBI GI g3080405
BLAST score 146
E value 2.0e-09
Match length 38
% identity 37

NCBI Description (AL022603) Lsd1 like protein [Arabidopsis thaliana]

>gi 4455269 emb CAB36805.1 (AL035527) Lsdl like protein

[Arabidopsis thaliana]

Seq. No. 140942

Seq. ID LIB25-081-Q1-E1-E9

Method BLASTX
NCBI GI g115767
BLAST score 538
E value 3.0e-55
Match length 103
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 140943

Seq. ID LIB25-081-Q1-E1-F10

Method BLASTX
NCBI GI g3819710
BLAST score 457
E value 8.0e-46
Match length 86
% identity 97

NCBI Description (AJ224161) delta-8 sphingolipid desaturase [Arabidopsis

thalianal

Seq. No. 140944

Seq. ID LIB25-081-Q1-E1-F5

Method BLASTN NCBI GI g2642152



```
BLAST score
                  356
                  0.0e+00
E value
                  371
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T5I7 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  140945
Seq. No.
                  LIB25-081-Q1-E1-F8
Seq. ID
Method
                  BLASTX
                  g3023742
NCBI GI
                  172
BLAST score
                  2.0e-12
E value
Match length
                  36
% identity
                  100
                  FERREDOXIN 2 PRECURSOR >qi 1931646 (U95973) ferredoxin
NCBI Description
                  precusor isolog [Arabidopsis thaliana]
                  140946
Seq. No.
                  LIB25-081-Q1-E1-G10
Seq. ID
Method
                  BLASTX
                  g1762428
NCBI GI
BLAST score
                  468
                  4.0e-47
E value
                  91
Match length
% identity
                  100
                  (U59467) aromatic rich glycoprotein JP630 [Arabidopsis
NCBI Description
                  thaliana]
                  140947
Seq. No.
                  LIB25-081-Q1-E1-G12
Seq. ID
                  BLASTN
Method
                  g3766106
NCBI GI
                  74
BLAST score
E value
                  2.0e-33
Match length
                  358
                  99
% identity
                  Arabidopsis thaliana chromosome 1 BAC F9K20 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  140948
Seq. No.
                  LIB25-081-Q1-E1-G8
Seq. ID
Method
                  BLASTX
                  g3219938
NCBI GI
BLAST score
                  151
                  8.0e-10
E value
Match length
                  58
                  40
% identity
                  HYPOTHETICAL 34.9 KD PROTEIN C57A10.11C IN CHROMOSOME I
NCBI Description
                  >gi 2058378 emb CAB08174 (Z94864) hypothetical protein
```

[Schizosaccharomyces pombe]

140949 Seq. No. Seq. ID

LIB25-081-Q1-E1-H5

Method BLASTX NCBI GI g1703227 BLAST score 279



7.0e-25 E value Match length 68 % identity 76

NCBI Description ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)

(ALAAT-2) >gi_629770_pir__S42535 alanine transaminase (EC 2.6.1.2) - barley >gi 469148 emb CAA81231 (Z26322) alanine

aminotransferase [Hordeum vulgare]

Seq. No. 140950

LIB25-082-Q1-E1-D12 Seq. ID

Method BLASTN g2182286 NCBI GI BLAST score 205 E value 1.0e-111 Match length 381 % identity 100

Sequence of BAC F20P5 from Arabidopsis thaliana chromosome NCBI Description

1, complete sequence [Arabidopsis thaliana]

Seq. No. 140951

LIB25-082-Q1-E1-D9 Seq. ID

Method BLASTN NCBI GI g4589435 BLAST score - 328 E value 0.0e+00349 Match length % identity 98

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MOE17, complete sequence

Seq. No. 140952

LIB25-082-Q1-E1-E10 Seq. ID

Method BLASTX NCBI GI g2289001 BLAST score 631 4.0e-66 E value Match length 128 % identity 95

(AC002335) small nuclear ribonucleoprotein isolog NCBI Description

[Arabidopsis thaliana]

140953 Seq. No.

LIB25-082-Q1-E1-E3 Seq. ID

Method BLASTX NCBI GI g464621 BLAST score 368 2.0e-35 E value Match length 94 % identity 74

60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 NCBI Description

ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16

[Mesembryanthemum crystallinum]

Seq. No. 140954

LIB25-082-Q1-E1-F11 Seq. ID



```
Method BLASTN
NCBI GI g2564046
BLAST score 180
E value 6.0e-97
Match length 211
% identity 95
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MGI19, complete sequence [Arabidopsis thaliana]

Seq. No. 140955

Seq. ID LIB25-082-Q1-E1-F5

Method BLASTX
NCBI GI g1350956
BLAST score 560
E value 8.0e-58
Match length 109
% identity 100

NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No. 140956

Seq. ID LIB25-082-Q1-E1-G10

Method BLASTN
NCBI GI g4757405
BLAST score 297
E value 1.0e-166
Match length 392
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MOJ10, complete sequence

Seq. No. 140957

Seq. ID LIB25-082-Q1-E1-G6

Method BLASTX
NCBI GI g4204265
BLAST score 317
E value 2.0e-29
Match length 112
% identity 61

NCBI Description (AC005223) 45643 [Arabidopsis thaliana]

Seq. No. 140958

Seq. ID LIB25-082-Q1-E1-H4

Method BLASTX
NCBI GI g3831457
BLAST score 437
E value 2.0e-43
Match length 88
% identity 100

NCBI Description (AC005700) putative ion channel protein [Arabidopsis

thaliana]

Seq. No. 140959

Seq. ID LIB25-082-Q1-E1-H8

Method BLASTN
NCBI GI g4512646
BLAST score 296
E value 1.0e-166



Match length 300
% identity 100
NCBI Description Arabidopsis thaliana chromosome II BAC F23N11 genomic sequence, complete sequence

Seq. No. 140960
Seq. ID LIB25-083-Q1-E1-A12
Method BLASTX

NCBI GI g2129759
BLAST score 504
E value 3.0e-51
Match length 101
% identity 100

NCBI Description UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana >gi 1143392 emb CAA90941 (Z54214) uridine diphosphate

glucose epimerase [Arabidopsis thaliana]

Seq. No. 140961

Seq. ID LIB25-083-Q1-E1-A9

Method BLASTX
NCBI GI g4759280
BLAST score 202
E value 8.0e-16
Match length 61
% identity 66

NCBI Description U5 snRNP-specific protein, 116 kD >gi_434759_dbj_BAA04699_

(D21163) similar to human elongation factor 2 mRNA (HSEF2).

[Homo sapiens]

Seq. No. 140962

Seq. ID LIB25-083-Q1-E1-B10

Method BLASTX
NCBI GI g3150415
BLAST score 459
E value 6.0e-46
Match length 89
% identity 35

NCBI Description (AC004165) sec13-related protein [Arabidopsis thaliana]

>gi 3420046 (AC004680) sec13-related protein [Arabidopsis

thaliana]

Seq. No. 140963

Seq. ID LIB25-083-Q1-E1-B7

Method BLASTX
NCBI GI g2245107
BLAST score 104
E value 2.0e-36
Match length 96
% identity 70

NCBI Description (Z97343) thioesterase homolog [Arabidopsis thaliana]

Seq. No. 140964

Seq. ID LIB25-083-Q1-E1-C10

Method BLASTX
NCBI GI g131398
BLAST score 523
E value 2.0e-53



Match length 88 % identity

NCBI Description

PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor

- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 140965

LIB25-083-Q1-E1-C11 Seq. ID

Method BLASTX NCBI GI g2275202 BLAST score 576 1.0e-59 E value 124 Match length % identity 89

(ACO02337) acyl-CoA synthetase isolog [Arabidopsis NCBI Description

thaliana]

140966 Seq. No.

LIB25-083-Q1-E1-C12 Seq. ID

Method BLASTX g115385 NCBI GI BLAST score 643 E value 2.0e-67 124 Match length 100 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting

chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 140967

LIB25-083-Q1-E1-C9 Seq. ID

Method BLASTN g2760164 NCBI GI 330 BLAST score E value 0.0e+00 Match length 367 % identity 100

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K18P6, complete sequence [Arabidopsis thaliana]

140968 Seq. No.

LIB25-083-Q1-E1-D11 Seq. ID

Method BLASTX NCBI GI g1323704 BLAST score 177 7.0e-13 E value 93 Match length % identity 42

(U55387) similar to C. elegans F38E1.9 gene product encoded NCBI Description

by GenBank Accession Number U41996 [Cricetulus griseus]



```
Seq. No. 140969
```

Seq. ID LIB25-083-Q1-E1-E4

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 48
% identity 67

% identity 67
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 140970

Seq. ID LIB25-083-Q1-E1-F10

Method BLASTX
NCBI GI g1170091
BLAST score 549
E value 2.0e-56
Match length 107
% identity 100

NCBI Description GLUTATHIONE S-TRANSFERASE PM24 (24 KD AUXIN-BINDING PROTEIN) (CLASS PHI) >gi_479736_pir__S35268 glutathione transferase (EC 2.5.1.18) gst2 - Arabidopsis thaliana >gi_166723 (L07589) glutathione S-transferase [Arabidopsis thaliana] >gi_347212 (L11601) glutathione S-transferase [Arabidopsis thaliana] >gi_407090 emb CAA53051_ (X75303)

glutathione S-transferase [Arabidopsis thaliana]

>gi 2262152 gb AAC78264.1 AAC78264 (AC002330) Atpm24.1

glutathione S transferase [Arabidopsis thaliana]

Seq. No. 140971

Seq. ID LIB25-083-Q1-E1-F11

Method BLASTN
NCBI GI g4056429
BLAST score 259
E value 1.0e-144
Match length 259
% identity 100

NCBI Description Arabidopsis thaliana chromosome 1 BAC F508 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 140972

Seq. ID LIB25-083-Q1-E1-H6

Method BLASTX
NCBI GI g399091
BLAST score 381
E value 8.0e-37
Match length 94
% identity 83

NCBI Description PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP

(PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)

(H+-PPASE) >gi_282878_pir__A38230 inorganic pyrophosphatase (EC 3.6.1.1), H+-translocating pyrophosphate-energized -

Arabidopsis thaliana >gi 166634 (M81892) vacuolar

H+-phosphatase [Arabidopsis thaliana]

Seq. No. 140973

Seq. ID LIB25-084-Q1-E1-A1

Method BLASTN



```
q3299824
NCBI GI
BLAST score
                  198
E value
                  1.0e-107
Match length
                  253
% identity
                  96
                  Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,
NCBI Description
                  near 17 cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  140974
Seq. ID
                  LIB25-084-Q1-E1-A3
Method
                  BLASTN
NCBI GI
                  g4589450
BLAST score
                  196
E value
                  1.0e-106
Match length
                  219
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  T31K7, complete sequence
                  140975
Seq. No.
Seq. ID
                  LIB25-084-Q1-E1-A4
Method
                  BLASTN
NCBI GI
                  g4406776
BLAST score
                  215
E value
                  1.0e-118
Match length
                  223
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC F14H20 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  140976
Seq. No.
                  LIB25-084-Q1-E1-A6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4218109
                  214
BLAST score
                  1.0e-117
E value
Match length
                  214
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16
NCBI Description
                   (ESSAII project)
Seq. No.
                  140977
                  LIB25-084-Q1-E1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4160346
BLAST score
                  197
E value
                  1.0e-15
Match length
                  73
                  51
% identity
```

(AL035216) nucleolar protein involved in pre-rRNA NCBI Description

processing [Schizosaccharomyces pombe]

140978 Seq. No.

LIB25-084-Q1-E1-B11 Seq. ID

Method BLASTX NCBI GI g4539332

BLAST score 277



```
7.0e-25
E value
Match length
                   55
% identity
                   100
                   (AL035539) glycosyltransferase like protein (fragment)
NCBI Description
                   [Arabidopsis thaliana]
                   140979
Seq. No.
Seq. ID
                  LIB25-084-Q1-E1-B3
```

Method BLASTN NCBI GI g4454587 BLAST score 50 E value 3.0e-19 Match length 110

86 % identity

Arabidopsis thaliana BAC F21A20 from chromosome V near 61 NCBI Description cM, complete sequence [Arabidopsis thaliana]

140980 Seq. No. LIB25-084-Q1-E1-B4 Seq. ID BLASTX Method q1170040 NCBI GI BLAST score 276

7.0e-25 E value 81 Match length % identity 63

GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE) NCBI Description

>gi 451198 dbj BAA03137 (D14049) glutathione reductase precursor [Arabidopsis thaliana] >gi_1944448_dbj_BAA19653_ (D89620) glutathione reductase precursor [Arabidopsis thaliana] >qi 740576 prf 2005376A glutathione reductase

[Arabidopsis thaliana]

Seq. No. 140981

LIB25-084-Q1-E1-B7 Seq. ID

Method BLASTN NCBI GI g4757412 BLAST score 219 E value 1.0e-120 Match length 246 % identity 96

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MXK23, complete sequence

140982 Seq. No.

LIB25-084-Q1-E1-B8 Seq. ID

BLASTN Method NCBI GI g2264303 BLAST score 223 1.0e-122 E value 223 Match length 100 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MBB18, complete sequence [Arabidopsis thaliana]

140983 Seq. No.

LIB25-084-Q1-E1-B9 Seq. ID

Method BLASTX



NCBI GI g2911073 BLAST score 244 E value 6.0e-21 Match length 59 % identity 90

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 140984

Seq. ID LIB25-084-Q1-E1-C1

Method BLASTX
NCBI GI g115767
BLAST score 353
E value 7.0e-34
Match length 69
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 140985

Seq. ID LIB25-084-Q1-E1-C11

Method BLASTX
NCBI GI g3540194
BLAST score 279
E value 4.0e-25
Match length 60
% identity 100

NCBI Description (AC004260) AtVPS45p [Arabidopsis thaliana]

Seq. No. 140986

Seq. ID LIB25-084-Q1-E1-C12

Method BLASTX
NCBI GI g542157
BLAST score 409
E value 2.0e-40
Match length 94
% identity 82

NCBI Description ribosomal 5S RNA-binding protein - Rice

Seq. No. 140987

Seq. ID LIB25-084-Q1-E1-C2

Method BLASTX
NCBI GI g3980401
BLAST score 419
E value 1.0e-41
Match length 83
% identity 99

NCBI Description (AC004561) putative tropinone reductase [Arabidopsis

thaliana]

Seq. No. 140988

Seq. ID LIB25-084-Q1-E1-C3

Method BLASTN



```
g3831437
NCBI GI
BLAST score
                  117
                  3.0e-59
E value
                  210
Match length
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC T3A4 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  140989
Seq. No.
Seq. ID
                  LIB25-084-Q1-E1-C5
Method
                  BLASTX
NCBI GI
                  g1864017
BLAST score
                  351
                  1.0e-33
E value
                  68
Match length
% identity
                  100
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
NCBI Description
                  140990
Seq. No.
Seq. ID
                  LIB25-084-Q1-E1-C8
                  BLASTX
Method
NCBI GI
                  q481132
                  233
BLAST score
                  8.0e-20
E value
Match length
                  61
% identity
                  sucrose transport protein SUC1 - Arabidopsis thaliana
NCBI Description
                  >gi_407094_emb_CAA53147_ (X75365) sucrose-proton symporter
                   [Arabidopsis thaliana]
Seq. No.
                  140991
Seq. ID
                  LIB25-084-Q1-E1-C9
Method
                  BLASTX
NCBI GI
                  q4584546
BLAST score
                  336
                  9.0e-32
E value
Match length
                  94
% identity
                   63
                  (AL049608) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  140992
                  LIB25-084-Q1-E1-D4
Seq. ID
Method
                  BLASTN
                  q3250737
NCBI GI
                  114
BLAST score
                   1.0e-57
E value
                  204
Match length
% identity
                   88
NCBI Description Arabidopsis thaliana ASKbeta gene, complete CDS
                   140993
Seq. No.
                  LIB25-084-Q1-E1-E1
Seq. ID
```

Method BLASTN g3135250 NCBI GI 184 BLAST score E value 3.0e-99 Match length 249



% identity 84

NCBI Description Arabidopsis thaliana chromosome II BAC F27F23 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 140994

Seq. ID LIB25-084-Q1-E1-E10

Method BLASTN
NCBI GI g1490552
BLAST score 278
E value 1.0e-155
Match length 278
% identity 100

% identity 100
NCBI Description Arabidopsis thaliana S-adenosylmethionine decarboxylase

(SAMdc) mRNA, complete cds

Seq. No. 140995

Seq. ID LIB25-084-Q1-E1-E3

Method BLASTX
NCBI GI g2119848
BLAST score 417
E value 2.0e-41
Match length 82
% identity 100

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 -

Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]

Seq. No. 140996

Seq. ID LIB25-084-Q1-E1-E4

Method BLASTX
NCBI GI g2642159
BLAST score 177
E value 3.0e-13
Match length 35
% identity 100

NCBI Description (AC003000) putative mannose-1-phosphate guanyltransferase

[Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose

pyrophosphorylase [Arabidopsis thaliana] >gi 4151925

(AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No. 140997

Seq. ID LIB25-084-Q1-E1-F10

Method BLASTX
NCBI GI g4585977
BLAST score 171
E value 2.0e-12
Match length 44
% identity 70

NCBI Description (AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No. 140998

Seq. ID LIB25-084-Q1-E1-F11



```
Method
                  BLASTX
                  g1172977
NCBI GI
BLAST score
                  424
                  4.0e-42
E value
Match length
                  88
% identity
                  98
NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
                  ribosomal protein L18 [Arabidopsis thaliana]
                  140999
Seq. No.
Seq. ID
                  LIB25-084-Q1-E1-F12
Method
                  BLASTN
NCBI GI
                  g4455321
BLAST score
                  267
                  1.0e-148
E value
Match length
                  267
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10
                  (ESSAII project)
                  141000
Seq. No.
Seq. ID
                  LIB25-084-Q1-E1-F3
Method
                  BLASTN
NCBI GI
                  g3687221
                  129
BLAST score
                  2.0e-66
E value
Match length
                  247
% identity
                  96
NCBI Description Arabidopsis thaliana chromosome II BAC F6F22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  141001
Seq. No.
Seq. ID
                  LIB25-084-Q1-E1-F4
                  BLASTX
Method
NCBI GI
                  q4056469
BLAST score
                  187
E value
                  2.0e-14
Match length
                  39
% identity
                  100
                  (AC005990) Strong similarity to gb M95166 ADP-ribosylation
NCBI Description
                  factor from Arabidopsis thaliana. ESTs gb_Z25826,
                  gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,
                  gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and
                  gb Z25043 come from t
                  141002
Seq. No.
                  LIB25-084-Q1-E1-F5
Seq. ID
Method
                  BLASTN
                  g710625
NCBI GI
BLAST score
                  222
```

1.0e-122 E value 243 Match length % identity 97

NCBI Description Arabidopsis thaliana mRNA for ERD15 protein, complete cds

141003 Seq. No.

LIB25-084-Q1-E1-G1 Seq. ID



Method BLASTN
NCBI GI g4220640
BLAST score 205
E value 1.0e-112
Match length 224
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MPE11, complete sequence [Arabidopsis thaliana]

Seq. No. 141004

Seq. ID LIB25-084-Q1-E1-G10

Method BLASTX
NCBI GI g3641837
BLAST score 408
E value 3.0e-40
Match length 90
% identity 93

NCBI Description (AL023094) Nonclathrin coat protein gamma - like protein

[Arabidopsis thaliana]

Seq. No. 141005

Seq. ID LIB25-084-Q1-E1-G11

Method BLASTN
NCBI GI g3449313
BLAST score 283
E value 1.0e-158
Match length 283
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21P3, complete sequence [Arabidopsis thaliana]

Seq. No. 141006

Seq. ID LIB25-084-Q1-E1-G12

Method BLASTX
NCBI GI g2160168
BLAST score 300
E value 2.0e-27
Match length 61
% identity 87

NCBI Description (AC000132) Strong similarity to R. communis

phosphoglycerate mutase (gb X70652). ESTs

gb T41853, gb T76648 come from this gene. [Arabidopsis

thaliana]

Seq. No. 141007

Seq. ID LIB25-084-Q1-E1-G5

Method BLASTX
NCBI GI g124224
BLAST score 289
E value 2.0e-26
Match length 62
% identity 87

NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)

>gi_100345_pir__S21060 translation initiation factor eIF-5A

- common tobacco >gi_19887_emb_CAA45105_ (X63543)

eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

```
Seq. No.
                  141008
                  LIB25-084-Q1-E1-H5
Seq. ID
Method
                 BLASTN
NCBI GI
                  g2062705
BLAST score
                  20
                  2.0e-01
E value
Match length
                  37
% identity
                  34
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  141009
Seq. No.
                  LIB25-085-Q1-E1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2351068
BLAST score
                  146
E value
                  2.0e-76
Match length
                  338
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRH10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141010
                  LIB25-085-Q1-E1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1871185
BLAST score
                  217
E value
                  1.0e-17
Match length
                  101
% identity
                  40
                  (U90439) seven in absentia isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  141011
                  LIB25-085-Q1-E1-C6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4757414
BLAST score
                  258
                  1.0e-143
E value
Match length
                  258
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MYF24, complete sequence
                  141012
Seq. No.
Seq. ID
                  LIB25-085-Q1-E1-D1
Method
                  BLASTN
                  g3128135
```

NCBI GI BLAST score 146 8.0e-77 E value Match length 146 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19E1, complete sequence [Arabidopsis thaliana]

Seq. No. 141013

Seq. ID LIB25-085-Q1-E1-E12

Method BLASTX NCBI GI g4725956



```
BLAST score
                  270
                  8.0e-24
E value
Match length
                  52
% identity
                  98
NCBI Description
                  (AL049730) polyubiquitin-like protein (fragment)
                  [Arabidopsis thaliana]
Seq. No.
                  141014
                  LIB25-085-Q1-E1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244750
BLAST score
                  489
E value
                  2.0e-49
Match length
                  109
% identity
                  87
NCBI Description
                  (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                  >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                  [Arabidopsis thaliana]
Seq. No.
                  141015
Seq. ID
                  LIB25-085-Q1-E1-F10
Method
                  BLASTN
NCBI GI
                  g3128166
BLAST score
                  282
E value
                  1.0e-157
Match length
                  282
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F4I1 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141016
                  LIB25-085-Q1-E1-F2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1149572
BLAST score
                  183
E value
                  9.0e-99
Match length
                  183
% identity
                  100
NCBI Description
                  A.thaliana rpl21 mRNA for chloroplast ribosomal large
                  subunit protein L21
Seq. No.
                  141017
                  LIB25-085-Q1-E1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1806146
BLAST score
                  441
E value
                  7.0e-44
Match length
                  108
% identity
                  80
NCBI Description
                  (X97317) cdc2MsF [Medicago sativa]
Seq. No.
                  141018
```

Seq. ID LIB25-085-Q1-E1-G11

Method BLASTX
NCBI GI g730645
BLAST score 282
E value 3.0e-25



Match length % identity 84

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_(Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_(Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_(AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No. 141019

Seq. ID LIB25-085-Q1-E1-G3

Method BLASTX
NCBI GI g2194126
BLAST score 304
E value 7.0e-28
Match length 102
% identity 62

NCBI Description (AC002062) EST gb T43335 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 141020

Seq. ID LIB25-085-Q1-E1-G9

Method BLASTX
NCBI GI g2462832
BLAST score 637
E value 8.0e-67
Match length 130
% identity 87

NCBI Description (AF000657) similar to Bacillus CotA [Arabidopsis thaliana]

Seq. No. 141021

Seq. ID LIB25-085-Q1-E1-H6

Method BLASTX
NCBI GI g1183004
BLAST score 692
E value 3.0e-73
Match length 133
% identity 39

NCBI Description (D45848) calmodulin-related protein [Arabidopsis thaliana]

>qi 3402707 (AC004261) calmodulin-related protein

[Arabidopsis thaliana]

Seq. No. 141022

Seq. ID LIB25-086-Q1-E1-A1

Method BLASTN
NCBI GI g4220637
BLAST score 224
E value 1.0e-123
Match length 224
% identity 18

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MIE1, complete sequence [Arabidopsis thaliana]

Seq. No. 141023

Seq. ID LIB25-086-Q1-E1-A8



```
Method
                  g2102691
NCBI GI
BLAST score
                  166
                  4.0e-12
E value
                  71
Match length
                  44
% identity
                  (U64817) fructokinase [Lycopersicon esculentum]
NCBI Description
                  141024
Seq. No.
                  LIB25-086-Q1-E1-A9
Seq. ID
                  BLASTN
Method
                  g2288979
NCBI GI
                  214
BLAST score
                  1.0e-117
E value
Match length
                  214
                  60
% identity
                  Arabidopsis thaliana chromosome II BAC T01024 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  141025
Seq. No.
                  LIB25-086-Q1-E1-B1
Seq. ID
                  BLASTX
Method
                  g2828267
NCBI GI
                  334
BLAST score
                  1.0e-31
E value
Match length
                  74
                  85
% identity
                  (Y14044) geranylgeranyl reductase [Arabidopsis thaliana]
NCBI Description
                   141026
Seq. No.
                  LIB25-086-Q1-E1-B10
Seq. ID
                   BLASTN
Method
                   g2815404
NCBI GI
                   206
BLAST score
                   1.0e-112
E value
                   206
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MMG4, complete sequence [Arabidopsis thaliana]
Seq. No.
                   141027
                   LIB25-086-Q1-E1-B11
Seq. ID
                   BLASTX
Method
                   g99752
NCBI GI
BLAST score
                   261
                   3.0e-23
E value
Match length
                   54
                   100
% identity
                   protochlorophyllide reductase (EC 1.3.1.33) precursor -
NCBI Description
                   Arabidopsis thaliana
```

LIB25-086-Q1-E1-B4 Seq. ID

BLASTN Method NCBI GI g4006885 BLAST score 205 1.0e-112 E value



Match length 226 % identity 97

Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig NCBI Description

fragment No

141029 Seq. No.

LIB25-086-Q1-E1-B6 Seq. ID

Method BLASTX NCBI GI g2341034 258 BLAST score 6.0e-23 E value Match length 52 100 % identity

NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No. 141030

LIB25-086-Q1-E1-C1 Seq. ID

BLASTN Method NCBI GI g4539415 BLAST score 47 E value 8.0e-18 Match length 59

% identity 95

Arabidopsis thaliana DNA chromosome 4, BAC clone NCBI Description

project)

Seq. No. 141031

Seq. ID LIB25-086-Q1-E1-C2

Method BLASTX NCBI GI q1170121 297 BLAST score 2.0e-27 E value 59 Match length 100 % identity

GLUTATHIONE S-TRANSFERASE 103-1A >gi 2129602 pir S66354 NCBI Description

glutathione transferase (EC 2.5.1.18), auxin-inducible -Arabidopsis thaliana >gi_895700_emb_CAA61504_ (X89216) glutathione transferase [Arabidopsis thaliana] >gi 929957 (U30489) glutathione S-transferase [Arabidopsis thaliana] >gi_940381_dbj_BAA07917_ (D44465) Glutathione S-Transferase [Arabidopsis thaliana] >gi_3980390 (AC004561) glutathione

S-transferase [Arabidopsis thaliana]

Seq. No. 141032

LIB25-086-Q1-E1-C4 Seq. ID

Method BLASTX g3342382 NCBI GI BLAST score 236 3.0e-20 E value Match length 74 % identity 61

(AF059678) VIP-receptor-gene repressor protein [Rattus NCBI Description

norvegicus]

Seq. No. 141033

Seq. ID LIB25-086-Q1-E1-D11

Method BLASTX



```
NCBI GI g3513727
BLAST score 351
E value 7.0e-34
Match length 72
% identity 68
```

NCBI Description (AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >qi 4539358 emb CAB40052.1 (AL049525) putative

protein [Arabidopsis thaliana]

Seq. No. 141034

Seq. ID LIB25-086-Q1-E1-D12

Method BLASTN
NCBI GI g2832639
BLAST score 216
E value 1.0e-118
Match length 216
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12

(ESSAII project)

Seq. No. 141035

Seq. ID LIB25-086-Q1-E1-D2

Method BLASTX
NCBI GI g256963
BLAST score 184
E value 3.0e-14
Match length 69
% identity 64

NCBI Description (S45910) glyceraldehyde-3-phosphate-dehydrogenase subunit

GapA {N-terminal} [Arabidopsis thaliana, Peptide
Chloroplast Partial, 68 aa] [Arabidopsis thaliana]

Seq. No. 141036

Seq. ID LIB25-086-Q1-E1-D3

Method BLASTX
NCBI GI g4262240
BLAST score 364
E value 2.0e-35
Match length 69
% identity 100

NCBI Description (AC006200) putative stress protein [Arabidopsis thaliana]

Seq. No. 141037

Seq. ID LIB25-086-Q1-E1-D4

Method BLASTN
NCBI GI g4454004
BLAST score 94
E value 1.0e-45
Match length 227
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6

(ESSAII project)

Seq. No. 141038

Seq. ID LIB25-086-Q1-E1-D5



Method BLASTX
NCBI GI g2943789
BLAST score 187
E value 1.0e-14
Match length 35
% identity 100

NCBI Description (AB000875) RD22BP1 [Arabidopsis thaliana]

Seq. No. 141039

Seq. ID LIB25-086-Q1-E1-E1

Method BLASTN
NCBI GI g3643588
BLAST score 147
E value 3.0e-77
Match length 212
% identity 63

NCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 141040

Seq. ID LIB25-086-Q1-E1-E10

Method BLASTX
NCBI GI g3063459
BLAST score 367
E value 1.0e-35
Match length 71
% identity 96

NCBI Description (AC003981) F22013.21 [Arabidopsis thaliana]

Seq. No. 141041

Seq. ID LIB25-086-Q1-E1-E2

Method BLASTN
NCBI GI 94063730
BLAST score 227
E value 1.0e-125
Match length 227
% identity 100

NCBI Description Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete

sequence [Arabidopsis thaliana]

Seq. No. 141042

Seq. ID LIB25-086-Q1-E1-E3

Method BLASTX
NCBI GI g4262179
BLAST score 379
E value 4.0e-37
Match length 74
% identity 100

NCBI Description (AC005508) 27668 [Arabidopsis thaliana]

Seq. No. 141043

Seq. ID LIB25-086-Q1-E1-F11

Method BLASTX
NCBI GI g1695717
BLAST score 206
E value 7.0e-17



Match length 43 % identity 100

NCBI Description (D89341) luminal binding protein [Arabidopsis thaliana]

Seq. No. 141044

Seq. ID LIB25-086-Q1-E1-F3

Method BLASTN
NCBI GI g857373
BLAST score 222
E value 1.0e-122
Match length 222
% identity 100

NCBI Description Arabidopsis thaliana mRNA for phosphoinositide specific

phospholipase C, complete cds

Seq. No. 141045

Seq. ID LIB25-086-Q1-E1-F5

Method BLASTN
NCBI GI g1418334
BLAST score 179
E value 2.0e-96
Match length 179
% identity 100

NCBI Description A.thaliana mRNA for ZAT11 protein

Seq. No. 141046

Seq. ID LIB25-086-Q1-E1-F6

Method BLASTN
NCBI GI g2264317
BLAST score 218
E value 1.0e-119
Match length 218
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUG13, complete sequence [Arabidopsis thaliana]

Seq. No. 141047

Seq. ID LIB25-086-Q1-E1-F8

Method BLASTN
NCBI GI g1946354
BLAST score 198
E value 1.0e-107
Match length 218
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T06B20 genomic

sequence, complete sequence

Seq. No. 141048

Seq. ID LIB25-086-Q1-E1-G1

Method BLASTN
NCBI GI g2351070
BLAST score 93
E value 5.0e-45
Match length 161
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTH12, complete sequence [Arabidopsis thaliana]



```
141049
Seq. No.
                  LIB25-086-Q1-E1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q544425
                  310
BLAST score
                  6.0e-29
E value
                  59
Match length
                  100
% identity
                  GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN)
NCBI Description
                  >gi 419756_pir__S30148 glycine-rich protein (clone AtGRP8)
                  - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988)
                  glycine rich protein [Arabidopsis thaliana] >gi_166658
                  (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649)
                  RNA-binding protein [Arabidopsis thaliana]
Seq. No.
                  141050
                  LIB25-086-Q1-E1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1350768
BLAST score
                  182
E value
                  5.0e-14
Match length
                  33
                  100
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L7A
Seq. No.
                  141051
Seq. ID
                  LIB25-086-Q1-E1-G6
Method
                  BLASTN
                  q4006885
NCBI GI
BLAST score
                  211
                  1.0e-115
E value
Match length
                  219
                  99
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                  fragment No
                  141052
Seq. No.
                  LIB25-086-Q1-E1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4151924
                  217
BLAST score
                  1.0e-119
E value
                  217
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana CYT1 protein (cyt1) mRNA, complete cds
```

Seq. ID LIB25-086-Q1-E1-H11

Method BLASTN
NCBI GI g1490552
BLAST score 217
E value 1.0e-119
Match length 217
% identity 100

NCBI Description Arabidopsis thaliana S-adenosylmethionine decarboxylase

(SAMdc) mRNA, complete cds



```
Seq. No.
                  141054
                  LIB25-086-Q1-E1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3522932
                  111
BLAST score
E value
                  7.0e-56
Match length
                  139
                  95
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F14M4 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  141055
Seq. No.
Seq. ID
                  LIB25-086-Q1-E1-H6
Method
                  BLASTN
                  g2224930
NCBI GI
BLAST score
                  215
                  1.0e-118
E value
Match length
                  219
% identity
                  100
                  Arabidopsis thaliana ethylene-insensitive3-like3 (EIL3)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  141056
Seq. ID
                  LIB25-087-Q1-E1-A12
Method
                  BLASTX
NCBI GI
                  g3785983
                  300
BLAST score
E value
                  7.0e-28
Match length
                  57
                  100
% identity
NCBI Description
                  (AC005560) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  141057
                  LIB25-087-Q1-E1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1168548
BLAST score
                  236
                  2.0e-20
E value
Match length
                  62
                  79
% identity
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-7 (HD-ZIP PROTEIN
NCBI Description
                  ATHB-7) >gi_629527_pir__S47137 homeotic protein Athb-7 -
                  Arabidopsis thaliana >gi_499164_emb_CAA47425_ (X67032) orf
                  [Arabidopsis thaliana]
Seq. No.
                  141058
Seq. ID
                  LIB25-087-Q1-E1-B1
Method
                  BLASTX
NCBI GI
                  q3702332
BLAST score
                  186
E value
                  2.0e-14
Match length
                  53
                  77
% identity
```

141059

Seq. No.

17177

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]



```
LIB25-087-Q1-E1-B10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2264307
BLAST score
                  117
E value
                  2.0e-59
                  213
Match length
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MED24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141060
                  LIB25-087-Q1-E1-B12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g166695
BLAST score
                  150
E value
                  5.0e-79
Match length
                  170
% identity
                  97
                  Arabidopsis thaliana recombination and DNA-damage
NCBI Description
                  resistance protein (DRT112) mRNA, complete cds
Seq. No.
                  141061
                  LIB25-087-Q1-E1-B2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2584827
BLAST score
                  111
E value
                  6.0e-56
Match length
                  145
% identity
                  99
                  Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  141062
                  LIB25-087-Q1-E1-D10
Seq. ID
Method
                  BLASTN
                  g1495268
NCBI GI
BLAST score
                  181
                  1.0e-97
E value
Match length
                  181
% identity
                  100
NCBI Description A.thaliana mRNA (orf19) from chromosome III
Seq. No.
                  141063
                  LIB25-087-Q1-E1-D12
Seq. ID
Method
                  BLASTN
                  g3327922
NCBI GI
BLAST score
                  207
                  1.0e-113
E value
Match length
                  207
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T31E10 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```

Seq. ID LIB25-087-Q1-E1-D7

Method BLASTN NCBI GI g4159706



BLAST score 109 E value 8.0e-55 Match length 137 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGL6, complete sequence

Seq. No. 141065

Seq. ID LIB25-087-Q1-E1-E10

Method BLASTX
NCBI GI g1168200
BLAST score 176
E value 2.0e-13
Match length 36
% identity 100

NCBI Description 14-3-3-LIKE PROTEIN GF14 PSI (14-3-3-LIKE PROTEIN RCI1)

>gi_1361988_pir__S57277 GF14 protein psi chain -

Arabidopsis thaliana >gi_166717 (L09110) GF14 psi chain [Arabidopsis thaliana] >gi_487789 (U09375) GF14psi isoform

[Arabidopsis thaliana]

Seq. No. 141066

Seq. ID LIB25-087-Q1-E1-E11

Method BLASTX
NCBI GI g1710401
BLAST score 344
E value 5.0e-33
Match length 70
% identity 91

NCBI Description RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN

(RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)

>gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase

R2 [Nicotiana tabacum]

Seq. No. 141067

Seq. ID LIB25-087-Q1-E1-E3

Method BLASTN
NCBI GI g2618605
BLAST score 136
E value 8.0e-71
Match length 152
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUK11, complete sequence [Arabidopsis thaliana]

Seq. No. 141068

Seq. ID LIB25-087-Q1-E1-F10

Method BLASTX
NCBI GI g2894599
BLAST score 139
E value 5.0e-09
Match length 44
% identity 61

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 141069

Seq. ID LIB25-087-Q1-E1-F3



Method BLASTX
NCBI GI g1109600
BLAST score 241
E value 6.0e-21
Match length 43
% identity 100

NCBI Description (D16628) ATSEH [Arabidopsis thaliana] >gi 2760840

(AC003105) soluble epoxide hydrolase [Arabidopsis thaliana]

Seq. No. 141070

Seq. ID LIB25-087-Q1-E1-G12

Method BLASTN
NCBI GI g4220633
BLAST score 158
E value 8.0e-84
Match length 158
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K7J8, complete sequence [Arabidopsis thaliana]

Seq. No. 141071

Seq. ID LIB25-087-Q1-E1-G8

Method BLASTN
NCBI GI g4220635
BLAST score 124
E value 1.0e-63
Match length 140
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDB19, complete sequence [Arabidopsis thaliana]

Seq. No. 141072

Seq. ID LIB25-087-Q1-E1-H10

Method BLASTN
NCBI GI g2656028
BLAST score 101
E value 8.0e-50
Match length 183
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNF13

Seq. No. 141073

Seq. ID LIB25-087-Q1-E1-H11

Method BLASTN
NCBI GI g4538949
BLAST score 211
E value 1.0e-115
Match length 211
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24

(ESSA project)

Seq. No. 141074

Seq. ID LIB25-087-Q1-E1-H12

Method BLASTX NCBI GI g4539292



```
BLAST score
E value
                  3.0e-23
Match length
                  52
                  90
% identity
                  (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                  thaliana]
                  141075
Seq. No.
                  LIB25-087-Q1-E1-H3
Seq. ID
Method
                  BLASTN
                  g4689466
NCBI GI
                  136
BLAST score
E value
                  9.0e-71
Match length
                  152
% identity
                  29
                  Arabidopsis thaliana chromosome II BAC T23015 genomic
NCBI Description
                  sequence, complete sequence
                  141076
Seq. No.
                  LIB25-088-Q1-E1-A8
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3687221
BLAST score
                  154
E value
                  3.0e-81
Match length
                  289
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC F6F22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  141077
Seq. No.
                  LIB25-088-Q1-E1-B9
Seq. ID
Method
                  BLASTX
                  g1076303
NCBI GI
BLAST score
                  483
E value
                  1.0e-48
                  112
Match length
% identity
                  87
NCBI Description
                  RNA-binding protein cp29 precursor - Arabidopsis thaliana
                  >gi 681902 dbj BAA06518 (D31710) cp29 [Arabidopsis
                  thaliana]
                  141078
Seq. No.
                  LIB25-088-Q1-E1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4559381
                  235
BLAST score
                  1.0e-19
E value
Match length
                  135
% identity
                  44
                  (AC006526) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. ID LIB25-088-Q1-E1-C10

Method BLASTX NCBI GI g2119846 BLAST score 632 E value 3.0e-66



122 Match length % identity 98 chlorophyll a/b-binding protein type I precursor Lhb1B2 -NCBI Description Arabidopsis thaliana >gi 16364 emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi 3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] Seq. No. 141080 LIB25-088-Q1-E1-C11 Seq. ID Method BLASTN NCBI GI q166695 BLAST score 49 E value 1.0e-19 Match length 49 % identity 100 Arabidopsis thaliana recombination and DNA-damage NCBI Description resistance protein (DRT112) mRNA, complete cds Seq. No. 141081 Seq. ID LIB25-088-Q1-E1-C8 Method BLASTN g4103242 NCBI GI 75 BLAST score E value 1.0e-34 99 Match length 94 % identity NCBI Description Arabidopsis thaliana BIPOSTO (BIP) mRNA, complete cds 141082 Seq. No. LIB25-088-Q1-E1-E8 Seq. ID Method BLASTN NCBI GI g4235150 BLAST score 348 E value 0.0e + 00Match length 376 % identity 55 Arabidopsis thaliana chromosome I BAC T25B24 genomic NCBI Description sequence, complete sequence Seq. No. 141083 LIB25-088-Q1-E1-F3 Seq. ID BLASTN Method NCBI GI g2351064 BLAST score 57 7.0e-24 E value 93

Match length 90 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MDJ22, complete sequence [Arabidopsis thaliana]

141084 Seq. No.

LIB25-089-Q1-E1-A9 Seq. ID

Method BLASTN NCBI GI g2288979



```
BLAST score
E value
                  3.0e-84
Match length
                  306
                  96
% identity
                  Arabidopsis thaliana chromosome II BAC T01024 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  141085
Seq. No.
                  LIB25-089-Q1-E1-D11
Seq. ID
                  BLASTX
Method
                  g1742961
NCBI GI
BLAST score
                  641
E value
                  3.0e-67
Match length
                  132
% identity
                  96
                  (X94756) cystathionine gamma-synthase [Arabidopsis
NCBI Description
                  thaliana]
                  141086
Seq. No.
                  LIB25-089-Q1-E1-D12
Seq. ID
Method
                  BLASTX
                  g4038034
NCBI GI
BLAST score
                  341
                  4.0e-32
E value
Match length
                  81
% identity
                  83
                  (AC005936) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  141087
                  LIB25-089-Q1-E1-E1
Seq. ID
Method
                  BLASTX
                  g3176874
NCBI GI
BLAST score
                  162
                  1.0e-11
E value
Match length
                  45
                  69
% identity
                  (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                  thaliana]
                  141088
Seq. No.
Seq. ID
                  LIB25-089-Q1-E1-G2
Method
                  BLASTN
NCBI GI
                  g4159704
BLAST score
                  97
E value
                  1.0e-47
Match length
                  117
                  96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MCB17, complete sequence
Seq. No.
                  141089
                  LIB25-090-Q1-E1-A10
Seq. ID
```

Method BLASTN NCBI GI g3869071 BLAST score 173 E value 2.0e-92 Match length 317

E value

7.5

Match length

% identity

4.0e-61

130

91



```
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MIL23, complete sequence [Arabidopsis thaliana]
                  141090
Seq. No.
                  LIB25-090-Q1-E1-A11
Seq. ID
Method
                  BLASTX
                  q2492681
NCBI GI
BLAST score
                  304
E value
                  1.0e-27
Match length
                  137
                  43
% identity
                  PROBABLE COATOMER BETA SUBUNIT (BETA-COAT PROTEIN)
NCBI Description
                   (BETA-COP) >gi 1432173 (U62960) CopB [Dictyostelium
                  discoideum]
Seq. No.
                  141091
                  LIB25-090-Q1-E1-A3
Seq. ID
Method
                  BLASTN
                  g2264317
NCBI GI
BLAST score
                  97
                  3.0e-47
E value
Match length
                  278
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUG13, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141092
                  LIB25-090-Q1-E1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3128141
BLAST score
                  327
                  0.0e+00
E value
                  399
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQD22, complete sequence [Arabidopsis thaliana]
                  141093
Seq. No.
                  LIB25-090-Q1-E1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3482933
BLAST score
                  448
E value
                  8.0e-45
Match length
                  100
% identity
                  86
                   (AC003970) Similar to cdc2 protein kinases [Arabidopsis
NCBI Description
                  thaliana]
                  141094
Seq. No.
Seq. ID
                  LIB25-090-Q1-E1-D9
                                                  ΰ,
Method
                  BLASTX
NCBI GI
                  q730645
BLAST score
                  589
```



NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15

[Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb R29788,gb ATTS0365 come from this gene. [Arabidopsis

thaliana]

Seq. No. 141095

Seq. ID LIB25-090-Q1-E1-E4

Method BLASTN
NCBI GI 94753195
BLAST score 74
E value 9.0e-34

Match length 147 % identity 100

NCBI Description Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5

cM, complete sequence

Seq. No. 141096

Seq. ID LIB25-090-Q1-E1-F12

Method BLASTN
NCBI GI g3292807
BLAST score 179
E value 4.0e-96
Match length 351
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19

(ESSAII project)

Seq. No. 141097

Seq. ID LIB25-090-Q1-E1-G11

Method BLASTX
NCBI GI g2746341
BLAST score 488
E value 3.0e-49
Match length 132
% identity 68

NCBI Description (AF037590) ATA27 [Arabidopsis thaliana]

Seq. No. 141098

Seq. ID LIB25-090-Q1-E1-G3

Method BLASTN
NCBI GI g2924733
BLAST score 131
E value 2.0e-67
Match length 405
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUF9, complete sequence [Arabidopsis thaliana]

Seq. No. 141099

Seq. ID LIB25-090-Q1-E1-G7

Method BLASTN
NCBI GI g2351061
BLAST score 158



E value 2.0e-83 Match length 418 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAF19, complete sequence [Arabidopsis thaliana]

Seq. No. 141100

Seq. ID LIB25-091-Q1-E1-A6

Method BLASTN
NCBI GI g3386593
BLAST score 39
E value 1.0e-12
Match length 59
% identity 92

NCBI Description Arabidopsis thaliana chromosome II BAC F4I18 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 141101

Seq. ID LIB25-091-Q1-E1-B11

Method BLASTX
NCBI GI g280386
BLAST score 317
E value 2.0e-29
Match length 59
% identity 100

NCBI Description ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana

>gi_166930 (J05507) ubiquitin extension protein (UBQ1)
[Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin

extension protein (UBQ2) [Arabidopsis thaliana] >qi 4678227 qb AAD26972.1 AC007135 8 (AC007135)

ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]

Seq. No. 141102

Seq. ID LIB25-091-Q1-E1-B3

Method BLASTX
NCBI GI g2119846
BLAST score 522
E value 2.0e-53
Match length 102
% identity 98

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 141103

Seq. ID LIB25-091-Q1-E1-B6

Method BLASTX
NCBI GI g4725941
BLAST score 288
E value 6.0e-26
Match length 55
% identity 100

NCBI Description (AL049730) putative pollen-specific protein [Arabidopsis

% identity

NCBI Description

96



thaliana]

141104 Seq. No. LIB25-091-Q1-E1-B8 Seq. ID BLASTN Method g4757403 NCBI GI BLAST score 164 4.0e-87 E value Match length 324 100 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MJL12, complete sequence Seq. No. 141105 LIB25-091-Q1-E1-C1 Seq. ID Method BLASTN g2244829 NCBI GI 282 BLAST score 1.0e-157 E value Match length 282 % identity 100 Arabidopsis thaliana DNA chromosome 4, ESSA I contig NCBI Description fragment No 141106 Seq. No. Seq. ID LIB25-091-Q1-E1-D11 Method BLASTN g2264314 NCBI GI BLAST score 243 1.0e-134 E value Match length 359 98 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MQK4, complete sequence [Arabidopsis thaliana] Seq. No. 141107 LIB25-091-Q1-E1-D12 Seq. ID. BLASTX Method g4204295 NCBI GI BLAST score 623 3.0e-65 E value 117 Match length 99 % identity (AC003027) 1cl prt seq No definition line found NCBI Description [Arabidopsis thaliana] Seq. No. 141108 LIB25-091-Q1-E1-D6 Seq. ID Method BLASTN NCBI GI g4220641 BLAST score 144 2.0e-75 E value Match length 165

17187

MUL3, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



```
Seq. No.
Seq. ID
                  LIB25-091-Q1-E1-G10
Method
                  BLASTX
NCBI GI
                  g2129538
BLAST score
                  331
E value
                  6.0e-31
Match length
                  64
                  100
% identity
NCBI Description
                  AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232)
                  AT103 [Arabidopsis thaliana]
                  141110
Seq. No.
Seq. ID
                  LIB25-091-Q1-E1-G9
Method
                  BLASTX
NCBI GI
                  q1644291
BLAST score
                  140
E value
                  1.0e-08
Match length
                  105
% identity
NCBI Description
                  (Z73295) receptor-like protein kinase [Catharanthus roseus]
Seq. No.
                  141111
Seq. ID
                  LIB25-092-Q1-E1-A1
Method
                  BLASTX
NCBI GI
                  g541848
BLAST score
                  385
                  8.0e-38
E value
Match length
                  73
% identity
                  100
                  amino acid transport protein I - Arabidopsis thaliana
NCBI Description
                  >gi 22641 emb CAA47603 (X67124) amino acid permease I
                  [Arabidopsis thaliana] >gi 404019 (L16240) amino acid
                  transporter [Arabidopsis thaliana]
Seq. No.
                  141112
Seq. ID
                  LIB25-092-Q1-E1-A11
Method
                  BLASTN
NCBI GI
                  g559399
BLAST score
                  145
                  4.0e-76
E value
Match length
                  145
                  100
% identity
NCBI Description A.thaliana PP1bg gene encoding protein phosphatase
                  141113
Seq. No.
                  LIB25-092-Q1-E1-A8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220638
BLAST score
                  180
                  6.0e-97
E value
Match length
                  210
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

Seq. ID LIB25-092-Q1-E1-A9

MIF21, complete sequence [Arabidopsis thaliana]

BLAST score

E value

103

5.0e-51



```
Method
                  BLASTX
NCBI GI
                  g1800223
BLAST score
                  137
E value
                  9.0e-09
                  50
Match length
                  50
% identity
                  (U65018) mannosyltransferase [Dictyostelium discoideum]
NCBI Description
                  141115
Seq. No.
                  LIB25-092-Q1-E1-B1
Seq. ID
                  BLASTN
Method
                  g2924732
NCBI GI
BLAST score
                  47
E value
                  1.0e-17
                  119
Match length
                  92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUA2, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141116
                  LIB25-092-Q1-E1-B12
Seq. ID
Method
                  BLASTN
                  g4049332
NCBI GI
BLAST score
                  113
E value
                  5.0e-57
Match length
                  180
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4
NCBI Description
                  (ESSAII project)
Seq. No.
                  141117
                  LIB25-092-Q1-E1-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4678371
BLAST score
                  166
E value
                  1.0e-88
Match length
                  215
% identity
                  43
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15
                  (ESSA project)
                  141118
Seq. No.
                  LIB25-092-Q1-E1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2245062
                  286
BLAST score
                  3.0e-26
E value
                  59
Match length
% identity
                  100
                  (Z97342) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  141119
Seq. No.
Seq. ID
                  LIB25-092-Q1-E1-B7
Method
                  BLASTN
NCBI GI
                  g2264302
```



Match length 220 % identity 100 NCBI Description

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAC12, complete sequence [Arabidopsis thaliana]

141120 Seq. No.

Seq. ID LIB25-092-Q1-E1-B8

Method BLASTN g17681 NCBI GI BLAST score 25 8.0e-05 E value Match length 77 % identity 94

NCBI Description A.thaliana mRNA for Wilm's tumor suppressor homologue

Seq. No. 141121

Seq. ID LIB25-092-Q1-E1-B9

Method BLASTN NCBI GI q4586024 BLAST score 69 9.0e-31 E value Match length 172 100 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC T13C7 genomic

sequence, complete sequence

141122 Seq. No.

Seq. ID LIB25-092-Q1-E1-C10

Method BLASTN NCBI GI q4538949 BLAST score 193 E value 1.0e-105 Match length 193 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24

(ESSA project)

Seq. No. 141123

Seq. ID LIB25-092-Q1-E1-C11

Method BLASTN NCBI GI q2864607 BLAST score 120 E value 3.0e-61 Match length 190 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6

(ESSAII project)

Seq. No. 141124

Seq. ID LIB25-092-Q1-E1-C3

Method BLASTN NCBI GI g4220468 BLAST score 217 E value 1.0e-119 Match length 217 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T8011 genomic



sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  141125
Seq. ID
                  LIB25-092-Q1-E1-C5
Method
                  BLASTN
                  q3132469
NCBI GI
                  217
BLAST score
                  1.0e-119
E value
Match length
                  217
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC T29F13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  141126
Seq. No.
Seq. ID
                  LIB25-092-Q1-E1-C7
Method
                  BLASTX
                  g4490732
NCBI GI
BLAST score
                  388
E value
                  3.0e-38
Match length
                  71
% identity
                  100
                  (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  141127
Seq. ID
                  LIB25-092-Q1-E1-D10
Method
                  BLASTN
NCBI GI
                  q4159707
BLAST score
                  194
                  1.0e-105
E value
                  194
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MJK13, complete sequence
Seq. No.
                  141128
                  LIB25-092-Q1-E1-D11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2924733
BLAST score
                  149
                  2.0e-78
E value
Match length
                  149
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUF9, complete sequence [Arabidopsis thaliana]
                  141129
Seq. No.
                  LIB25-092-Q1-E1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g832876
BLAST score
                   251
                   4.0e-22
E value
Match length
                   55
% identity
                  (L41345) ascorbate free radical reductase [Solanum
NCBI Description
```

radical reductase [Lycopersicon esculentum]
17191

 $lycopersicum] > gi_1097368_prf_2113407A \ ascorbate \ free$



```
Seq. No.
                  141130
Seq. ID
                  LIB25-092-Q1-E1-D3
Method
                  BLASTX
                  q267073
NCBI GI
BLAST score
                  254
                  2.0e-22
E value
Match length
                  46
                  100
% identity
                  TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin
NCBI Description
                  beta chain - Arabidopsis thaliana >gi_166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
Seq. No.
                  141131
                  LIB25-092-Q1-E1-D4
Seq. ID
                  BLASTN
Method
                  g1871173
NCBI GI
BLAST score
                  216
E value
                  1.0e-118
Match length
                  216
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T06D20 genomic
                  sequence, complete sequence
                  141132
Seq. No.
                  LIB25-092-Q1-E1-D5
Seq. ID
Method
                  BLASTX
                  g1351272
NCBI GI
BLAST score
                  362
                  4.0e-35
E value
Match length
                  71
                  100
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550
NCBI Description
                   (U02949) cytosolic triose phosphate isomerase [Arabidopsis
                   thaliana] >gi_742408_prf__2009415A triose phosphate
                   isomerase [Arabidopsis thaliana]
                  141133
Seq. No.
                  LIB25-092-Q1-E1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3250679
BLAST score
                  243
E value
                  3.0e-21
Match length
                  43
                  100
% identity
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]
Seq. No.
                   141134
                  LIB25-092-Q1-E1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2924733
BLAST score
                   151
                  1.0e-79
E value
                  216
Match length
% identity
                   100
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

141140





```
MUF9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141135
Seq. ID
                  LIB25-092-Q1-E1-D8
Method
                  BLASTX
NCBI GI
                  g4678328
BLAST score
                  370
                  4.0e-36
E value
Match length
                  70
% identity
                  100
                  (ALO49658) aldehyde dehydrogenase (NAD+)-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  141136
Seq. No.
Seq. ID
                  LIB25-092-Q1-E1-D9
Method
                  BLASTN
NCBI GI
                  q2351063
BLAST score
                  156
E value
                  1.0e-82
Match length
                  177
% identity
                  96
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCL19, complete sequence [Arabidopsis thaliana]
                  141137
Seq. No.
Seq. ID
                  LIB25-092-Q1-E1-E10
Method
                  BLASTX
NCBI GI
                  g3021336
BLAST score
                  265
E value
                  9.0e-24
Match length
                  59
% identity
                  81
                  (AJ224957) RGA-like [Arabidopsis thaliana]
NCBI Description
                  141138
Seq. No.
                  LIB25-092-Q1-E1-E11
Seq. ID
Method
                  BLASTX
                  g2462746
NCBI GI
BLAST score
                  186
E value
                  2.0e-14
Match length
                  40
                  93
% identity
                  (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  141139
                  LIB25-092-Q1-E1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4510323
BLAST score
                  192
E value
                  1.0e-104
                  192
Match length
% identity
                  51
NCBI Description Arabidopsis thaliana BAC T7B11 from chromosome IV near 10
                  cM, complete sequence
```



Seq. ID LIB25-092-Q1-E1-E4

Method BLASTN
NCBI GI g4581084
BLAST score 140
E value 4.0e-73
Match length 171
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC T30F21 genomic

sequence, complete sequence

Seq. No. 141141

Seq. ID LIB25-092-Q1-E1-E5

Method BLASTX
NCBI GI g2500193
BLAST score 199
E value 5.0e-16
Match length 43
% identity 93

NCBI Description RAC-LIKE GTP BINDING PROTEIN ARAC4 (GTP BINDING PROTEIN

ROP2) >gi_1304417 (U45236) Description: rac-like protein; GTP binding protein; Method: conceptual translation supplied by author. [Arabidopsis thaliana] >gi_1777764 (U49972) GTP binding protein Rop2At [Arabidopsis thaliana]

Seq. No. 141142

Seq. ID LIB25-092-Q1-E1-E8

Method BLASTX
NCBI GI g166867
BLAST score 272
E value 1.0e-24
Match length 70
% identity 79

NCBI Description (J05216) ribosomal protein S11 (probable start codon at bp

67) [Arabidopsis thaliana]

Seq. No. 141143

Seq. ID LIB25-092-Q1-E1-E9

Method BLASTX
NCBI GI g4741952
BLAST score 178
E value 1.0e-13
Match length 37
% identity 100

NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No. 141144

Seq. ID LIB25-092-Q1-E1-F4

Method BLASTN
NCBI GI g2924651
BLAST score 134
E value 2.0e-69
Match length 155
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K2A18, complete sequence [Arabidopsis thaliana]

Seq. No. 141145

Seq. ID

Method

NCBI GI

BLAST score

141150

BLASTN

177

g4741959

LIB25-092-Q1-E1-G5



```
Seq. ID
                  LIB25-092-Q1-E1-F5
Method
                  BLASTN
                  g3668073
NCBI GI
BLAST score
                  80
                  3.0e-37
E value
Match length
                  216
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T4C15 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141146
                  LIB25-092-Q1-E1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2832358
BLAST score
                  137
E value
                  3.0e-71
Match length
                  141
                  99
% identity
NCBI Description Arabidopsis thaliana mRNA for HMG betal protein
Seq. No.
                  141147
                  LIB25-092-Q1-E1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1708312
BLAST score
                  174
E value
                  4.0e-13
Match length
                  36
                  100
% identity
NCBI Description HEAT SHOCK PROTEIN 81-1 (HSP81-1) (HEAT SHOCK PROTEIN 83)
Seq. No.
                  141148
Seq. ID
                  LIB25-092-Q1-E1-G2
Method
                  BLASTN
NCBI GI
                  g4539309
BLAST score
                  192
E value
                  1.0e-104
Match length
                  219
% identity
                  96
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22
                  (ESSA project)
                  141149
Seq. No.
Seq. ID
                  LIB25-092-Q1-E1-G4
Method
                  BLASTX
NCBI GI
                  g295792
BLAST score
                  416
E value
                  2.0e-41
Match length
                  72
% identity
                  100
NCBI Description
                  (X13611) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
```

4.0e-95 E value Match length 207 % identity 96 Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete NCBI Description cds 141151 Seq. No. LIB25-092-Q1-E1-G6 Seq. ID Method BLASTN NCBI GI g1877523 BLAST score 115 E value 4.0e-58 Match length 188 % identity 73 Arabidopsis thaliana BAC T7I23, complete sequence NCBI Description [Arabidopsis thaliana] Seq. No. 141152 Seq. ID LIB25-092-Q1-E1-G8 Method BLASTN NCBI GI g3985931 BLAST score 97 E value 2.0e-47 Match length 208 % identity 100 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K21H1, complete sequence [Arabidopsis thaliana] Seq. No. 141153 Seq. ID LIB25-092-Q1-E1-G9 Method BLASTN NCBI GI g2760167 BLAST score 136 E value 9.0e-71 Match length 184 % identity 100 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana] Seq. No. 141154 Seq. ID LIB25-092-Q1-E1-H1 Method BLASTX NCBI GI g4741952 BLAST score 247 E value 1.0e-21

48 Match length % identity 100

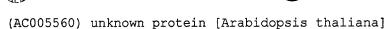
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No. 141155

Seq. ID LIB25-092-Q1-E1-H10

Method BLASTX NCBI GI g3785989 BLAST score 200 E value 4.0e-16 63 Match length % identity 62





NCBI Description

Seq. ID LIB25-092-Q1-E1-H12

Method BLASTX
NCBI GI g131381
BLAST score 311
E value 4.0e-29
Match length 63
% identity 100

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 99745_pir__S11852

photosystem II oxygen-evolving complex protein 1 precursor - Arabidopsis thaliana >gi_22571_emb_CAA36675_ (X52428) 33

kDa oxygen-evolving protein [Arabidopsis thaliana]

Seq. No. 141157

Seq. ID LIB25-092-Q1-E1-H2

Method BLASTX
NCBI GI g1755164
BLAST score 258
E value 6.0e-23
Match length 66
% identity 76

NCBI Description (U75193) germin-like protein [Arabidopsis thaliana]

>gi_1755168 (U75195) germin-like protein [Arabidopsis
thaliana] >gi_2239042_emb_CAA73213_ (Y12673) GLP3 protein
[Arabidopsis thaliana] >gi_4666250_dbj_BAA77208.1_ (D89374)

germin-like protein 2 precursor [Arabidopsis thaliana]

Seq. No. 141158

Seq. ID LIB25-092-Q1-E1-H3

Method BLASTN
NCBI GI g16375
BLAST score 157
E value 3.0e-83
Match length 157
% identity 100

NCBI Description A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding

protein

Seq. No. 141159

Seq. ID LIB25-092-Q1-E1-H5

Method BLASTN
NCBI GI g4490324
BLAST score 209
E value 1.0e-114
Match length 209
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14

(ESSA project)

Seq. No. 141160

Seq. ID LIB25-092-Q1-E1-H8

Method BLASTX NCBI GI g1346702



```
BLAST score
E value
                  1.0e-13
Match length
                  46
                  83
% identity
                  EXOPOLYGALACTURONASE CLONE GBGA483 PRECURSOR (EXOPG)
NCBI Description
                  (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi 421832 pir S34200 exopolygalacturonase (clone GBGa483)
                  - Arabidopsis thaliana >gi_313684_emb_CAA51033_ (X72292)
                  exopolygalacturonase [Arabidopsis thaliana]
Seq. No.
                  141161
Seq. ID
                  LIB25-093-Q1-E1-A3
Method
                  BLASTN
NCBI GI
                  a4733957
                  195
BLAST score
                  1.0e-106
E value
                  203
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T26C18 genomic
NCBI Description
                  sequence, complete sequence
                  141162
Seq. No.
Seq. ID
                  LIB25-093-Q1-E1-A5
Method
                  BLASTN
                  q4056476
NCBI GI
                  197
BLAST score
                  1.0e-107
E value
                  197
Match length
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC F3G5 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141163
```

LIB25-093-Q1-E1-A6 Seq. ID Method BLASTN g2854069 NCBI GI BLAST score 131 E value 9.0e-68 Match length 139 % identity 99

Arabidopsis thaliana putative histone deacetylase (HD2) NCBI Description mRNA, complete cds

Seq. No. 141164 LIB25-093-Q1-E1-A8 Seq. ID Method BLASTN

NCBI GI q2459406 BLAST score 179 2.0e-96 E value Match length 179 100 % identity

Arabidopsis thaliana chromosome II BAC F4P9 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

141165 Seq. No.

Seq. ID LIB25-093-Q1-E1-A9

BLASTN Method



NCBI GI g4835223
BLAST score 131
E value 9.0e-68
Match length 175
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3

(ESSA project)

Seq. No. 141166

Seq. ID LIB25-093-Q1-E1-B3

Method BLASTN
NCBI GI g3399678
BLAST score 144
E value 2.0e-75
Match length 197
% identity 100

NCBI Description Arabidopsis thaliana chromosome 1 BAC F13M7 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 141167

Seq. ID LIB25-093-Q1-E1-B4

Method BLASTX
NCBI GI g2118222
BLAST score 231
E value 9.0e-20
Match length 62
% identity 77

NCBI Description H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain

(clone AVA-P4) - Arabidopsis thaliana >gi_926935 (L44584) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis

thaliana]

Seq. No. 141168

Seq. ID LIB25-093-Q1-E1-B5

Method BLASTX
NCBI GI g1076678
BLAST score 213
E value 1.0e-17
Match length 51
% identity 84

NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No. 141169

Seq. ID LIB25-093-Q1-E1-B7

Method BLASTN
NCBI GI g3128143
BLAST score 130
E value 4.0e-67
Match length 186
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTI20, complete sequence [Arabidopsis thaliana]

Seq. No. 141170

Seq. ID LIB25-093-Q1-E1-B9

Method BLASTX NCBI GI g4105794



```
BLAST score
                  191
E value
                  4.0e-15
                  40
Match length
                  68
% identity
                 (AF049928) PGP224 [Petunia x hybrida]
NCBI Description
Seq. No.
                  141171
Seq. ID
                  LIB25-093-Q1-E1-C1
Method
                  BLASTN
NCBI GI
                  g3449320
BLAST score
                  185
E value
                  1.0e-100
Match length
                  193
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRB17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141172
Seq. ID
                  LIB25-093-Q1-E1-D1
Method
                  BLASTX
NCBI GI
                  g2687686
BLAST score
                  279
E value
                  2.0e-25
Match length
                  56
% identity
                  100
NCBI Description
                  (AJ000110) cystatin [Arabidopsis thaliana]
Seq. No.
                  141173
                  LIB25-093-Q1-E1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499973
BLAST score
                  192
E value
                  3.0e-15
Match length
                  41
% identity
                  95
                  PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)
NCBI Description
                  >gi 1465366 emb CAA66701 (X98078) photosystem II
                   [Arabidopsis thaliana]
                  141174
Seq. No.
Seq. ID
                  LIB25-093-Q1-E1-D2
Method
                  BLASTN
NCBI GI
                  g166643
                  \bar{2}01
BLAST score
                  1.0e-109
E value
Match length
                  201
% identity
                  100
NCBI Description Arabidopsis thaliana chlorophyll A/B-binding protein gene,
                  complete cds
                  141175
Seq. No.
Seq. ID
                  LIB25-093-Q1-E1-D4
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1695717
BLAST score 216
E value 5.0e-18
Match length 45

NCBI Description



% identity NCBI Description (D89341) luminal binding protein [Arabidopsis thaliana] Seq. No. 141176 LIB25-093-Q1-E1-D6 Seq. ID Method BLASTN g4468103 NCBI GI BLAST score 185 1.0e-100 E value Match length 185 % identity 100 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project) Seq. No. 141177 Seq. ID LIB25-093-Q1-E1-D9 Method BLASTN NCBI GI g497420 BLAST score 180 E value 5.0e-97 Match length 187 99 % identity NCBI Description Arabidopsis thaliana (strain Columbia) phenylalanine ammonia-lyase (PAL2) gene, complete cds Seq. No. 141178 Seq. ID LIB25-093-Q1-E1-E1 Method BLASTN NCBI GI g4760411 BLAST score 178 E value 9.0e-96 Match length 178 % identity 100 Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, NCBI Description complete sequence Seq. No. 141179 Seq. ID LIB25-093-Q1-E1-E11 Method BLASTN NCBI GI q4586241 BLAST score 83 2.0e-39 E value Match length 127 % identity 91 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project) Seq. No. 141180 Seq. ID LIB25-093-Q1-E1-E2 Method BLASTN q4220633 NCBI GI BLAST score 137 3.0e-71E value Match length 137 100 % identity

17201

K7J8, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

```
Seq. No.
                  141181
Seq. ID
                  LIB25-093-01-E1-E3
Method
                  BLASTN
NCBI GI
                  q4415905
BLAST score
                  148
E value
                  7.0e-78
Match length
                  156
                  99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13K3 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141182
Seq. ID
                  LIB25-093-Q1-E1-E6
Method
                  BLASTN
NCBI GI
                  g2232147
BLAST score
                  146
E value
                  1.0e-76
Match length
                  182
                  100
% identity
NCBI Description Arabidopsis thaliana 14-3-3-like protein GF14 upsilon
                  (GRF5) gene, complete cds
Seq. No.
                  141183
                  LIB25-093-Q1-E1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2495256
BLAST score
                  285
E value
                  4.0e-26
Match length
                  61
% identity
                  93
NCBI Description
                  STRUCTURE-SPECIFIC RECOGNITION PROTEIN 1 HOMOLOG (HMG
                  [Catharanthus roseus]
```

PROTEIN) >gi_481756_pir__S39242 HMG protein - Madagascar periwinkle >gi_433872_emb_CAA82251_ (Z28410) HMG protein

Seq. No. 141184

Seq. ID LIB25-093-Q1-E1-F10

Method BLASTN NCBI GI q1246400 BLAST score 157 3.0e-83 E value Match length 157 % identity 100

NCBI Description A.thaliana mRNA for ferritin

Seq. No. 141185

Seq. ID LIB25-093-Q1-E1-F5

Method BLASTX NCBI GI g4581139 BLAST score 343 E value 7.0e-33 Match length 64 % identity 98

(AC006919) putative ABC transporter [Arabidopsis thaliana] NCBI Description

Seq. No. 141186

NCBI GI

E value

BLAST score

g4314378

1.0e-11

162



```
LIB25-093-Q1-E1-F7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1669386
                  70
BLAST score
                  2.0e-31
E value
                  143
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana actin 2 (ACT2) gene, complete cds
                  141187
Seq. No.
                  LIB25-093-Q1-E1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2288979
BLAST score
                  163
                  7.0e-87
E value
Match length
                  187
                  96
% identity
                  Arabidopsis thaliana chromosome II BAC T01024 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  141188
Seq. No.
                  LIB25-093-Q1-E1-G10 .
Seq. ID
Method
                  BLASTN
NCBI GI
                  g16440
                  170
BLAST score
                  5.0e-91
E value
Match length
                  182
                  98
% identity
NCBI Description A.thaliana PRKase gene for Ribulose-5-phosphate kinase
                  141189
Seq. No.
                  LIB25-093-Q1-E1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1495251
BLAST score
                  323
E value
                  1.0e-30
Match length
                  66
                  100
% identity
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  141190
                  LIB25-093-Q1-E1-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3449331
BLAST score
                  199
E value
                  1.0e-108
Match length
                  199
% identity
                  37
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNC17, complete sequence [Arabidopsis thaliana]
                  141191
Seq. No.
                  LIB25-093-Q1-E1-G7
Seq. ID
                  BLASTX
Method
```



Match length 54 % identity 65

NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 141192

Seq. ID LIB25-093-Q1-E1-G8

Method BLASTX
NCBI GI g2119846
BLAST score 269
E value 3.0e-24
Match length 53
% identity 100

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 141193

Seq. ID LIB25-093-Q1-E1-H10

Method BLASTN
NCBI GI g4733952
BLAST score 106
E value 7.0e-53
Match length 176
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F23H11 genomic

sequence, complete sequence

Seq. No. 141194

Seq. ID LIB25-093-Q1-E1-H2

Method BLASTN
NCBI GI g4580745
BLAST score 87
E value 2.0e-41
Match length 127
% identity 99

NCBI Description Arabidopsis thaliana chromosome 1 BAC F1003 sequence,

complete sequence

Seq. No. 141195

Seq. ID LIB25-093-Q1-E1-H3

Method BLASTX
NCBI GI g119350
BLAST score 233
E value 5.0e-20
Match length 47
% identity 100

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis

thaliana >gi_16271_emb_CAA41114_ (X58107) enolase

[Arabidopsis thaliana]

>gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase
(2-phospho-D-glycerate hydroylase);identical to P25696



[Arabidopsis thaliana]

Seq. No. 141196

Seq. ID LIB25-093-Q1-E1-H4

Method BLASTX
NCBI GI g730526
BLAST score 271
E value 2.0e-24
Match length 48
% identity 100

NCBI Description 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)

>gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis
thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein

[Arabidopsis thaliana]

Seq. No. 141197

Seq. ID LIB25-093-Q1-E1-H5

Method BLASTX
NCBI GI g2119846
BLAST score 254
E value 2.0e-22
Match length 50
% identity 100

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 141198

Seq. ID LIB25-093-Q1-E1-H6

Method BLASTN
NCBI GI 94567259
BLAST score 67
E value 1.0e-29
Match length 191
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F3K23 genomic

sequence, complete sequence

Seq. No. 141199

Seq. ID LIB25-093-Q1-E1-H7

Method BLASTN
NCBI GI g2980757
BLAST score 197
E value 1.0e-107
Match length 197
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18

(ESSAII project)

Seq. No. 141200

Seq. ID LIB25-093-Q1-E1-H9

Method BLASTN NCBI GI g17674



BLAST score 90 E value 1.0e-43 Match length 90 % identity 100

NCBI Description A.thaliana U4.2 snRNA gene

Seq. No. 141201

Seq. ID LIB25-094-Q1-E1-A12

Method BLASTN
NCBI GI g217870
BLAST score 197
E value 1.0e-107
Match length 197
% identity 100

NCBI Description A. thaliana mRNA for t-complex polypeptide 1 homologue,

complete cds

Seq. No. 141202

Seq. ID LIB25-094-Q1-E1-A2

Method BLASTN
NCBI GI g4741961
BLAST score 199
E value 1.0e-108
Match length 199
% identity 100

NCBI Description Arabidopsis thaliana PsbS protein (PsbS) mRNA, complete cds

Seq. No. 141203

Seq. ID LIB25-094-Q1-E1-A3

Method BLASTN
NCBI GI g3776004
BLAST score 192
E value 1.0e-104
Match length 192
% identity 100

NCBI Description Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH15

Seq. No. 141204

Seq. ID LIB25-094-Q1-E1-B10

Method BLASTN
NCBI GI g2696018
BLAST score 151
E value 1.0e-79
Match length 188
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXC9, complete sequence [Arabidopsis thaliana]

Seq. No. 141205

Seq. ID LIB25-094-Q1-E1-B11

Method BLASTX
NCBI GI g4006865
BLAST score 354
E value 3.0e-34
Match length 64
% identity 100

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]



```
Seq. No.
                  141206
                  LIB25-094-Q1-E1-B12
Seq. ID
Method
                  BLASTX
                  g2281095
NCBI GI
                  184
BLAST score
                  3.0e-14
E value
                  46
Match length
% identity
                  83
                  (ACO02333) cysteine synthase, cpACS1 [Arabidopsis thaliana]
NCBI Description
                  141207
Seq. No.
                  LIB25-094-Q1-E1-B4
Seq. ID
Method
                  BLASTX
                  g2119846
NCBI GI
                  308
BLAST score
                  8.0e-29
E value
                  60
Match length
                  100
% identity
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
NCBI Description
                  Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
                  141208
Seq. No.
                  LIB25-094-Q1-E1-B5
Seq. ID
Method
                  BLASTX
                  g4454567
NCBI GI
BLAST score
                  254
                  2.0e-22
E value
                  50
Match length
% identity
                  100
                 (AF128407) EDS1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  141209
                  LIB25-094-Q1-E1-B7
Seq. ID
Method
                  BLASTN
                  q1785618
NCBI GI
                   99
BLAST score
                  1.0e-48
E value
Match length
                  126
                  100
% identity
NCBI Description Artificial sequence; A.thaliana DNA; pGV1048 T-DNA; GUS
                  fusion protein (1348 bp)
Seq. No.
                  141210
                  LIB25-094-Q1-E1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                   q3250673
BLAST score
                   195
                   1.0e-106
E value
Match length
                   195
% identity
                   100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5
```

Match length

NCBI Description

% identity

55 100



(ESSAII project)

```
Seq. No.
                  141211
                  LIB25-094-Q1-E1-B9
Seq. ID
Method
                  BLASTN
                  g3402695
NCBI GI
BLAST score
                  199
                  1.0e-108
E value
Match length
                  199
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T3K9 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141212
                  LIB25-094-Q1-E1-C3
Seq. ID
Method
                  BLASTX
                  q407992
NCBI GI
BLAST score
                  136
E value
                  1.0e-08
Match length
                   60
                   48
% identity
NCBI Description
                  (L25125) RNA helicase [Mus musculus]
Seq. No.
                  141213
                  LIB25-094-Q1-E1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                   q4760411
BLAST score
                   201
E value
                   1.0e-109
                   201
Match length
                   100
% identity
                  Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,
NCBI Description
                   complete sequence
Seq. No.
                   141214
Seq. ID
                   LIB25-094-Q1-E1-C5
Method
                   BLASTX
NCBI GI
                   g3915823
BLAST score
                   275
E value
                   6.0e-25
                   53
Match length
                   98
% identity
                  [Segment 1 of 2] 60S RIBOSOMAL PROTEIN L5
NCBI Description
Seq. No.
                   141215
Seq. ID
                   LIB25-094-Q1-E1-C6
Method
                   BLASTX
NCBI GI
                   g2119846
BLAST score
                   278
E value
                   3.0e-25
```

chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis



thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

```
Seq. No.
                  141216
                  LIB25-094-Q1-E1-C8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2058281
                  157
BLAST score
                  3.0e-83
E value
Match length
                  157
% identity
                  100
NCBI Description
                  A.thaliana mRNA for AtRanBPla protein
                  141217
Seq. No.
                  LIB25-094-Q1-E1-C9
Seq. ID
Method
                  BLASTN
                  q905390
NCBI GI
BLAST score
                  199
                  1.0e-108
E value
Match length
                  199
                  100
% identity
                  Arabidopsis thaliana serine acetyltransferase (Sat-52)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  141218
                  LIB25-094-Q1-E1-D10
Seq. ID
Method
                  BLASTX
                  q4689386
NCBI GI
BLAST score
                  180
                   9.0e-14
E value
                   39
Match length
                  87
% identity
                   (AF139468) photosystem I reaction center subunit III [Vigna
NCBI Description
                   radiata]
Seq. No.
                   141219
Seq. ID
                   LIB25-094-Q1-E1-D12
Method
                   BLASTN
NCBI GI
                   q4490324
BLAST score
                   180
E value
                   5.0e-97
Match length
                   201
                   97
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14
NCBI Description
                   (ESSA project)
Seq. No.
                   141220
Seq. ID
                   LIB25-094-Q1-E1-D3
Method
                   BLASTN
NCBI GI
                   g1532162
BLAST score
                   141
                   1.0e-73
E value
Match length
                   204
% identity
                   100
                  Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3,
NCBI Description
                   AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14
```

genes, partial cds, AT.I.24-7, ascorbate peroxidase



(ATHAPX1), EF-lalpha-A1, -A2 and -A3 (EF-lalpha) and AT.I

Seq. No. 141221 LIB25-094-Q1-E1-D5 Seq. ID BLASTN Method q2618600 NCBI GI BLAST score 180 5.0e-97 E value 180 Match length 100 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MDC12, complete sequence [Arabidopsis thaliana] 141222 Seq. No. LIB25-094-01-E1-D7 Seq. ID Method BLASTX q3688799 NCBI GI BLAST score 230 1.0e-19 E value 46 Match length 100 % identity (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis NCBI Description thaliana] Seq. No. 141223 LIB25-094-Q1-E1-D9 Seq. ID Method BLASTX a124224 NCBI GI BLAST score 272 1.0e-24 E value 55 Match length 96 % identity INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) NCBI Description >gi 100345 pir S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105 (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum] Seq. No. 141224 Seq. ID LIB25-094-Q1-E1-E1 Method BLASTN NCBI GI q3831448 BLAST score 201 1.0e-109 E value Match length 201 % identity 100 Arabidopsis thaliana chromosome II BAC T32F6 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 141225 Seq. No. LIB25-094-Q1-E1-E4 Seq. ID BLASTX Method NCBI GI q401169 BLAST score 212 1.0e-17 E value Match length 40 100 % identity

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)



Seq. No. 141226

Seq. ID LIB25-094-Q1-E1-E5

Method BLASTN
NCBI GI g2924729
BLAST score 193
E value 1.0e-105
Match length 193
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNA5, complete sequence [Arabidopsis thaliana]

Seq. No. 141227

Seq. ID LIB25-094-Q1-E1-E6

Method BLASTX
NCBI GI g1076366
BLAST score 267
E value 5.0e-24
Match length 51
% identity 100

NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis

thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi_992643 (U32186)

cyclophilin [Arabidopsis thaliana]

>gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase

[Arabidopsis thaliana]

Seq. No. 141228

Seq. ID LIB25-094-Q1-E1-E9

Method BLASTX
NCBI GI g119143
BLAST score 330
E value 2.0e-31
Match length 65
% identity 95

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_81606_pir__S06724 translation elongation factor eEF-1
alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
(X16430) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1369927_emb_CAA34454_ (X16431) elongation factor
1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_
(X16431) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana]
>gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana]
>gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No. 141229

Seq. ID LIB25-094-Q1-E1-F1

Method BLASTN
NCBI GI g2618677
BLAST score 201
E value 1.0e-109
Match length 201
% identity 100

NCBI Description Arabidopsis thaliana BAC F21B7 chromosome 1, complete

sequence [Arabidopsis thaliana]



```
141230
Seq. No.
Seq. ID
                  LIB25-094-Q1-E1-F10
Method
                  BLASTX
NCBI GI
                  q4587543
                   302
BLAST score
                   4.0e-28
E value
Match length
                   59
                  100
% identity
                   (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase
NCBI Description
                  with GDSL-motif family. EST gb_AB015099 comes from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  141231
Seq. ID
                  LIB25-094-Q1-E1-F11
                  BLASTN
Method
                  q3212846
NCBI GI
                   166
BLAST score
E value
                   1.0e-88
                   188
Match length
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   141232
                  LIB25-094-Q1-E1-F12
Seq. ID
Method
                  BLASTN
                   q2262097
NCBI GI
                   185
BLAST score
E value
                   1.0e-100
                   185
Match length
                   100
% identity
                  Arabidopsis thaliana chromosome IV BAC T19F6 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   141233
Seq. ID
                   LIB25-094-Q1-E1-F3
Method
                   BLASTN
NCBI GI
                   g3123744
BLAST score
                   52
                   1.0e-20
E value
Match length
                   100
% identity
                   88
NCBI Description Brassica napus mRNA for aluminum-induced, complete cds
Seq. No.
                   141234
Seq. ID
                   LIB25-094-Q1-E1-F5
Method
                   BLASTX
NCBI GI
                   q730544
BLAST score
                   240
                   8.0e-21
E value
                   45
Match length
                   100
% identity
```

NCBI Description 60S RIBOSOMAL PROTEIN L24

Seq. No. 141235

Seq. ID LIB25-094-Q1-E1-F7

Method BLASTN



NCBI GI g3885325 BLAST score 195 1.0e-106 E value Match length 195 100 % identity Arabidopsis thaliana chromosome II BAC T20P8 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 141236 Seq. No. Seq. ID LIB25-094-Q1-E1-F8 Method BLASTX NCBI GI q2244807 BLAST score 218 E value 3.0e-18 69 Match length 61 % identity (Z97336) hypothetical protein [Arabidopsis thaliana] NCBI Description 141237 Seq. No. LIB25-094-Q1-E1-G1 Seq. ID Method BLASTN q4586241 NCBI GI BLAST score 170 E value 5.0e-91 203 Match length 100 % identity Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 NCBI Description (ESSA project) 141238 Seq. No. LIB25-094-Q1-E1-G3 Seq. ID Method BLASTX NCBI GI g2062167 BLAST score 345 E value 4.0e-33 Match length 66 % identity 100 (AC001645) Proline-rich protein APG isolog [Arabidopsis NCBI Description thaliana] 141239 Seq. No. LIB25-094-Q1-E1-G4 Seq. ID BLASTN Method NCBI GI g2058281 BLAST score 159 2.0e-84 E value Match length 159 % identity 100 NCBI Description A.thaliana mRNA for AtRanBPla protein 141240 Seq. No. LIB25-094-Q1-E1-G5 Seq. ID BLASTN Method

Method BLASTN
NCBI GI g4049332
BLAST score 115
E value 3.0e-58
Match length 197



```
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4
NCBI Description
                   (ESSAII project)
Seq. No.
                  141241
                  LIB25-094-Q1-E1-H1
Seq. ID
Method
                  BLASTN
                  g4538990
NCBI GI
BLAST score
                  103
E value
                  5.0e-51
Match length
                  207
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19
NCBI Description
                   (ESSA project)
                  141242
Seq. No.
                  LIB25-094-Q1-E1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2454184
BLAST score
                   311
                   4.0e-29
E value
Match length
                   64
                   100
% identity
                   (U80186) pyruvate dehydrogenase E1 beta subunit
NCBI Description
                   [Arabidopsis thaliana]
                   141243
Seq. No.
                  LIB25-094-Q1-E1-H12
Seq. ID
Method
                   BLASTX
                   q974216
NCBI GI
                   323
BLAST score
                   1.0e-30
E value
                   65
Match length
% identity
                   52
NCBI Description (X90652) TATA-box binding protein [Zea mays]
Seq. No.
                   141244
Seq. ID
                   LIB25-094-Q1-E1-H2
Method
                   BLASTX
NCBI GI
                   q3298542
BLAST score
                   184
                   3.0e-14
E value
Match length
                   65
                   52
% identity
                   (AC004681) putative cellulose synthase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   141245
                   LIB25-094-Q1-E1-H4
Seq. ID
Method
                   BLASTX
                   g3341676
NCBI GI
BLAST score
                   287
                   2.0e-26
E value
                   57
Match length
                   100
% identity
                   (AC003672) putative glycosyl hydrolase [Arabidopsis
NCBI Description
```

17214

thaliana]



Seq. No. 141246 LIB25-094-Q1-E1-H5 Seq. ID Method BLASTN NCBI GI g4159707 BLAST score 198 E value 1.0e-107 Match length 198 100 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MJK13, complete sequence Seq. No. 141247 LIB25-094-Q1-E1-H7 Seq. ID Method BLASTN NCBI GI q2642214 BLAST score 196 E value 1.0e-106 196 Match length 100 % identity NCBI Description Arabidopsis thaliana NOI protein mRNA, complete cds Seq. No. 141248 Seq. ID LIB25-094-Q1-E1-H8 Method BLASTX NCBI GI q115767 BLAST score 249 7.0e-22 E value Match length 50 100 % identity CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana] Seq. No. 141249 LIB25-095-Q1-E1-A1 Seq. ID BLASTX Method g2738248 NCBI GI 227 BLAST score 3.0e-19 E value 64 Match length 75 % identity (U97200) cobalamin-independent methionine synthase NCBI Description [Arabidopsis thaliana] Seq. No. 141250 LIB25-095-Q1-E1-A10 Seq. ID BLASTN Method

NCBI GI g3702724
BLAST score 41
E value 5.0e-14
Match length 161
% identity 86

NCBI Description



```
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K17N15, complete sequence [Arabidopsis thaliana]
                  141251
Seq. No.
                  LIB25-095-Q1-E1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2149051
                  222
BLAST score
                  1.0e-18
E value
Match length
                  42
                  100
% identity
                  (U73810) small Ras-like GTP-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  141252
Seq. No.
                  LIB25-095-Q1-E1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2351073
BLAST score
                  168
                  8.0e-90
E value
                  203
Match length
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141253
                  LIB25-095-Q1-E1-A4
Seq. ID
Method
                  BLASTX
                   g3080392
NCBI GI
                   209
BLAST score
E value
                   4.0e-17
                   53
Match length
                   83
% identity
                  (AL022603) glucose transporter [Arabidopsis thaliana]
NCBI Description
                   141254
Seq. No.
                   LIB25-095-Q1-E1-A5
Seq. ID
                   BLASTN
Method
                   q4519183
NCBI GI
BLAST score
                   191
                   1.0e-103
E value
                   218
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K15C23, complete sequence
                   141255
Seq. No.
Seq. ID
                   LIB25-095-Q1-E1-B1
Method
                   BLASTN
NCBI GI
                   q4538990
BLAST score
                   69
                   1.0e-30
E value
Match length
                   158
                   100
% identity
```

(ESSA project)

Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19

Match length

% identity

213



```
141256
Seq. No.
                  LIB25-095-Q1-E1-B2
Seq. ID
Method
                  BLASTX
                  q629602
NCBI GI
BLAST score
                  382
                  2.0e-37
E value
                  73
Match length
                  99
% identity
                  probable imbibition protein - wild cabbage
NCBI Description
                  >gi 488787 emb CAA55893_ (X79330) putative imbibition
                  protein [Brassica oleracea]
                  141257
Seq. No.
                  LIB25-095-Q1-E1-B4
Seq. ID
Method
                  BLASTX
                  g2118017
NCBI GI
                  254
BLAST score
                  2.0e-22
E value
                  60
Match length
                  72
% identity
                  non-S-RNase (EC 3.1.-.-) - Japanese pear
NCBI Description
                   >gi_1526417_dbj_BAA08475_ (D49529) ribonuclease [Pyrus
                  pyrifolia]
Seq. No.
                   141258
                  LIB25-095-Q1-E1-B5
Seq. ID
Method
                  BLASTN
                   g3128143
NCBI GI
BLAST score
                   219
                   1.0e-120
E value
                   219
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MTI20, complete sequence [Arabidopsis thaliana]
                   141259
Seq. No.
                   LIB25-095-Q1-E1-B7
Seq. ID
Method
                   BLASTX
                   q137465
NCBI GI
BLAST score
                   339
E value
                   2.0e-32
Match length
                   73
                   95
% identity
                   VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT)
NCBI Description
                   (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir_ A31886
                   H+-transporting ATPase (EC 3.6.1.35) 57K chain -
                   Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding
                   subunit of vacuolar ATPase [Arabidopsis thaliana]
                   141260
Seq. No.
Seq. ID
                   LIB25-095-Q1-E1-B8
                   BLASTN
Method
NCBI GI
                   q1181530
BLAST score
                   213
                   1.0e-116
E value
```



```
NCBI Description Arabidopsis thaliana thionin (Thi2.1) mRNA, complete cds
                  141261
Seq. No.
                  LIB25-095-Q1-E1-B9
Seq. ID
                  BLASTX
Method
                  q2160168
NCBI GI
                  261
BLAST score
                  3.0e-23
E value
                  47
Match length
                  100
% identity
                  (AC000132) Strong similarity to R. communis
NCBI Description
                  phosphoglycerate mutase (gb_X70652). ESTs
                  gb_T41853,gb_T76648 come from this gene. [Arabidopsis
                  thaliana]
                  141262
Seq. No.
                  LIB25-095-Q1-E1-C1
Seq. ID
                  BLASTN
Method
                  g2062705
NCBI GI
                   36
BLAST score
                   5.0e-11
E value
                   49
Match length
                   56
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                   141263
Seq. No.
                   LIB25-095-Q1-E1-C10
Seq. ID
                   BLASTN
Method
                   g2746340
NCBI GI
BLAST score
                   199
                   1.0e-108
E value
                   199
Match length
                   100
% identity
NCBI Description Arabidopsis thaliana ATA27 mRNA, complete cds
                   141264
Seq. No.
                   LIB25-095-Q1-E1-C11
Seq. ID
                   BLASTN
Method
                   q2832689
NCBI GI
                   205
BLAST score
                   1.0e-112
E value
                   205
Match length
                   100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21
                   (ESSAII project)
                   141265
Seq. No.
                   LIB25-095-Q1-E1-C2
Seq. ID
Method
                   BLASTN
                   q4468801
NCBI GI
BLAST score
                   89
                   9.0e-43
E value
                   158
Match length
                   100
 % identity
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17
```

(ESSA project)



```
141266
Seq. No.
                  LIB25-095-Q1-E1-C5
Seq. ID
                  BLASTX
Method
                  q1946367
NCBI GI
                  357
BLAST score
                  1.0e-34
E value
                  71
Match length
                  100
% identity
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]
                  141267
Seq. No.
                  LIB25-095-Q1-E1-C6
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3869069
                   149
BLAST score
                   2.0e-78
E value
                   218
Match length
                   98
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MEB5, complete sequence [Arabidopsis thaliana]
                   141268
Seq. No.
                   LIB25-095-Q1-E1-C8
Seq. ID
                   BLASTX
Method
                   g4741954
NCBI GI
                   308
BLAST score
                   8.0e-29
E value
                   60
Match length
                   100
% identity
                   (AF134127) Lhcb4.2 protein [Arabidopsis thaliana]
NCBI Description
                   141269
Seq. No.
                   LIB25-095-Q1-E1-D10
Seq. ID
                   BLASTN
Method
                   g4454447
NCBI GI
                   201
BLAST score
                   1.0e-109
E value
                   201
Match length
                   100
 % identity
                   Arabidopsis thaliana chromosome II BAC F5H14 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   141270
 Seq. No.
                   LIB25-095-Q1-E1-D12
 Seq. ID
Method
                   BLASTN
                   q2832667
 NCBI GI
                   187
 BLAST score
                   1.0e-101
 E value
 Match length
                   187
                   100
 % identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14
 NCBI Description
                    (ESSAII project)
```

Seq. No. 141271

Seq. ID LIB25-095-Q1-E1-D5

Method BLASTX NCBI GI g1175013



```
BLAST score
                  3.0e-23
E value
                  49
Match length
                  100
% identity
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi 629542_pir S44084
NCBI Description
                  plasma membrane intrinsic protein 2a - Arabidopsis thaliana
                  >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic
                  protein 2a [Arabidopsis thaliana]
                  141272
Seq. No.
                  LIB25-095-Q1-E1-D9
Seq. ID
                  BLASTN
Method
                  g4220638
NCBI GI
                  171
BLAST score
E value
                   1.0e-91
                   201
Match length
% identity
                   95
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIF21, complete sequence [Arabidopsis thaliana]
                   141273
Seq. No.
                   LIB25-095-Q1-E1-E1
Seq. ID
                   BLASTX
Method
                   g4567286
NCBI GI
                   209
BLAST score
                   4.0e-17
E value
                   58
Match length
                   74
% identity
                   (AC006841) putative coatomer alpha subunit [Arabidopsis
NCBI Description
                   thaliana]
                   141274
Seq. No.
                   LIB25-095-Q1-E1-E10
Seq. ID
                   BLASTN
Method
                   g4220510
NCBI GI
                   174
BLAST score
                   2.0e-93
E value
                   201
Match length
 % identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
NCBI Description
                   (ESSAII project)
                   141275
 Seq. No.
                   LIB25-095-Q1-E1-E2
 Seq. ID
                   BLASTN
 Method
                   q2924651
 NCBI GI
                   176
 BLAST score
                   2.0e-94
 E value
                   176
 Match length
                   100
```

% identity

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K2A18, complete sequence [Arabidopsis thaliana]

141276 Seq. No.

LIB25-095-Q1-E1-E4 Seq. ID

Method BLASTX NCBI GI g1491615

```
BLAST score
                  1.0e-17
E value
                  56
Match length
                  75
% identity
                  (X99923) male sterility 2-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  141277
Seq. No.
                  LIB25-095-Q1-E1-E8
Seq. ID
                  BLASTN
Method
                  g2651294
NCBI GI
                  77
BLAST score
                  2.0e-35
E value
Match length
                  221
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T2P4 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  141278
Seq. No.
                  LIB25-095-Q1-E1-E9
Seq. ID
                  BLASTN
Method
                  g4159703
NCBI GI
                   106
BLAST score
                   8.0e-53
E value
Match length
                   143
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K5F14, complete sequence
                   141279
Seq. No.
                   LIB25-095-Q1-E1-F10
Seq. ID
                   BLASTN
Method
                   q3510343
NCBI GI
BLAST score
                   105
E value
                   3.0e-52
Match length
                   128
                   100
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MJC20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   141280
                   LIB25-095-Q1-E1-F11
Seq. ID
                   BLASTX
Method
                   q1345594
NCBI GI
BLAST score
                   149
                   4.0e-10
E value
                   61
Match length
```

% identity 94

14-3-3-LIKE PROTEIN GF14 KAPPA >gi_1022780 (U36447) GF14 NCBI Description

Kappa isoform [Arabidopsis thaliana]

141281 Seq. No.

LIB25-095-Q1-E1-F12 Seq. ID

BLASTX Method g401169 NCBI GI 216 BLAST score 5.0e-18 E value



41 Match length 100 % identity NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

141282 Seq. No.

LIB25-095-Q1-E1-F2 Seq. ID

BLASTN Method g1935913 NCBI GI 215 BLAST score 1.0e-118 E value 222 Match length 100 % identity

NCBI Description Arabidopsis thaliana lethal leaf-spot 1 homolog (Lls1)

mRNA, partial cds

141283 Seq. No.

LIB25-095-Q1-E1-F3 Seq. ID

BLASTX Method g464987 NCBI GI 261 BLAST score 3.0e-23 E value 49 Match length 100 % identity

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN NCBI Description

LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)

>gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana

>gi 297878 emb CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin

conjugating enzyme [Arabidopsis thaliana]

141284 Seq. No.

LIB25-095-Q1-E1-F5 Seq. ID

BLASTX Method g3892712 NCBI GI 369 BLAST score 6.0e-36 E value 72 Match length 100 % identity

(AL033545) adenine phosphoribosyltransferase (EC NCBI Description

2.4.2.7) - like protein [Arabidopsis thaliana]

141285 Seq. No.

LIB25-095-Q1-E1-F6 Seq. ID

BLASTN Method g2288886 NCBI GI 202 BLAST score 1.0e-110 E value 202 Match length % identity

Arabidopsis thaliana mRNA for mevalonate diphosphate NCBI Description

decarboxylase

141286 Seq. No.

LIB25-095-Q1-E1-F8 Seq. ID

Method BLASTX q3461848 NCBI GI

Match length

% identity

216 100



```
BLAST score
                  6.0e-35
E value
                  71
Match length
                  100
% identity
                 (AC005315) putative ATPase [Arabidopsis thaliana]
NCBI Description
                  141287
Seq. No.
                  LIB25-095-Q1-E1-G1
Seq. ID
                  BLASTN
Method
                  g3212102
NCBI GI
                  157
BLAST score
                   3.0e-83
E value
                   181
Match length
                   100
% identity
NCBI Description Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM,
                   complete sequence [Arabidopsis thaliana]
                   141288
Seq. No.
                   LIB25-095-Q1-E1-G10
Seq. ID
                   BLASTX
Method
                   g3776029
NCBI GI
                   320
BLAST score
                   3.0e-30
E value
                   63
Match length
                   100
% identity
                   (AJ010476) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   141289
Seq. No.
                   LIB25-095-Q1-E1-G12
Seq. ID
                   BLASTX
Method
                   q3688799
NCBI GI
                   271
BLAST score
                   2.0e-24
E value
                   64
Match length
                   80
% identity
                   (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
NCBI Description
                   thaliana]
                   141290
 Seq. No.
                   LIB25-095-Q1-E1-G2
 Seq. ID
                   BLASTN
 Method
                   g4757414
 NCBI GI
                   101
 BLAST score
                   8.0e-50
 E value
                   220
 Match length
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
 NCBI Description
                   MYF24, complete sequence
                   141291
 Seq. No.
                   LIB25-095-Q1-E1-G6
 Seq. ID
                   BLASTN
 Method
                    q4376087
 NCBI GI
 BLAST score
                    216
                    1.0e-118
 E value
```



NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No. 141292

Seq. ID LIB25-095-Q1-E1-G8

Method BLASTN
NCBI GI 94335744
BLAST score 41

E value 5.0e-14 Match length 77 8 identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC T4M8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 141293

Seq. ID LIB25-095-Q1-E1-H1

Method BLASTN
NCBI GI 94249393
BLAST score 181
E value 2.0e-97
Match length 220
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T9J23 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 141294

Seq. ID LIB25-095-Q1-E1-H4

Method BLASTX
NCBI GI g2129944
BLAST score 210
E value 3.0e-17
Match length 46
% identity 83

NCBI Description RNA-binding protein RZ-1 - wood tobacco

>gi_1395193_dbj_BAA12064_ (D83696) RNA-binding protein RZ-1
[Nicotiana sylvestris] >gi 1435062 dbj BAA06012 (D28861)

RNA binding protein, RZ-1 [Nicotiana sylvestris]

Seq. No. 141295

Seq. ID LIB25-095-Q1-E1-H5

Method BLASTX
NCBI GI g544424
BLAST score 204
E value 1.0e-16
Match length 39
% identity 97

NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147

glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301 emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding

protein [Arabidopsis thaliana]

>gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)

glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No. 141296

Seq. ID LIB25-095-Q1-E1-H8

Method BLASTN



```
q4220635
NCBI GI
                  214
BLAST score
                  1.0e-117
E value
                  214
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDB19, complete sequence [Arabidopsis thaliana]
                  141297
Seq. No.
                  LIB25-095-Q1-E1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267146
BLAST score
                  332
                  1.0e-31
E value
                   66
Match length
                   95
% identity
                  DNA TOPOISOMERASE I >gi 99762 pir S22864 DNA topoisomerase
NCBI Description
                   (EC 5.99.1.2) I - Arabidopsis thaliana
                   >gi_16558_emb_CAA40763_ (X57544) topoisomerase I
                   [Arabidopsis thaliana] >gi_445137_prf__1908437A
                   topoisomerase I [Arabidopsis thaliana]
                   141298
Seq. No.
                   LIB25-096-Q1-E1-A10
Seq. ID
                   BLASTX
Method
                   q2586157
NCBI GI
                   330
BLAST score
                   2.0e-31
E value
Match length
                   66
                   100
% identity
                   (AF002220) kinesin-like calmodulin-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   141299
Seq. No.
                   LIB25-096-Q1-E1-A4
Seq. ID
                   BLASTX
Method
                   g2914701
NCBI GI
                   356
BLAST score
                   2.0e-34
E value
Match length
                   66
                   100
 % identity
                   (AC003974) putative cytochrome b5 [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   141300
                   LIB25-096-Q1-E1-A6
 Seq. ID
                   BLASTX
 Method
                   g1246019
 NCBI GI
                   290
 BLAST score
                   1.0e-26
 E value
                   56
 Match length
                   100
 % identity
                   (S80554) chalcone synthase, CHS [Arabidopsis, Landsberg
 NCBI Description
                   erecta, tt4, Peptide Mutant, 395 aa] [Arabidopsis]
```

Seq. No. 141301

Seq. ID LIB25-096-Q1-E1-A8

Method BLASTN



NCBI GI q1546699 BLAST score 214 E value 1.0e-117 Match length 214 % identity 100 NCBI Description A.thaliana mRNA for peroxidase ATP18a Seq. No. 141302 LIB25-096-Q1-E1-A9 Seq. ID Method BLASTX g228456 NCBI GI BLAST score 282 9.0e-26 E value Match length 50 % identity 100

NCBI Description Gln synthetase [Arabidopsis thaliana]

141303 Seq. No.

LIB25-096-Q1-E1-B5 Seq. ID

Method BLASTX NCBI GI g4105798 BLAST score 257 8.0e-23 E value Match length 70 % identity 59

(AF049930) PGP237-11 [Petunia x hybrida] NCBI Description

141304 Seq. No.

Seq. ID LIB25-096-Q1-E1-B6

Method BLASTX NCBI GI g1171991 BLAST score 353 E value 4.0e-34 73 Match length % identity 96

PHENYLALANINE AMMONIA-LYASE 1 >gi 1076369 pir S52990 NCBI Description

phenylalanine ammonia-lyase (EC 4.3.1.5) - Arabidopsis thaliana >gi 497419 (L33677) phenylalanine ammonia lyase

[Arabidopsis thaliana]

Seq. No. 141305

Seq. ID LIB25-096-Q1-E1-B7

Method BLASTX NCBI GI q2961390 BLAST score 261 E value 3.0e-23Match length 50 % identity 100

(AL022141) beta-galactosidase like protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 141306

LIB25-096-Q1-E1-B8 Seq. ID

Method BLASTN g2980757 NCBI GI BLAST score 194 E value 1.0e-105



```
Match length
                  97
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18
NCBI Description
                   (ESSAII project)
                  141307
Seq. No.
                  LIB25-096-Q1-E1-C11
Seq. ID
                  BLASTX
Method
                  g1145697
NCBI GI
                   339
BLAST score
E value
                   2.0e-32
Match length
                   67
% identity
                   100
                   (U39485) delta tonoplast integral protein [Arabidopsis
NCBI Description
                   thaliana]
                   141308
Seq. No.
                   LIB25-096-Q1-E1-C12
Seq. ID
                   BLASTX
Method
                   q4741929
NCBI GI
BLAST score
                   215
                   7.0e-18
E value
                   62
Match length
                   65
% identity
                   (AF130253) membrane related protein CP5 [Arabidopsis
NCBI Description
                   thaliana]
                   141309
Seq. No.
                   LIB25-096-Q1-E1-C2
Seq. ID
                   BLASTN
Method
                   g511080
NCBI GI
                   112
BLAST score
                   2.0e-56
E value
Match length
                   112
 % identity
                   100
NCBI Description A.thaliana HEM15 mRNA for ferrochelatase
                   141310
 Seq. No.
                   LIB25-096-Q1-E1-C4
 Seq. ID
                   BLASTX
 Method
                   q4490705
 NCBI GI
                   359
 BLAST score
                   8.0e-35
 E value
 Match length
                   72
                   100
 % identity
                   (AL035680) ribosomal protein L14-like protein [Arabidopsis
 NCBI Description
                   thaliana]
                    141311
```

Seq. No.

LIB25-096-Q1-E1-C6 Seq. ID

BLASTN Method g3335331 NCBI GI 191 BLAST score 1.0e-103 E value 191 Match length 100 % identity

NCBI Description Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,





complete sequence [Arabidopsis thaliana]

141312 Seq. No. Seq. ID LIB25-096-Q1-E1-C7 Method BLASTX NCBI GI g3128175 BLAST score 167 3.0e-12 E value Match length 57 % identity 49 (AC004521) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 141313 Seq. ID LIB25-096-Q1-E1-C8

Method BLASTX
NCBI GI g999542

NCBI GI g999542
BLAST score 204
E value 1.0e-16
Match length 58
% identity 66

NCBI Description Spinacia oleracea >gi_999543_pdb_1GYL_B Spinacia oleracea

Seq. No. 141314

Seq. ID LIB25-096-Q1-E1-D10

Method BLASTX
NCBI GI g1350680
BLAST score 237
E value 2.0e-20
Match length 53
% identity 89

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 141315

Seq. ID LIB25-096-Q1-E1-D2

Method BLASTN
NCBI GI g1495250
BLAST score 75
E value 3.0e-34
Match length 149
% identity 88

NCBI Description A.thaliana mRNA for heat-shock protein

Seq. No. 141316

Seq. ID LIB25-096-Q1-E1-D4

Method BLASTN
NCBI GI g3299824
BLAST score 192
E value 1.0e-104
Match length 222
% identity 95

NCBI Description Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,

near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No. 141317

Seq. ID LIB25-096-Q1-E1-D5

Method BLASTX NCBI GI g2440035

Match length

216



```
BLAST score
                  6.0e-32
E value
                  71
Match length
                  90
% identity
                  (X98544) endo-1,4-beta-glucanase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  141318
                  LIB25-096-Q1-E1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3093479
BLAST score
                  184
E value
                  2.0e-99
                  212
Match length
                  97
% identity
                  Arabidopsis thaliana nucleoside diphosphate kinase type 2
NCBI Description
                   (NDPK2) gene, complete cds
Seq. No.
                  141319
                  LIB25-096-Q1-E1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4218109
BLAST score
                  200
E value
                  1.0e-109
                  200
Match length
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16
NCBI Description
                   (ESSAII project)
Seq. No.
                  141320
Seq. ID
                  LIB25-096-Q1-E1-E12
Method
                  BLASTN
                  g4589418
NCBI GI
BLAST score
                  102
E value
                  2.0e-50
                  200
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21G20, complete sequence
                  141321
Seq. No.
                  LIB25-096-Q1-E1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2459406
BLAST score
                  182
                  3.0e-98
E value
Match length
                  182
% identity
                   100
                  Arabidopsis thaliana chromosome II BAC F4P9 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                   141322
Seq. No.
Seq. ID
                  LIB25-096-Q1-E1-E5
Method
                  BLASTN
NCBI GI
                   q4538949
BLAST score
                   216
E value
                   1.0e-118
```



 Seq. No.
 141323

 Seq. ID
 LIB25-096-Q1-E1-E6

 Method
 BLASTX

Method BLASIX
NCBI GI g1346523
BLAST score 311
E value 4.0e-29
Match length 59
% identity 98

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)

>gi_1084428_pir__S49491 methionine adenosyltransferase (EC 2.5.1.6) - garden petunia >gi_559506_emb_CAA57696_ (X82214)

methionine adenosyltransferase [Petunia x hybrida]

Seq. No. 141324

Seq. ID LIB25-096-Q1-E1-E7

Method BLASTN
NCBI GI g3449334
BLAST score 163
E value 8.0e-87
Match length 205
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MYH9, complete sequence [Arabidopsis thaliana]

Seq. No. 141325

Seq. ID LIB25-096-Q1-E1-E9

Method BLASTX
NCBI GI g132939
BLAST score 284
E value 5.0e-26
Match length 51
% identity 100

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal

protein L3 (ARP1) - Arabidopsis thaliana >gi 166858 (M32654) ribosomal protein [Arabidopsis thaliana]

Seq. No. 141326

Seq. ID LIB25-096-Q1-E1-F2

Method BLASTN
NCBI GI g3548797
BLAST score 158
E value 8.0e-84
Match length 158
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T18E12 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 141327

Seq. ID LIB25-096-Q1-E1-F6

MethodBLASTXNCBI GIg4105798BLAST score280

E value

Match length

8.0e-37



```
E value
                   2.0e-25
Match length
                   68
 % identity
                   60
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.
                   141328
Seq. ID
                   LIB25-096-Q1-E1-F7
Method
                   BLASTX
NCBI GI
                   g4056505
BLAST score
                   306
E value
                   1.0e-28
Match length
                   63
% identity
                   97
NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]
Seq. No.
                   141329
                   LIB25-096-Q1-E1-F8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4510360
BLAST score
                   108
E value
                   6.0e-54
Match length
                   108
% identity
                   100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F11F19 genomic
                  sequence, complete sequence
Seq. No.
                   141330
Seq. ID
                  LIB25-096-Q1-E1-F9
Method
                  BLASTX
NCBI GI
                  g1169201
BLAST score
                  228
E value
                  2.0e-19
Match length
                  54
% identity
                  93
NCBI Description
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
                  >gi_421830_pir__S33707 DRT112 protein - Arabidopsis
                  thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.
                  141331
Seq. ID
                  LIB25-096-Q1-E1-G10
Method
                  BLASTX
NCBI GI
                  g2501011
BLAST score
                  252
E value
                  3.0e-22
Match length
                  62
% identity
                  77
NCBI Description
                  ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS)
                  >gi_1652625_dbj_BAA17545_ (D90907) isoleucyl-tRNA
                  synthetase [Synechocystis sp.]
Seq. No.
                  141332
Seq. ID
                  LIB25-096-Q1-E1-G2
Method
                  BLASTX
NCBI GI
                  g4558549
BLAST score
                  377
```



% identity (AC007138) putative SecA-type chloroplast protein transport NCBI Description factor [Arabidopsis thaliana] Seq. No. 141333 Seq. ID LIB25-096-Q1-E1-G5 Method BLASTN NCBI GI g3449330 BLAST score 65 E value 2.0e-28 Match length 133 % identity 87 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MDJ14, complete sequence [Arabidopsis thaliana] Seq. No. 141334 Seq. ID LIB25-096-Q1-E1-G6 Method BLASTX NCBI GI g4490706 280 BLAST score 2.0e-25 E value Match length 60 % identity 90 (AL035680) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 141335 LIB25-096-Q1-E1-H10 Seq. ID Method BLASTX NCBI GI g2104957 304 BLAST score 2.0e-28 E value 55 Match length % identity 100 (U96924) immunophilin [Arabidopsis thaliana] NCBI Description 141336 Seq. No. LIB25-096-Q1-E1-H2 Seq. ID Method BLASTN g166645 NCBI GI 116 BLAST score E value 7.0e-59 Match length 160 % identity Arabidopsis thaliana light-harvesting chlorophyll NCBI Description a/b-binding protein (Cab4) mRNA, complete cds Seq. No. 141337 LIB25-096-Q1-E1-H5 Seq. ID BLASTN Method NCBI GI g3869067 BLAST score 215

E value 1.0e-118 215 Match length 100 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MCK7, complete sequence [Arabidopsis thaliana]

E value Match length

% identity

NCBI Description

```
Seq. No.
                  141338
                  LIB25-097-Q1-E1-A11
Seq. ID
Method
                  BLASTX
                  g2244959
NCBI GI
                  242
BLAST score
                  5.0e-21
E value
                  53
Match length
                  89
% identity
                  (Z97340) similar to B.vulgaris CMS-associated mitochondrial
NCBI Description
                  ... (reverse transcriptase) [Arabidopsis thaliana]
                  141339
Seq. No.
                  LIB25-097-Q1-E1-A2
Seq. ID
Method
                  BLASTX
                  g2853080
NCBI GI
                  296
BLAST score
                  3.0e-27
E value
                  66
Match length
                  88
% identity
                   (AL021768) TMV resistance protein N-like [Arabidopsis
NCBI Description
                  thaliana]
                  141340
Seq. No.
                  LIB25-097-Q1-E1-A4
Seq. ID
Method
                  BLASTN
                  g3414927
NCBI GI
                  200
BLAST score
                  1.0e-109
E value
                  212
Match length
                  99
% identity
                  Arabidopsis thaliana PsbY precursor (psbY) mRNA, nuclear
NCBI Description
                  gene encoding chloroplast protein, complete cds
Seq. No.
                   141341
                  LIB25-097-Q1-E1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2501056
                   274
BLAST score
                   8.0e-25
E value
Match length
                   54
                   100
% identity
                  SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)
NCBI Description
                   >gi_2129737_pir__S71293 seryl-tRNA synthetase - Arabidopsis
                   thaliana >gi 1359497 emb CAA94388 (Z70313) seryl-tRNA
                   Synthetase [Arabidopsis thaliana]
                   141342
Seq. No.
                   LIB25-097-Q1-E1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3337091
BLAST score
                   143
```

2.0e-09

unshiu]

47

55

(AB016204) polygalacturonase inhibitor (PGIP) [Citrus



```
141343
Seq. No.
Seq. ID
                  LIB25-097-Q1-E1-C9
Method
                  BLASTN
NCBI GI
                  q4263373
                  109
BLAST score
                  1.0e-54
E value
Match length
                  170
                  100
% identity
                  Arabidopsis thaliana BAC T15G18 from chromosome IV, near 25
NCBI Description
                  cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141344
Seq. ID
                  LIB25-097-Q1-E1-D12
                  BLASTX
Method
                  q730583
NCBI GI
                  148
BLAST score
                  5.0e-10
E value
Match length
                  46
% identity
                  67
                  60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 551267 emb CAA55047_
NCBI Description
                   (X78213) 60s acidic ribosomal protein P2 [Parthenium
                  argentatum]
Seq. No.
                  141345
                  LIB25-097-Q1-E1-D7
Seq. ID
Method
                  BLASTN
                  q4580530
NCBI GI
                  100
BLAST score
E value
                  2.0e-49
                  100
Match length
                  100
% identity
                  Arabidopsis thaliana scarecrow-like 14 (SCL14) mRNA,
NCBI Description
                  partial cds
Seq. No.
                  141346
Seq. ID
                  LIB25-097-Q1-E1-D9
Method
                  BLASTN
NCBI GI
                   q2854069
BLAST score
                   160
E value
                   5.0e-85
Match length
                   160
                   100
% identity
                  Arabidopsis thaliana putative histone deacetylase (HD2)
NCBI Description
                  mRNA, complete cds
Seq. No.
                   141347
Seq. ID
                  LIB25-097-Q1-E1-E10
Method
                  BLASTX
                   q3128228
NCBI GI
BLAST score
                   314
                   2.0e-29
E value
                   59
Match length
                   100
% identity
                   (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                   thaliana] >gi 3337376 (AC004481) putative ribosomal protein
```

L18A [Arabidopsis thaliana]

```
Seq. No.
                  141348
                  LIB25-097-Q1-E1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4240115
BLAST score
                  190
E value
                  1.0e-103
Match length
                  190
                  100
% identity
                  Arabidopsis thaliana mRNA for NADH-cytochrome b5 reductase,
NCBI Description
                  complete cds
Seq. No.
                  141349
Seq. ID
                  LIB25-097-Q1-E1-E12
Method
                  BLASTX
NCBI GI
                  a542200
BLAST score
                  248
E value
                  9.0e-22
Match length
                  67
                  69
% identity
                  hypothetical protein - garden asparagus
NCBI Description
                  >gi 452714 emb CAA54526_ (X77320) unknown [Asparagus
                  officinalis]
Seq. No.
                  141350
                  LIB25-097-Q1-E1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2507281
BLAST score
                  383
E value
                  3.0e-37
Match length
                  69
% identity
                  100
                  GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi 1668706 emb CAA66048_
NCBI Description
                  (X97380) atran2 [Arabidopsis thaliana]
Seq. No.
                  141351
                  LIB25-097-Q1-E1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g115767
                  249
BLAST score
                  7.0e-22
E value
                  50
Match length
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
                  141352
Seq. No.
Seq. ID
                  LIB25-097-Q1-E1-F9
Method
                  BLASTX
```

NCBI GI g1169544 BLAST score 343 E value 6.0e-33 Match length 68

Seq. No. 141353

Seq. ID LIB25-097-Q1-E1-G10

Method BLASTX
NCBI GI g3335353
BLAST score 223
E value 8.0e-19
Match length 64
% identity 64

NCBI Description (AC004512) Similar to cytochrome P450 gb_X90458 from A.

thaliana. [Arabidopsis thaliana]

Seq. No. 141354

Seq. ID LIB25-097-Q1-E1-H11

Method BLASTX
NCBI GI g1465368
BLAST score 306
E value 1.0e-28
Match length 66
% identity 85

NCBI Description (X99548) bHLH protein [Arabidopsis thaliana]

Seq. No. 141355

Seq. ID LIB25-098-Q1-E1-A2

Method BLASTN
NCBI GI g3128137
BLAST score 120
E value 2.0e-61
Match length 120
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9I9, complete sequence [Arabidopsis thaliana]

Seq. No. 141356

Seq. ID LIB25-098-Q1-E1-B2

Method BLASTX
NCBI GI 94432835
BLAST score 296
E value 6.0e-27
Match length 102
% identity 53

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 141357

Seq. ID LIB25-098-Q1-E1-C11

Method BLASTN
NCBI GI g430946
BLAST score 141
E value 7.0e-74
Match length 141
% identity 100

NCBI Description Arabidopsis thaliana PSI type III chlorophyll a/b-binding

protein (Lhca3*1) mRNA, complete cds

NCBI Description



```
Seq. No.
                  141358
                  LIB25-098-Q1-E1-D3
Seq. ID
Method
                  BLASTX
                  g2129577
NCBI GI
BLAST score
                  272
E value
                   4.0e-24
Match length
                   51
                   100
% identity
                  DnaJ homolog protein - Arabidopsis thaliana >gi 727357
NCBI Description
                   (U22340) DnaJ homolog [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB25-098-Q1-E1-F12
Method
                  BLASTN
NCBI GI
                   q3702734
BLAST score
                   245
E value
                   1.0e-135
                   377
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MNB8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   141360
                   LIB25-098-Q1-E1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1176604
BLAST score
                   174
E value
                   1.0e-12
Match length
                   102
% identity
                   HYPOTHETICAL 37.4 KD PROTEIN T09A5.9 IN CHROMOSOME III
NCBI Description
                   >gi_3879646_emb_CAA85336 (Z36753) similar to SDS22
                   protein; cDNA EST yk434d3.3 comes from this gene
                   [Caenorhabditis elegans]
Seq. No.
                   141361
Seq. ID
                   LIB25-098-Q1-E1-G5
Method
                   BLASTN
                   g2564049
NCBI GI
BLAST score
                   376
                   0.0e+00
E value
                   376
Match length
% identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MLE2, complete sequence [Arabidopsis thaliana]
                   141362
Seq. No.
Seq. ID
                   LIB25-098-Q1-E1-G7
                   BLASTX
Method
                   g2244935
NCBI GI
                   313
BLAST score
                   6.0e-29
E value
                   98
Match length
                   69
% identity
```

(Z97339) hypothetical protein [Arabidopsis thaliana]

Method



```
Seq. No.
                   141363
                  LIB25-098-Q1-E1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738257
BLAST score
                   349
E value
                   4.0e-33
Match length
                  76
% identity
                  89
                  (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
NCBI Description
Seq. No.
                   141364
Seq. ID
                  LIB25-099-Q1-E1-B11
Method
                  BLASTN
NCBI GI
                   q3193311
BLAST score
                   173
E value
                   1.0e-92
Match length
                   324
                   98
% identity
NCBI Description Arabidopsis thaliana BAC F6N15
                   141365
Seq. No.
Seq. ID
                  LIB25-099-Q1-E1-C4
Method
                  BLASTX
NCBI GI
                  q3738338
BLAST score
                   488
E value
                   2.0e-49
Match length
                   99
% identity
                   98
                   (AC005170) putative polygalacturonase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   141366
Seq. ID
                   LIB25-099-Q1-E1-C6
Method
                   BLASTN
                   g2924729
NCBI GI
BLAST score
                   201
                   1.0e-109
E value
                   327
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MNA5, complete sequence [Arabidopsis thaliana]
                   141367
Seq. No.
Seq. ID
                   LIB25-099-Q1-E1-C8
                   {\tt BLASTN}
Method
                   g2351067
NCBI GI
BLAST score
                   225
E value
                   1.0e-123
                   399
Match length
                   50
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MPO12, complete sequence [Arabidopsis thaliana]
                   141368
Seq. No.
Seq. ID
                   LIB25-099-Q1-E1-D3
```

17238

BLASTN

Method

NCBI GI

BLASTX q267079



```
NCBI GI
                  q2264314
BLAST score
                  416
                  0.0e+00
E value
Match length
                   416
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQK4, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141369
Seq. ID
                  LIB25-099-Q1-E1-D4
Method
                  BLASTX
NCBI GI
                  q4388717
BLAST score
                   415
E value
                  8.0e-41
Match length
                  119
                   28
% identity
NCBI Description
                   (AC006413) putative nuclear phosphoprotein (contains
                  multiple TPR repeats prosite:QDOC50005) [Arabidopsis
                  thaliana]
Seq. No.
                   141370
Seq. ID
                  LIB25-099-Q1-E1-D7
Method
                  BLASTX
NCBI GI
                   g733554
BLAST score
                   355
E value
                   9.0e - 34
Match length
                   112
                   59
% identity
NCBI Description
                   (U23450) similar to RNA-binding protein [Caenorhabditis
                   elegans]
                   141371
Seq. No.
Seq. ID
                   LIB25-099-Q1-E1-E7
Method
                   BLASTN
NCBI GI
                   g4580386
BLAST score
                   287
                   1.0e-160
E value
                   295
Match length
% identity
                   99
                  Arabidopsis thaliana chromosome II BAC T8018 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   141372
Seq. ID
                   LIB25-099-Q1-E1-E9
                   BLASTN
Method
                   g4079614
NCBI GI
BLAST score
                   180
                   1.0e-96
E value
                   373
Match length
                   100
% identity
                  Arabidopsis thaliana chromosome I BAC F21M11 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   141373
Seq. ID
                   LIB25-099-Q1-E1-F9
```

BLAST score

E value

158

7.0e-84



```
BLAST score
                  9.0e-62
E value
                  107
Match length
                  100
% identity
                  TUBULIN BETA-6 CHAIN >gi 320187 pir JQ1590 tubulin beta-6
NCBI Description
                  chain - Arabidopsis thaliana >gi 166904 (M84703) beta-6
                  tubulin [Arabidopsis thaliana]
                  141374
Seq. No.
Seq. ID
                  LIB25-100-Q1-E1-A9
                  BLASTX
Method
NCBI GI
                  g3953475
BLAST score
                  163
E value
                  3.0e-11
                  56
Match length
% identity
                  52
NCBI Description (AC002328) F2202.20 [Arabidopsis thaliana]
Seq. No.
                  141375
Seq. ID
                  LIB25-100-Q1-E1-D4
Method
                  BLASTX
NCBI GI
                  g3643598
BLAST score
                  556
                  2.0e-57
E value
                  107
Match length
                  100
% identity
                   (AC005395) putative poly(A) polymerase [Arabidopsis
NCBI Description
                  thaliana]
                  141376
Seq. No.
Seq. ID
                  LIB25-100-Q1-E1-F7
Method
                  BLASTX
                  g3420049
NCBI GI
BLAST score
                  635
                  1.0e-66
E value
Match length
                  122
% identity
                   (AC004680) putative protein phosphatase 2C [Arabidopsis
NCBI Description
                  thaliana]
                  141377
Seq. No.
Seq. ID
                  LIB25-100-Q1-E1-H9
Method
                  BLASTN
NCBI GI
                  q4376087
BLAST score
                  92
                  2.0e-44
E value
Match length
                  124
                   94
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                  fragment No
Seq. No.
                  141378
Seq. ID
                  LIB25-101-Q1-E1-B4
Method
                  BLASTN
NCBI GI
                  g2924505
```



Match length 202 % identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13

(ESSAII project)

Seq. No. 141379

Seq. ID LIB25-101-Q1-E1-D12

Method BLASTN
NCBI GI g4587986
BLAST score 59
E value 1.0e-24

Match length 71 % identity 96

NCBI Description Arabidopsis thaliana ABA-regulated gene cluster, complete

sequence

Seq. No. 141380

Seq. ID LIB25-102-Q1-E1-B1

Method BLASTN
NCBI GI g4558586
BLAST score 122
E value 4.0e-62
Match length 333
% identity 99

NCBI Description Arabidopsis thaliana chromosome 1 BAC T518 sequence,

complete sequence

Seq. No. 141381

Seq. ID LIB25-102-Q1-E1-D10

Method BLASTX
NCBI GI g115783
BLAST score 458
E value 6.0e-46
Match length 86
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 141382

Seq. ID LIB25-102-Q1-E1-D8

Method BLASTN
NCBI GI g3046855
BLAST score 339
E value 0.0e+00
Match length 339
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MSL1, complete sequence [Arabidopsis thaliana]

Seq. No. 141383

Seq. ID LIB25-102-Q1-E1-E11

Method BLASTN
NCBI GI g4467358
BLAST score 383
E value 0.0e+00



```
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana mRNA for Phosphatidylinositol 4-Kinase
                  141384
Seq. No.
Seq. ID
                  LIB25-102-Q1-E1-G7
                  BLASTN
Method
NCBI GI
                  g2583106
BLAST score
                  246
                  1.0e-136
E value
                  246
Match length
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC F4L23 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  141385
Seq. No.
Seq. ID
                  LIB25-102-Q1-E1-G8
                  BLASTX
Method
                  g1617013
NCBI GI
                  220
BLAST score
                  4.0e-18
E value
Match length
                  45
                  98
% identity
                  (Y07745) histone H2B like protein [Arabidopsis thaliana]
NCBI Description
                  141386
Seq. No.
Seq. ID
                  LIB25-103-Q1-E1-D1
Method
                  BLASTX
                  g3860262
NCBI GI
                  434
BLAST score
                  4.0e-43
E value
Match length
                  99
% identity
                  80
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                  141387
Seq. No.
Seq. ID
                  LIB25-103-Q1-E1-F1
                  BLASTX
Method
NCBI GI
                  g3152590
BLAST score
                  240
                  2.0e-20
E value
Match length
                  76
% identity
                  66
                  (AC002986) Similar to protein serine/threonine kinase NPK15
NCBI Description
                  gb_D31737 from Nicotiana tabacum. [Arabidopsis thaliana]
```

141388 Seq. No.

LIB25-103-Q1-E1-F7 Seq. ID

Method BLASTX q473874 NCBI GI BLAST score 152 E value 5.0e-10 116 Match length % identity

NCBI Description (U08285) a membrane-associated salt-inducible protein

[Nicotiana tabacum]



```
Seq. No.
                  141389
Seq. ID
                  LIB25-104-Q1-E1-A12
Method
                  BLASTN
NCBI GI
                  g4757403
BLAST score
                  140
E value
                  7.0e-73
Match length
                  337
                  100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MJL12, complete sequence
                  141390
Seq. No.
                  LIB25-104-Q1-E1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3510344
BLAST score
                  163
E value
                  1.0e-86
Match length
                  354
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MJG14, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141391
Seq. ID
                  LIB25-104-Q1-E1-B5
Method
                  BLASTX
NCBI GI
                  g1531762
                  155
BLAST score
E value
                  2.0e-10
Match length
                  44
                  70
% identity
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
                  141392
Seq. No.
Seq. ID
                  LIB25-104-Q1-E1-B8
Method
                  BLASTX
NCBI GI
                  g625977
BLAST score
                  471
                  2.0e-47
E value
Match length
                  92
% identity
                  100
                  p40 protein homolog - Arabidopsis thaliana >gi 402904
NCBI Description
                   (U01955) laminin receptor-like protein [Arabidopsis
                  thaliana]
                  141393
Seq. No.
Seq. ID
                  LIB25-104-Q1-E1-C11
Method
                  BLASTX
NCBI GI
                  q1617013
BLAST score
                  262
E value
                  6.0e-23
Match length
                  52
% identity
                  100
NCBI Description (Y07745) histone H2B like protein [Arabidopsis thaliana]
```

Seq. No. 141394

Seq. ID LIB25-104-Q1-E1-C3



```
Method
                  BLASTN
NCBI GI
                  q3176701
BLAST score
                  249
E value
                  1.0e-138
Match length
                  317
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC T20K24 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141395
Seq. ID
                  LIB25-104-Q1-E1-C5
Method
                  BLASTN
NCBI GI
                  q2351064
BLAST score
                  248
E value
                  1.0e-137
Match length
                  326
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDJ22, complete sequence [Arabidopsis thaliana]
                  141396
Seq. No.
Seq. ID
                  LIB25-104-Q1-E1-D6
Method
                  BLASTN
NCBI GI
                  g2264310
BLAST score
                  324
E value
                  0.0e + 00
                  324
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MKP11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   141397
Seq. ID
                  LIB25-104-Q1-E1-D8
Method
                  BLASTX
NCBI GI
                  g1362005
                   562
BLAST score
                   4.0e-58
E value
                   116
Match length
% identity
                   98
                  secY protein homolog precursor - Arabidopsis thaliana
NCBI Description
                   141398
Seq. No.
Seq. ID
                  LIB25-104-Q1-E1-E12
Method
                  BLASTN
NCBI GI
                   g2654008
BLAST score
                   142
                   4.0e-74
E value
Match length
                   242
                   100
% identity
                  Arabidopsis thaliana Rho-like GTP binding protein (Rop4)
NCBI Description
                  mRNA, complete cds
                   141399
Seq. No.
```

Seq. ID LIB25-104-Q1-E1-F8 BLASTN Method

NCBI GI g2098816 BLAST score 352



0.0e+00 E value 352 Match length 100 % identity

Arabidopsis thaliana BAC F19G10, complete sequence NCBI Description

Seq. No. 141400

LIB25-104-Q1-E1-F9 Seq. ID

BLASTN Method g2494106 NCBI GI BLAST score 295 1.0e-165 E value 332 Match length % identity 97

Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, NCBI Description

complete sequence [Arabidopsis thaliana]

Seq. No. 141401

LIB25-104-Q1-E1-G3 Seq. ID

Method BLASTX NCBI GI g131398 BLAST score 434 E value 4.0e-43 Match length 104 % identity 86

PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description

> >gi 72714 pir F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi 16447 emb CAA39441 (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi 3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400

come from this gene. [Arabidopsis

141402 Seq. No.

Seq. ID LIB25-104-Q1-E1-H10

BLASTX Method g2911075 NCBI GI 320 BLAST score 9.0e-30 E value 113 Match length 56 % identity

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

141403 Seq. No.

Seq. ID LIB25-104-Q1-E1-H5

BLASTX Method NCBI GI g4539316 BLAST score 486 E value 3.0e-49100 Match length % identity 100

(AL035679) putative fructose-bisphosphate aldolase NCBI Description

[Arabidopsis thaliana]

Seq. No. 141404

Seq. ID LIB25-104-Q1-E1-H9



100

BLASTX Method g4455156 NCBI GI BLAST score 538 2.0e-55 E value 102 Match length

% identity (AL021712) CDP-diacylglycerol synthetase-like protein NCBI Description

[Arabidopsis thaliana]

Seq. No. 141405

Seq. ID LIB25-105-Q1-E1-B12

BLASTN Method NCBI GI q3702732 351 BLAST score 0.0e + 00E value 351 Match length % identity 100

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MGF10, complete sequence [Arabidopsis thaliana]

141406 Seq. No.

LIB25-105-Q1-E1-B4 Seq. ID

Method BLASTN NCBI GI q2570223 BLAST score 209 1.0e-114 E value Match length 255 % identity 94

Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, NCBI Description

complete sequence [Arabidopsis thaliana]

Seq. No. 141407

Seq. ID LIB25-105-Q1-E1-B7

BLASTN Method g2564047 NCBI GI 314 BLAST score 1.0e-176 E value 314 Match length 100 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MJB21, complete sequence [Arabidopsis thaliana]

141408 Seq. No.

Seq. ID LIB25-105-Q1-E1-C7

Method BLASTN NCBI GI q4580744 BLAST score 174 4.0e-93 E value Match length 371 98 % identity

Sequence of BAC F15I1 from Arabidopsis thaliana chromosome NCBI Description

1, complete sequence

141409 Seq. No.

Seq. ID LIB25-105-Q1-E1-D12

Method BLASTX NCBI GI g1542941

```
BLAST score
E value
                  5.0e-15
Match length
                  64
% identity
                  62
NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
Seq. No.
                  141410
Seq. ID
                  LIB25-105-Q1-E1-D8
Method
                  BLASTN
NCBI GI
                  q2059328
BLAST score
                  179
E value
                  4.0e-96
Match length
                  372
                  98
% identity
NCBI Description A.thaliana gene encoding shaggy-like kinase gamma
Seq. No.
                  141411
Seq. ID
                  LIB25-105-Q1-E1-E8
Method
                  BLASTX
NCBI GI
                  q1707032
BLAST score
                  327
E value
                  2.0e-30
Match length
                  122
% identity
                  30
NCBI Description
                  (U80445) coded for by C. elegans cDNA yk13g5.3; coded for
                  by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA
                  CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for
                  by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA
                  yk65h8
Seq. No.
                  141412
Seq. ID
                  LIB25-105-Q1-E1-F4
Method
                  BLASTX
NCBI GI
                  g1585970
BLAST score
                  321
                  8.0e-30
E value
Match length
                  118
% identity
                  51
NCBI Description cellulase [Lathyrus odoratus]
Seq. No.
                  141413
```

Seq. ID LIB25-105-Q1-E1-F6

Method BLASTX NCBI GI g4038044 BLAST score 515 E value 1.0e-52 Match length 123 78 % identity

(AC005936) unknown protein [Arabidopsis thaliana] NCBI Description

>gi 4406788 gb AAD20098 (AC006532) unknown protein

[Arabidopsis thaliana]

141414 Seq. No.

Seq. ID LIB25-105-Q1-E1-G3

BLASTN Method NCBI GI g4757401 BLAST score 328



```
E value 0.0e+00
Match length 416
% identity 62
NCBL Description Arabido:
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGH6, complete sequence

Seq. No. 141415

Seq. ID LIB25-105-Q1-E1-G8

Method BLASTX
NCBI GI g639722
BLAST score 474
E value 9.0e-48
Match length 117
% identity 76

NCBI Description (L27484) calcium-dependent protein kinase [Zea mays]

Seq. No. 141416

Seq. ID LIB25-105-Q1-E1-H1

Method BLASTX
NCBI GI g3033375
BLAST score 544
E value 5.0e-56
Match length 110
% identity 99

NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis

thaliana]

Seq. No. 141417

Seq. ID LIB25-105-Q1-E1-H3

Method BLASTX
NCBI GI g1864017
BLAST score 512
E value 3.0e-52
Match length 102
% identity 94

NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No. 141418

Seq. ID LIB25-106-Q1-E1-E5

Method BLASTN
NCBI GI g1707006
BLAST score 250
E value 1.0e-138
Match length 298
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC T1B8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 141419

Seq. ID LIB25-106-Q1-E1-F6

Method BLASTX
NCBI GI 9417103
BLAST score 623
E value 4.0e-65
Match length 124
% identity 100

NCBI Description HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone



H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
(U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460)
histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone
H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2
[Medicago sativa] >gi_488577 (U09465) histone H3.2
[Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone
H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422)
histone H3 variant H3.3 [Lycopersicon esculentum]
>gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]
>gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana
tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]
>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia
coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone
H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_
(AL035708) Histon H3 [Arabidopsis thaliana]

```
141420
Seq. No.
Seq. ID
                  LIB25-106-Q1-E1-H11
Method
                  BLASTX
NCBI GI
                  q4335748
BLAST score
                  333
                  2.0e-31
E value
Match length
                   68
                  100
% identity
                   (AC006284) putative A3 protein [Vigna unguiculata]
NCBI Description
                   (integral membrane protein) [Arabidopsis thaliana]
Seq. No.
                  141421
Seq. ID
                  LIB25-107-Q1-E1-D6
Method
                  BLASTX
NCBI GI
                  q3776005
BLAST score
                  597
E value
                   4.0e-62
Match length
                  131
% identity
                   90
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]
Seq. No.
                   141422
Seq. ID
                  LIB25-107-Q1-E1-E11
Method
                  BLASTX
NCBI GI
                  g136636
BLAST score
                   406
                   8.0e-40
E value
Match length
                  76
% identity
                   99
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                  >gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -
```

[Arabidopsis thaliana]

Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme



Seq. No. Seq. ID

141423

LIB25-107-Q1-E1-E2

```
Method
                  BLASTN
NCBI GI
                  g2244991
BLAST score
                  306
E value
                   1.0e-172
Match length
                   306
                   100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
Seq. No.
                  141424
Seq. ID
                  LIB25-107-Q1-E1-F2
Method
                  BLASTN
NCBI GI
                  g2264317
BLAST score
                   306
E value
                   1.0e-172
Match length
                   306
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUG13, complete sequence [Arabidopsis thaliana]
Seq. No.
                   141425
Seq. ID
                  LIB25-107-Q1-E1-F5
Method
                  BLASTX
NCBI GI
                   q3522961
BLAST score
                   218
E value
                   3.0e-18
Match length
                   47
% identity
                   89
                   (AC004411) putative pto kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   141426
Seq. ID
                   LIB25-107-Q1-E1-F7
Method
                   BLASTN
                   g4581084
NCBI GI
                   149
BLAST score
                   2.0e-78
E value
                   181
Match length
% identity
                   96
                  Arabidopsis thaliana chromosome I BAC T30F21 genomic
NCBI Description
                   sequence, complete sequence
                   141427
Seq. No.
Seq. ID
                   LIB25-107-Q1-E1-G9
Method
                   BLASTX
                   g2911886
NCBI GI
BLAST score
                   162
E value
                   1.0e-11
                   52
Match length
                   67
% identity
                  (AF047663) contains similarity to signal recognition
NCBI Description
                   particle subunit 54 (SRP54)-type domains (Pfam; SRP54,
                   score; 71.31); partial CDS [Caenorhabditis elegans]
Seq. No.
                   141428
```

Method

NCBI GI

BLASTN

q2264307



```
LIB25-108-Q1-E1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4165488
                  554
BLAST score
                   4.0e-57
E value
Match length
                  102
% identity
                  100
                  (AJ132399) alpha-tubulin 3 [Hordeum vulgare]
NCBI Description
Seq. No.
                  141429
                  LIB25-108-Q1-E1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2924651
BLAST score
                  350
                  0.0e+00
E value
Match length
                  361
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K2A18, complete sequence [Arabidopsis thaliana]
Seq. No.
                   141430
Seq. ID
                  LIB25-108-Q1-E1-G11
Method
                  BLASTX
NCBI GI
                   g2832674
BLAST score
                   486
E value
                   5.0e-49
Match length
                   132
% identity
                   77
                   (AL021712) fibrillin precursor-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   141431
Seq. No.
Seq. ID
                  LIB25-108-Q1-E1-G8
                  BLASTN
Method
                   g3492855
NCBI GI
                   130
BLAST score
                   5.0e-67
E value
                   178
Match length
                   100
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F20N2,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   141432
Seq. ID
                  LIB25-109-Q1-E1-A12
Method
                  BLASTN
NCBI GI
                   g2264309
BLAST score
                   108
E value
                   4.0e-54
Match length
                   164
% identity
                   91
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
NCBI Description
                  MJJ3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   141433
Seq. ID
                  LIB25-109-Q1-E1-B10
```



```
BLAST score
                  1.0e-129
E value
                  258
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MED24, complete sequence [Arabidopsis thaliana]
                  141434
Seq. No.
Seq. ID
                  LIB25-109-Q1-E1-B7
Method
                  BLASTX
                  q1173045
NCBI GI
BLAST score
                  472
                  1.0e-47
E value
                  92
Match length
                  100
% identity
                  60S RIBOSOMAL PROTEIN L37A >gi 421866 pir S34661 ribosomal
NCBI Description
                  protein L37a - turnip >gi_347062 (L21897) ribosomal protein
                  [Brassica rapa] >gi_395077_emb_CAA80864_ (Z24739) ribosomal
                  protein L37a [Brassica rapa]
Seq. No.
                  141435
Seq. ID
                  LIB25-109-Q1-E1-C2
Method
                  BLASTN
NCBI GI
                  g3299824
BLAST score
                  128
E value
                  9.0e-66
Match length
                  317
% identity
                  100
                  Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,
NCBI Description
                  near 17 cM, complete sequence [Arabidopsis thaliana]
                  141436
Seq. No.
Seq. ID
                  LIB25-109-Q1-E1-D3
Method
                  BLASTN
NCBI GI
                  g4468801
                  90
BLAST score
                  2.0e-43
E value
Match length
                  118
                  92
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17
NCBI Description
                  (ESSA project)
Seq. No.
                  141437
                  LIB25-109-Q1-E1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4741952
BLAST score
                  500
E value
                  7.0e-51
Match length
                  94
% identity
                  100
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

Seq. ID LIB25-109-Q1-E1-E8

141438

Method BLASTN
NCBI GI g2252823
BLAST score 311

% identity

39



```
E value
                   1.0e-175
Match length
                  311
% identity
                  100
                  Arabidopsis thaliana BAC IG005I10
NCBI Description
Seq. No.
                  141439
                  LIB25-109-Q1-E1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3128135
BLAST score
                  79
                  7.0e-37
E value
Match length
                  119
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19E1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141440
Seq. ID
                  LIB25-109-Q1-E1-H11
Method
                  BLASTX
NCBI GI
                  q2499811
BLAST score
                  200
E value
                   1.0e-15
Match length
                   37
% identity
                   97
                  PROFILIN 2 >gi_1353766 (U43323) profilin 2 [Arabidopsis
NCBI Description
                   thaliana] >gi 1353772 (U43326) profilin 2 [Arabidopsis
                  thaliana]
Seq. No.
                   141441
Seq. ID
                  LIB25-110-Q1-E1-A8
Method
                   BLASTX
NCBI GI
                   g3250695
BLAST score
                   184
E value
                   1.0e-13
Match length
                   76
% identity
                   49
                  (AL024486) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   141442
Seq. ID
                   LIB25-110-Q1-E1-B11
                  BLASTN
Method
NCBI GI
                   g2264318
BLAST score
                   409
                   0.0e+00
E value
                   412
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUP24, complete sequence [Arabidopsis thaliana]
                   141443
Seq. No.
Seq. ID
                   LIB25-110-Q1-E1-B2
Method
                  BLASTX
NCBI GI
                   g4512663
BLAST score
                   638
                   5.0e-67
E value
                   119
Match length
```

E value Match length

% identity



```
(AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4544470 gb AAD22377.1 AC006580 9 (AC006580)
                  hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  141444
Seq. ID
                  LIB25-110-Q1-E1-B7
Method
                  BLASTN
                  g4309683
NCBI GI
BLAST score
                  352
E value
                  0.0e + 00
Match length
                  352
% identity
                  100
                  Arabidopsis thaliana chromosome 1 BAC T31J12 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  141445
Seq. ID
                  LIB25-110-Q1-E1-C10
Method
                  BLASTX
NCBI GI
                  q4559358
BLAST score
                  150
E value
                  1.0e-09
Match length
                  50
% identity
                  50
                   (AC006585) putative steroid binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  141446
Seq. ID
                  LIB25-110-Q1-E1-C2
Method
                  BLASTN
NCBI GI
                  g2351062
BLAST score
                  105
                  2.0e-52
E value
Match length
                  139
                  92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAH20, complete sequence [Arabidopsis thaliana]
                  141447
Seq. No.
Seq. ID
                  LIB25-110-Q1-E1-C9
Method
                  BLASTN
                  g4455262
NCBI GI
BLAST score
                  293
                  1.0e-164
E value
Match length
                   361
                   94
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
NCBI Description
                   (ESSAII project)
Seq. No.
                  141448
                  LIB25-110-Q1-E1-E9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g166787
BLAST score
                  121
```

17254

NCBI Description A.thaliana chloroplast ATP synthase gamma subunit (atpC2)

9.0e-62



gene, complete cds

```
Seq. No.
                  141449
Seq. ID
                  LIB25-110-Q1-E1-F5
Method
                  BLASTN
NCBI GI
                  g4063737
BLAST score
                  345
E value
                  0.0e + 00
Match length
                  345
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F24D13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141450
Seq. ID
                  LIB25-110-Q1-E1-H2
Method
                  BLASTN
NCBI GI
                  g3451055
BLAST score
                   331
E value
                  0.0e+00
Match length
                   376
% identity
                   57
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20
NCBI Description
                   (ESSAII project)
Seq. No.
                  141451
                  LIB25-111-Q1-E1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4567289
BLAST score
                   219
E value
                   6.0e-18
Match length
                   75
                   57
% identity
NCBI Description
                  (AC006841) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   141452
Seq. ID
                  LIB25-111-Q1-E1-A2
                  BLASTN
Method
                   q4220628
NCBI GI
BLAST score
                   373
                   0.0e+00
E value
                   389
Match length
                   77
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K24C1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   141453
                  LIB25-111-Q1-E1-B6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3242970
BLAST score
                   282
E value
                   1.0e-157
                   362
Match length
                   98
% identity
                  Arabidopsis thaliana BAC T4I9, chromosome IV, near 17 cM,
```

Seq. No. 141454

NCBI Description

complete sequence [Arabidopsis thaliana]



Seq. ID LIB25-111-Q1-E1-B8

Method BLASTX NCBI GI q2499610 BLAST score 450 E value 7.0e-45Match length 100 % identity

MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 6 (MAP KINASE 6) NCBI Description

(ATMPK6) >gi_629547_pir__S40472 mitogen-activated protein kinase 6 (EC 2.7.1.-) - Arabidopsis thaliana

>gi_457404_dbj_BAA04869_ (D21842) MAP kinase [Arabidopsis thaliana] >gi_2281091 (AC002333) MAP Kinase 6 [Arabidopsis

thaliana]

141455 Seq. No.

Seq. ID LIB25-111-Q1-E1-C9

Method BLASTN NCBI GI g166589 BLAST score 386 E value 0.0e + 00386 Match length 100 % identity

NCBI Description Arabidopsis thaliana transcription factor (AGL2) mRNA,

complete cds

Seq. No. 141456

Seq. ID LIB25-111-Q1-E1-D2

Method BLASTX NCBI GI g1071912 BLAST score 568 E value 1.0e-58 Match length 127 % identity 90

cysteine synthase (EC 4.2.99.8) cpACS1 - Arabidopsis NCBI Description

thaliana >gi 572517 emb CAA57344 (X81698) cysteine

synthase [Arabidopsis thaliana]

Seq. No. 141457

Seq. ID LIB25-111-Q1-E1-D4

BLASTN Method g2351066 NCBI GI 271 BLAST score E value 1.0e-151 413 Match length 98 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MOP9, complete sequence [Arabidopsis thaliana]

Seq. No. 141458

Seq. ID LIB25-111-Q1-E1-D5

Method BLASTX NCBI GI g2924521 BLAST score 513 3.0e-52 E value Match length 109 88 % identity

NCBI Description (AL022023) putative protein [Arabidopsis thaliana]



```
Seq. No.
                  141459
Seq. ID
                  LIB25-111-Q1-E1-D6
Method
                  BLASTX
                  g2829899
NCBI GI
                  374
BLAST score
E value
                  6.0e-36
                  107
Match length
% identity
                   65
                   (AC002311) similar to ripening-induced protein,
NCBI Description
                   gp AJ001449 2465015 and major#latex protein,
                  gp X91961 1107495 [Arabidopsis thaliana]
Seq. No.
                  141460
                  LIB25-111-Q1-E1-E7
Seq. ID
Method
                  BLASTN
                  q1877523
NCBI GI
BLAST score
                   211
                  1.0e-115
E value
                   390
Match length
% identity
                  Arabidopsis thaliana BAC T7I23, complete sequence
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   141461
                  LIB25-111-Q1-E1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                   a3461821
BLAST score
                   596
E value
                   5.0e-62
Match length
                   118
                   99
% identity
                   (AC004138) putative nucleoside triphosphatase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   141462
Seq. ID
                   LIB25-111-Q1-E1-F3
Method
                   BLASTN
NCBI GI
                   q3805839
BLAST score
                   167
E value
                   6.0e-89
Match length
                   391
% identity
                   100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14
                   (ESSAII project)
Seq. No.
                   141463
Seq. ID
                   LIB25-111-Q1-E1-F5
Method
                   BLASTN
NCBI GI
                   g2351071
BLAST score
                   291
                   1.0e-163
E value
                   320
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

MVA3, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                  141464
                  LIB25-111-Q1-E1-F6
Seq. ID
                  BLASTX
Method
                  g4033469
NCBI GI
                  399
BLAST score
E value
                  7.0e-39
                  75
Match length
% identity
                  58
                  ARGININE/SERINE-RICH SPLICING FACTOR RSP41
NCBI Description
                  >gi_1707370_emb_CAA67799_ (X99436) splicing factor
                  [Arabidopsis thaliana]
Seq. No.
                  141465
                  LIB25-111-Q1-E1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2344896
BLAST score
                  135
E value
                  6.0e-08
Match length
                  134
                  7
% identity
                  (AC002388) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  141466
                  LIB25-111-Q1-E1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3128137
BLAST score
                  220
E value
                  1.0e-121
Match length
                  244
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9I9, complete sequence [Arabidopsis thaliana]
                  141467
Seq. No.
Seq. ID
                  LIB25-111-Q1-E1-H7
                  BLASTN
Method
                  g2632104
NCBI GI
                  130
BLAST score
                  2.0e-67
E value
                  130
Match length
                  100
% identity
                  Arabidopsis thaliana gene encoding arginyl-tRNA synthetase,
NCBI Description
                  clone G7
                  141468
Seq. No.
Seq. ID
                  LIB25-112-Q1-E1-A2
```

BLASTN Method g3860243 NCBI GI BLAST score 402 0.0e+00E value 402 Match length 100 % identity

Arabidopsis thaliana chromosome II BAC F15K20 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

141469 Seq. No.

LIB25-112-Q1-E1-A8 Seq. ID



```
Method
                  BLASTX
NCBI GI
                  q4581146
BLAST score
                  607
                  3.0e-63
E value
                  121
Match length
                  100
% identity
                  (AC006919) putative fructose-bisphosphate aldolase,
NCBI Description
                  cytoplasmic [Arabidopsis thaliana]
                  141470
Seq. No.
                  LIB25-112-Q1-E1-B12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2062153
BLAST score
                  128
                  8.0e-66
E value
Match length
                  128
                  100
% identity
                  Arabidopsis thaliana chromosome III BAC T02004 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141471
                  LIB25-112-Q1-E1-B5
Seq. ID
Method
                  BLASTN
                  g2494106
NCBI GI
BLAST score
                  205
                  1.0e-112
E value
Match length
                  205
% identity
                  100
                  Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  141472
Seq. No.
                  LIB25-112-Q1-E1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4191774
BLAST score
                  255
E value
                  6.0e-22
Match length
                  96
% identity
                  (AC005917) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                  thaliana]
                  141473
Seq. No.
Seq. ID
                  LIB25-112-Q1-E1-C6
Method
                  BLASTX
NCBI GI
                  g4506717
BLAST score
                  224
                  2.0e-18
E value
Match length
                  54
% identity
                  72
NCBI Description
```

ribosomal protein S29 >gi_266972_sp_P30054_RS29_HUMAN 40S RIBOSOMAL PROTEIN S29 >gi_631884_pir__S30298 ribosomal protein S29 - rat >gi_1362934 pir__S55919 ribosomal protein S29 - human >gi_57133 emb_CAA41778_ (X59051) ribosomal protein S29 [Rattus norvegicus] >gi_550027 (U14973) ribosomal protein S29 [Homo sapiens] >gi_1220361 (L31610) homologous to antisense sequence of krev-1, anti oncogene





[Homo sapiens] >gi_1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi_1513230 (U66372) ribosomal protein S29 [Bos taurus] >gi_1096945_prf__2113200H ribosomal protein S29 [Homo sapiens]

Seq. No. 141474

Seq. ID LIB25-112-Q1-E1-C8

Method BLASTX
NCBI GI g4510399
BLAST score 377
E value 3.0e-36
Match length 65
% identity 100

NCBI Description (AC006587) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 141475

Seq. ID LIB25-112-Q1-E1-D11

Method BLASTN
NCBI GI g4191760
BLAST score 262
E value 1.0e-145
Match length 408
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17F8,

complete sequence [Arabidopsis thaliana]

Seq. No. 141476

Seq. ID LIB25-112-Q1-E1-D4

Method BLASTX
NCBI GI g119143
BLAST score 168
E value 8.0e-12
Match length 34
% identity 97

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_81606_pir__S06724 translation elongation factor eEF-1
alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
(X16430) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1369927_emb_CAA34454_ (X16431) elongation factor
1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_
(X16431) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
>gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
>gi_1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]

Seq. No. 141477

Seq. ID LIB25-112-Q1-E1-D6

Method BLASTX
NCBI GI g4826682
BLAST score 301
E value 2.0e-27
Match length 121
% identity 49

NCBI Description cystinosis, nephropathic >gi_3036840_emb_CAA11021_

(AJ222967) cystinosin [Homo sapiens]

>gi_3036851_emb_CAA75882_ (Y15924) cystinosin [Homo



sapiens]

Seq. No. 141478

Seq. ID LIB25-112-Q1-E1-E11

Method BLASTX
NCBI GI g4262235
BLAST score 413
E value 2.0e-40
Match length 105
% identity 77

NCBI Description (AC006200) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 141479

Seq. ID LIB25-112-Q1-E1-E2

Method BLASTX
NCBI GI g2341034
BLAST score 206
E value 2.0e-16
Match length 40
% identity 100

NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No. 141480

Seq. ID LIB25-112-Q1-E1-F10

Method BLASTN
NCBI GI g3927822
BLAST score 321
E value 0.0e+00
Match length 428
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F8N16 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 141481

Seq. ID LIB25-112-Q1-E1-F7

Method BLASTN
NCBI GI g3021263
BLAST score 223
E value 1.0e-122
Match length 434
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F21P8

(ESSAII project)

Seq. No. 141482

Seq. ID LIB25-112-Q1-E1-F8

Method BLASTX
NCBI GI g2252840
BLAST score 565
E value 3.0e-58
Match length 143
% identity 85

NCBI Description (AF013293) contains regions of similarity to Haemophilus

influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No. 141483



```
LIB25-112-Q1-E1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3522935
BLAST score
                  550
E value
                  1.0e-56
                  127
Match length
% identity
NCBI Description (AC004411) putative alcohol dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  141484
Seq. ID
                  LIB25-113-Q1-E1-A1
Method
                  BLASTX
NCBI GI
                  g2795809
BLAST score
                  531
E value
                  3.0e-54
Match length
                  101
% identity
                  97
NCBI Description (AC003674) putative expansin [Arabidopsis thaliana]
Seq. No.
                  141485
Seq. ID
                  LIB25-113-Q1-E1-B6
Method
                  BLASTX
NCBI GI
                  g2924779
BLAST score
                  662
E value
                  1.0e-69
Match length
                  139
% identity
                  94
NCBI Description (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
                  thaliana] >gi_2981616_dbj_BAA25248 (AB008854)
                  3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
                  >gi 2981618 dbj BAA25249 (AB008855) 3-ketoacyl-CoA
                  thiolase [Arabidopsis thaliana]
Seq. No.
                  141486
Seq. ID
                  LIB25-113-Q1-E1-B7
Method
                  BLASTX
NCBI GI
                  g2827714
BLAST score
                  163
E value
                  4.0e-11
Match length
                  142
                  5
% identity
NCBI Description (AL021684) receptor protein kinase - like protein
                  [Arabidopsis thaliana]
Seq. No.
                  141487
Seq. ID
                  LIB25-113-Q1-E1-C12
Method
                  BLASTN
NCBI GI
                  g4589450
BLAST score
                  279
E value
                  1.0e-156
Match length
                  304
                  97
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  T31K7, complete sequence
```

Seq. No. 141488

Seq. ID

Method



```
Seq. ID
                   LIB25-113-Q1-E1-C5
 Method
                   BLASTN
 NCBI GI
                   g3402695
BLAST score
                   59
E value
                   2.0e-24
Match length
                   115
% identity
                   88
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T3K9 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   141489
Seq. ID
                   LIB25-113-Q1-E1-C7
Method
                   BLASTN
NCBI GI
                   g3869069
BLAST score
                   51
E value
                   1.0e-19
Match length
                   79
% identity
                   91
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.
                   141490
Seq. ID
                   LIB25-113-Q1-E1-C8
Method
                   BLASTX
NCBI GI
                   g3687243
BLAST score
                   261
E value
                   1.0e-22
Match length
                   64
% identity
                   80
NCBI Description
                   (AC005169) putative ribosomal protein [Arabidopsis
                   thaliana]
Seq. No.
                   141491
Seq. ID
                  LIB25-113-Q1-E1-D5
Method
                  BLASTX
NCBI GI
                  g3600039
BLAST score
                  211
E value
                  8.0e-17
Match length
                  60
% identity
                   63
NCBI Description
                  (AF080119) similar to Schizosaccharomyces pombe isp4
                  protein (GB:D14061) [Arabidopsis thaliana]
Seq. No.
                  141492
Seq. ID
                  LIB25-113-Q1-E1-D7
Method
                  BLASTN
NCBI GI
                  g4757407
BLAST score
                  242
E value
                  1.0e-133
Match length
                  438
% identity
                  77
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MQD19, complete sequence
Seq. No.
                  141493
```

17263

LIB25-113-Q1-E1-E1

BLASTX



```
NCBI GI
                  q2351846
BLAST score
                  254
                  7.0é-22
E value
                  95
Match length
                  56
% identity
NCBI Description (U93050) poly(A) binding protein II [Mus musculus]
                  141494
Seq. No.
                  LIB25-113-Q1-E1-E7
Seq. ID
Method
                  BLASTX /
NCBI GI
                  q4678946
BLAST score
                  544
E value
                  8.0e-56
                  108
Match length
                  98
% identity
NCBI Description (AL049711) putative protein [Arabidopsis thaliana]
                  141495
Seq. No.
                  LIB25-113-Q1-E1-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q16151
BLAST score
                  119
E value
                  1.0e-60
Match length
                  119
% identity
                  100
NCBI Description Arabidopsis thaliana gene for acyl carrier protein
                  141496
Seq. No.
Seq. ID
                  LIB25-113-Q1-E1-F12
Method
                  BLASTN
NCBI GI
                  q2244901
BLAST score
                  178
                  1.0e-95
E value
Match length
                  329
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  141497
Seq. ID
                  LIB25-113-Q1-E1-G1
Method
                  BLASTX
NCBI GI
                  g3983125
BLAST score
                  640
E value
                  4.0e-67
Match length
                  146
% identity
                  84
                  (AF097648) phosphate/triose-phosphate translocator
NCBI Description
                  precursor [Arabidopsis thaliana]
Seq. No.
                  141498
Seq. ID
                  LIB25-113-Q1-E1-G7
                  BLASTN
Method
NCBI GI
                  g4589424
BLAST score
                  93
                  1.0e-44
E value
Match length
                  175
```

17264

89

% identity



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8E10, complete sequence

Seq. No. 141499

Seq. ID LIB25-113-Q1-E1-H1

Method BLASTX
NCBI GI g3522958
BLAST score 744
E value 3.0e-79
Match length 147
% identity 99

NCBI Description (AC004411) putative pectinesterase [Arabidopsis thaliana]

Seq. No. 141500

Seq. ID LIB25-113-Q1-E1-H3

Method BLASTX
NCBI GI g198884
BLAST score 153
E value 5.0e-10
Match length 119
% identity 35

NCBI Description (M63848) leukotriene A-4 hydrolase [Mus musculus]

Seq. No. 141501

Seq. ID LIB25-114-Q1-E1-C6

Method BLASTX
NCBI GI g4539307
BLAST score 379
E value 1.0e-36
Match length 105
% identity 75

NCBI Description (AL049480) putative acidic ribosomal protein [Arabidopsis

thaliana]

Seq. No. 141502

Seq. ID LIB25-114-Q1-E1-D8

Method BLASTX
NCBI GI g3297821
BLAST score 472
E value 2.0e-47
Match length 134
% identity 27

NCBI Description (AL031032) extensin-like protein [Arabidopsis thaliana]

Seq. No. 141503

Seq. ID LIB25-114-Q1-E1-F6

Method BLASTX
NCBI GI 94262149
BLAST score 474
E value 8.0e-48
Match length 92
% identity 100

NCBI Description (AC005275) putative xyloglucan endotransglycosylase

[Arabidopsis thaliana]

Seq. No. 141504

Seq. ID LIB25-114-Q1-E1-G11



Method BLASTN
NCBI GI g2760167
BLAST score 336
E value 0.0e+00
Match length 366
% identity 100
NCBI Description Arabidop

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCO15, complete sequence [Arabidopsis thaliana]

Seq. No. 141505

Seq. ID LIB25-115-Q1-E1-A4

Method BLASTX
NCBI GI g115767
BLAST score 563
E value 3.0e-58
Match length 107
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 141506

Seq. ID LIB25-115-Q1-E1-A9

Method BLASTX
NCBI GI g4115381
BLAST score 609
E value 2.0e-63
Match length 116
% identity 100

NCBI Description (AC005967) putative limonene cyclase [Arabidopsis thaliana]

Seq. No. 141507

Seq. ID LIB25-115-Q1-E1-C10

Method BLASTX
NCBI GI g4768978
BLAST score 249
E value 3.0e-21
Match length 122
% identity 46

NCBI Description (AF140489) kiaa0078 protein [Oryza sativa]

Seq. No. 141508

Seq. ID LIB25-115-Q1-E1-C8

Method BLASTN
NCBI GI g4757407
BLAST score 381
E value 0.0e+00
Match length 381
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQD19, complete sequence

Seq. No. 141509

Seq. No.

Seq. ID Method



```
LIB25-115-Q1-E1-D4
Seq. ID
                  BLASTX
Method
                  g4510400
NCBI GI
BLAST score
                  291
E value
                  2.0e-26
Match length
                   60
                   97
% identity
                   (AC006587) putative vacuolar-type H(+)-ATPase [Arabidopsis
NCBI Description
                  thaliana]
                  141510
Seq. No.
                  LIB25-115-Q1-E1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2829899
BLAST score
                  224
                   2.0e-18
E value
                   62
Match length
% identity
                   65
                   (AC002311) similar to ripening-induced protein,
NCBI Description
                  gp AJ001449 2465015 and major#latex protein,
                  gp X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                  141511
                  LIB25-115-Q1-E1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1762130
BLAST score
                  152
                   5.0e-10
E value
                   49
Match length
% identity
                   69
NCBI Description
                  (U46136) chaperonin-60 beta subunit [Solanum tuberosum]
Seq. No.
                  141512
Seq. ID
                  LIB25-115-Q1-E1-H2
Method
                  BLASTX
NCBI GI
                   g1531758
BLAST score
                   285
                   7.0e-26
E value
Match length
                   79
% identity
                   68
NCBI Description
                   (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)
                   unknown protein [Arabidopsis thaliana]
Seq. No.
                   141513
                   LIB25-115-Q1-E1-H9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3201608
BLAST score
                   217
                   1.0e-119
E value
Match length
                  217
                   100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7F1 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
```

17267

141514

BLASTN

LIB25-116-Q1-E1-A3



```
NCBI GI
BLAST score
                  247
E value
                  1.0e-137
                  251
Match length
                  100
% identity
NCBI Description A.thaliana mRNA for mevalonate kinase
                  141515
Seq. No.
Seq. ID
                  LIB25-116-Q1-E1-B1
Method
                  BLASTX
NCBI GI
                  q3688799
                  250
BLAST score
E value
                  5.0e-22
                  50
Match length
                  100
% identity
```

(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis NCBI Description thaliana]

Seq. No. 141516

Seq. ID LIB25-116-Q1-E1-B3

Method BLASTX NCBI GI g4220450 BLAST score 231 E value 2.0e-19 Match length 103 % identity 13

(AC006216) Identical to gb D85194 mRNA which is similar to NCBI Description

gb_AF054906 myrosinase-binding protein homolog from Arabidopsis thaliana. ESTs gb Z34045 and gb Z34877 come

from this gene. [Arabidopsis thaliana]

141517 Seq. No.

LIB25-116-Q1-E1-E6 Seq. ID

Method BLASTN q3413696 NCBI GI BLAST score 313 1.0e-176 E value Match length 313 100 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC T19L18 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 141518

Seq. ID LIB25-116-Q1-E1-F7

Method BLASTN NCBI GI q3869066 BLAST score 214 1.0e-117 E value Match length 214 100 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBM17, complete sequence [Arabidopsis thaliana]

Seq. No. 141519

Seq. ID LIB25-116-Q1-E1-F9

Method BLASTN NCBI GI q3449320

BLAST score 1.0e-156 E value 317 Match length 100 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MRB17, complete sequence [Arabidopsis thaliana] 141520 Seq. No. LIB25-117-Q1-E1-A9 Seq. ID Method BLASTX NCBI GI q132939 BLAST score 611 9.0e-64 E value 123 Match length 93 % identity 60S RIBOSOMAL PROTEIN L3 >gi 81657 pir JQ0771 ribosomal NCBI Description protein L3 (ARP1) - Arabidopsis thaliana >gi_166858 (M32654) ribosomal protein [Arabidopsis thaliana] 141521 Seq. No. Seq. ID LIB25-117-Q1-E1-C1 Method BLASTN NCBI GI g4544381 339 BLAST score 0.0e + 00E value 366 Match length 98 % identity Arabidopsis thaliana chromosome II BAC F16F14 genomic NCBI Description sequence, complete sequence 141522 Seq. No. LIB25-117-Q1-E1-E7 Seq. ID Method BLASTX NCBI GI g2995949 BLAST score 228 3.0e-19 E value Match length 45 % identity 56 (AF053563) ubiquitin [Mesembryanthemum crystallinum] NCBI Description Seq. No. 141523 LIB3168-001-P1-K1-A1 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g112681
BLAST score 673
E value 6.0e-71
Match length 154
% identity 85

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141524

Seq. ID LIB3168-001-P1-K1-A10

Method BLASTX



NCBI GI g1628583
BLAST score 78
E value 3.8e-01
Match length 74
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141525

Seq. ID LIB3168-001-P1-K1-A11

Method BLASTX
NCBI GI g112741
BLAST score 371
E value 5.0e-37
Match length 97
% identity 82

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 141526

Seq. ID LIB3168-001-P1-K1-A12

Method BLASTX
NCBI GI g1628583
BLAST score 852
E value 7.0e-92
Match length 165
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141527

Seq. ID LIB3168-001-P1-K1-A2

Method BLASTX
NCBI GI g3915961
BLAST score 635
E value 2.0e-66
Match length 157
% identity 82

NCBI Description HYPOTHETICAL 267 KD PROTEIN (ORF 2280)

>gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi 2924285 emb CAA77438 (Z00044) hypothetical

protein [Nicotiana tabacum]

Seq. No. 141528

Seq. ID LIB3168-001-P1-K1-A5

Method BLASTX
NCBI GI g1903034
BLAST score 285
E value 2.0e-25
Match length 128



% identity 44
NCBI Description (X94625) amp-binding protein [Brassica napus]

Seq. No. 141529

Seq. ID LIB3168-001-P1-K1-A6

Method BLASTX
NCBI GI g1628583
BLAST score 674
E value 4.0e-81
Match length 155
% identity 96

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141530

Seq. ID LIB3168-001-P1-K1-A8

Method BLASTN
NCBI GI g2564048
BLAST score 168
E value 2.0e-89
Match length 276
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MKD15, complete sequence [Arabidopsis thaliana]

Seq. No. 141531

Seq. ID LIB3168-001-P1-K1-A9

Method BLASTX
NCBI GI g1628583
BLAST score 642
E value 3.0e-67
Match length 123
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141532

Seq. ID LIB3168-001-P1-K1-B1

Method BLASTX
NCBI GI g1171577
BLAST score 195
E value 8.0e-15
Match length 108
% identity 40

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 141533

Seq. ID LIB3168-001-P1-K1-B10

Method BLASTX
NCBI GI g1628583
BLAST score 382
E value 9.0e-37
Match length 96
% identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis





thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

141534 Seq. No. Seq. ID LIB3168-001-P1-K1-B11 Method BLASTX g112739 NCBI GI BLAST score 660 E value 3.0e-69 Match length 166 78 % identity 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi_68854_pir_ NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana] Seq. No. 141535 LIB3168-001-P1-K1-B12 Seq. ID Method BLASTX NCBI GI q112741 BLAST score 885 E value 1.0e-95 Match length 1.64 % identity 99 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868 (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana] Seq. No. 141536 LIB3168-001-P1-K1-B2 Seq. ID Method BLASTX NCBI GI q112741 BLAST score 800 8.0e-86 E value Match length 150 99 % identity NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

 Seq. No.
 141537

 Seq. ID
 LIB3168-001-P1-K1-B3

 Method
 BLASTX

 NCBI GI
 g2129659

 BLAST score
 453

4.0e-45

E value

17272

13%



Match length 70 % identity

oleosin, isoform 21K - Arabidopsis thaliana >gi 725260 NCBI Description

(L40954) oleosin [Arabidopsis thaliana]

Seq. No.

141538

Seq. ID

LIB3168-001-P1-K1-B4

Method NCBI GI BLAST score BLASTX q1628583 500

E value Match length

4.0e-64 155

% identity NCBI Description

(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.

141539

Seq. ID Method

LIB3168-001-P1-K1-B5

NCBI GI BLAST score BLASTX q1628583 102

E value Match length

1.0e-45 96

% identity

NCBI Description

(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.

141540

Seq. ID

LIB3168-001-P1-K1-B6

Method NCBI GI BLASTX q1628583

BLAST score E value

45 3.0e-68

Match length

163 83

% identity NCBI Description

(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.

141541

Seq. ID

LIB3168-001-P1-K1-B7

Method BLASTX NCBI GI q112681 BLAST score 637 1.0e-66 E value 157 Match length

81 % identity NCBI Description

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.

141542

Seq. ID

LIB3168-001-P1-K1-B8



Method BLASTX
NCBI GI g1628583
BLAST score 680
E value 1.0e-71
Match length 165
% identity 81

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141543

Seq. ID LIB3168-001-P1-K1-B9

Method BLASTX
NCBI GI g112737
BLAST score 584
E value 2.0e-60
Match length 140
% identity 81

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi 68853_pir NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 141544

Seq. ID LIB3168-001-P1-K1-C10

Method BLASTX
NCBI GI g1628583
BLAST score 322
E value 1.0e-32
Match length 83
% identity 89

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141545

Seq. ID LIB3168-001-P1-K1-C11

Method BLASTX
NCBI GI g112739
BLAST score 369
E value 2.0e-67
Match length 145
% identity 89

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68854_pir__ NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 141546

Seq. ID LIB3168-001-P1-K1-C12

Method BLASTX



NCBI GI g1628583 BLAST score 642 E value 3.0e-67 Match length 123 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141547

Seq. ID LIB3168-001-P1-K1-C2

Method BLASTX
NCBI GI g2129659
BLAST score 496
E value 4.0e-50
Match length 143
% identity 73

NCBI Description oleosin, isoform 21K - Arabidopsis thaliana >gi_725260

(L40954) oleosin [Arabidopsis thaliana]

Seq. No. 141548

Seq. ID LIB3168-001-P1-K1-C3

Method BLASTX
NCBI GI g1628583
BLAST score 633
E value 4.0e-66
Match length 170
% identity 76

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141549

Seq. ID LIB3168-001-P1-K1-C4

Method BLASTX
NCBI GI g112737
BLAST score 636
E value 2.0e-66
Match length 164
% identity 67

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710 emb_CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 141550

Seq. ID LIB3168-001-P1-K1-C5

Method BLASTX
NCBI GI g1628583
BLAST score 616
E value 3.0e-64
Match length 121
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis



thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

 Seq. No.
 141551

 Seq. ID
 LIB3168-001-P1-K1-C6

 Method
 BLASTX

 NCBI GI
 g2642159

BLAST score 286
E value 2.0e-59
Match length 128
% identity 97

% identity 97
NCBI Description (AC003000) putative mannose-1-phosphate guanyltransferase

[Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose

pyrophosphorylase [Arabidopsis thaliana] >gi_4151925

(AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No. 141552

Seq. ID LIB3168-001-P1-K1-C7

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141553

Seq. ID LIB3168-001-P1-K1-C8

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141554

Seq. ID LIB3168-001-P1-K1-C9

Method BLASTX
NCBI GI g1628583
BLAST score 624
E value 4.0e-65
Match length 119
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141555

Seq. ID LIB3168-001-P1-K1-D1

Method BLASTX NCBI GI g1628583 BLAST score 842

17276



E value 1.0e-90 Match length 171 % identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141556

Seq. ID LIB3168-001-P1-K1-D10

Method BLASTX
NCBI GI g112743
BLAST score 713
E value 1.0e-75
Match length 148
% identity 90

NCBI Description 2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_

(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]

>gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4

precursor [Arabidopsis thaliana]

Seq. No. 141557

Seq. ID LIB3168-001-P1-K1-D11

Method BLASTX
NCBI GI g1628583
BLAST score 359
E value 6.0e-78
Match length 160
% identity 94

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141558

Seq. ID LIB3168-001-P1-K1-D12

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141559

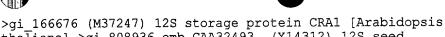
Seq. ID LIB3168-001-P1-K1-D2

Method BLASTX
NCBI GI g112681
BLAST score 212
E value 3.0e-17
Match length 42
% identity 100

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana





thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seg. No. 141560

LIB3168-001-P1-K1-D3 Seq. ID

Method BLASTX q112682 NCBI GI 741 BLAST score 7.0e-79 E value 164 Match length 85

% identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>qi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

141561 Seq. No.

LIB3168-001-P1-K1-D4 Seq. ID

BLASTN Method NCBI GI g2842474 BLAST score 240 1.0e-132 E value 240 Match length 100 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009

(ESSAII project)

141562 Seq. No.

Seq. ID LIB3168-001-P1-K1-D5

Method BLASTX NCBI GI g4204299 BLAST score 510 E value 1.0e-54 136 Match length 84 % identity

(AC003027) 1cl prt seq No definition line found NCBI Description

[Arabidopsis thaliana]

Seq. No. 141563

LIB3168-001-P1-K1-D6 Seq. ID

Method BLASTX q461841 NCBI GI BLAST score 312 3.0e-51E value Match length 151 61 % identity

CRUCIFERIN CRU4 PRECURSOR (11S GLOBULIN) (12S STORAGE NCBI Description

PROTEIN)

141564 Seq. No.

LIB3168-001-P1-K1-D7 Seq. ID

Method BLASTX q112681 NCBI GI BLAST score 712 1.0e-75 E value

17278



Match length 96 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

141565 Seq. No.

LIB3168-001-P1-K1-D9 Seq. ID

BLASTX Method NCBI GI q1628583 901 BLAST score 1.0e-97 E value 174 Match length 99 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141566

Seq. ID LIB3168-001-P1-K1-E1

Method BLASTX q112682 NCBI GI 610 BLAST score 2.0e-63 E value 157 Match length % identity 76

12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

141567 Seq. No.

Seq. ID LIB3168-001-P1-K1-E10

Method BLASTX NCBI GI g1628583 BLAST score 625 3.0e-65 E value 120 Match length % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141568

LIB3168-001-P1-K1-E12 Seq. ID

BLASTX Method g1628583 NCBI GI BLAST score 642 E value 3.0e-67 Match length 123 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]



141569 Seq. No. Seq. ID LIB3168-001-P1-K1-E2 BLASTX Method NCBI GI g1628583 603 BLAST score 8.0e-63 E value 115 Match length 100 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 141570 Seq. No. LIB3168-001-P1-K1-E3 Seq. ID BLASTX Method g1628583 NCBI GI 743 BLAST score 5.0e-79 E value Match length 178 % identity 83 (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 141571 LIB3168-001-P1-K1-E4 Seq. ID Method BLASTX g112737 NCBI GI 648 BLAST score 4.0e-70 E value 163 Match length % identity 83 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana] Seq. No. 141572 Seq. ID LIB3168-001-P1-K1-E5 Method BLASTX NCBI GI g2492515 BLAST score 366 7.0e - 35E value 87 Match length 85 % identity CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR NCBI Description >gi 2129924 pir _S58298 ATPase - pepper (fragment)

>gi_929013_emb_CAA62084_ (X90472) ATPase [Capsicum annuum]

Seq. No. 141573

Seq. ID LIB3168-001-P1-K1-E6

Method BLASTX NCBI GI g267136

% identity

NCBI Description

98



```
BLAST score
                  1.0e-58
E value
                  156
Match length
                  78
% identity
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2C (WATER-STRESS INDUCED
NCBI Description
                  TONOPLAST INTRINSIC PROTEIN) (WSI-TIP)
                  >qi 217869 dbj BAA02520 (D13254) transmembrane channel
                  protein [Arabidopsis thaliana] >gi_4371283_gb_AAD18141
                  (AC006260) putative plasma membrane intrinsic protein 2C
                  [Arabidopsis thaliana] >gi_384324_prf__1905411A
                  transmembrane channel [Arabidopsis thaliana]
                  141574
Seq. No.
                  LIB3168-001-P1-K1-E7
Seq. ID
Method
                  BLASTX
                  g4204299
NCBI GI
BLAST score
                  758
                  7.0e-81
E value
Match length
                  162
% identity
                  90
                  (AC003027) lcl prt seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
                  141575
Seq. No.
                  LIB3168-001-P1-K1-E8
Seq. ID
                  BLASTX
Method
                  q1628583
NCBI GI
                  625
BLAST score
                  3.0e-65
E value
                  120
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  141576
Seq. No.
                  LIB3168-001-P1-K1-E9
Seq. ID
                  BLASTX
Method
                  g1628583
NCBI GI
BLAST score
                  626
                  2.0e-65
E value
Match length
                  129
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  141577
Seq. No.
                  LIB3168-001-P1-K1-F1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q112682
BLAST score
                  518
                   4.0e-53
E value
Match length
                   98
```

12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana



>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
storage protein [Arabidopsis thaliana]

141578 Seq. No. Seq. ID LIB3168-001-P1-K1-F10 Method BLASTX g1345973 NCBI GI 408 BLAST score 7.0e-40 E value Match length 123 % identity 75

NCBI Description

OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC

1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)

omega-3 fatty acid desaturase [Arabidopsis thaliana]

>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase

[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)

microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

 Seq. No.
 141579

 Seq. ID
 LIB3168-001-P1-K1-F11

 Method
 BLASTX

 NCBI GI
 g1345592

 BLAST score
 348

 E value
 9.0e-55

 Match length
 124

 % identity
 95

•

Seq. No. 141580

Seq. ID LIB3168-001-P1-K1-F12

Method BLASTX
NCBI GI g1628583
BLAST score 536
E value 9.0e-55
Match length 101
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141581

Seq. ID LIB3168-001-P1-K1-F2

Method BLASTX
NCBI GI g133406
BLAST score 164
E value 3.0e-11
Match length 34
% identity 88

NCBI Description DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN

>gi 81501 pir C23525 DNA-directed RNA polymerase (EC

2.7.7.6) alpha chain - spinach chloroplast

>gi_12265_emb_CAA27214_ (X03496) pot. RNA polymerase alpha



subunit (aa 1-335) [Spinacia oleracea]

```
Seq. No.
                  141582
                  LIB3168-001-P1-K1-F3
Seq. ID
                  BLASTX
Method
                  q1628583
NCBI GI
BLAST score
                  399
                  1.0e-38
E value
                  109
Match length
                  75
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  141583
Seq. No.
                  LIB3168-001-P1-K1-F4
Seq. ID
                  BLASTN
Method
                  g2264311
NCBI GI
                  70
BLAST score
                  7.0e-31
E value
                  93
Match length
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141584
Seq. ID
                  LIB3168-001-P1-K1-F5
                  BLASTX
Method
                  g112681
NCBI GI
                  612
BLAST score
E value
                  9.0e-64
Match length
                  160
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__$08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  141585
Seq. No.
Seq. ID
                  LIB3168-001-P1-K1-F6
                  BLASTX
Method
NCBI GI
                  g112741
BLAST score
                  865
                   2.0e-93
E value
Match length
                   164
% identity
                   97
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                   3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
```

17283

141586

LIB3168-001-P1-K1-F7

Seq. No.

Seq. ID



```
BLASTX
Method
                  q1628583
NCBI GI
                  67
BLAST score
                  7.0e-31
E value
                  135
Match length
                  59
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  141587
Seq. No.
                  LIB3168-001-P1-K1-F8
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
                  594
BLAST score
```

Method BLASTX
NCBI GI g1628583
BLAST score 594
E value 5.0e-62
Match length 123
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

 Seq. No.
 141588

 Seq. ID
 LIB3168-001-P1-K1-F9

 Method
 BLASTX

 NCBI GI
 g1628583

 BLAST score
 642

BLAST score 642 E value 3.0e-67 Match length 123 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141589

Seq. ID LIB3168-001-P1-K1-G1

Method BLASTX
NCBI GI g112681
BLAST score 590
E value 3.0e-61
Match length 148
% identity 80

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141590

Seq. ID LIB3168-001-P1-K1-G10

Method BLASTX
NCBI GI g112741
BLAST score 605
E value 6.0e-63
Match length 144
% identity 82

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE



PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No. 141591

Seq. ID LIB3168-001-P1-K1-G11

Method BLASTX
NCBI GI g1628583
BLAST score 343
E value 3.0e-32
Match length 90
% identity 76

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141592

Seq. ID LIB3168-001-P1-K1-G12

Method BLASTX
NCBI GI g112681
BLAST score 679
E value 1.0e-71
Match length 164
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141593

Seq. ID LIB3168-001-P1-K1-G2

Method BLASTX
NCBI GI g3047098
BLAST score 161
E value 8.0e-11
Match length 90
% identity 42

NCBI Description (AF058826) similar to eukaryotic protein kinase domains

(Pfam: pkinase.hmm, score: 171.43) [Arabidopsis thaliana]

Seq. No. 141594

Seq. ID LIB3168-001-P1-K1-G3

Method BLASTX
NCBI GI g3281855
BLAST score 510
E value 1.0e-53
Match length 138
% identity 79

NCBI Description (AL031004) hypothetical protein [Arabidopsis thaliana]

Seq. No. 141595

Seq. ID LIB3168-001-P1-K1-G4

Method BLASTX

17285



```
NCBI GI
                  q1072480
BLAST score
                  413
                  4.0e-59
E value
                  154
Match length
% identity
NCBI Description cruciferin 1 precursor - rape
                  141596
Seq. No.
                  LIB3168-001-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  548
E value
                  3.0e-56
Match length
                  171
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  141597
Seq. No.
                  LIB3168-001-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  642
                  3.0e-67
E value
                  123
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  141598
Seq. No.
Seq. ID
                  LIB3168-001-P1-K1-G8
                  BLASTX
Method
NCBI GI
                  q112741
                  879
BLAST score
                  5.0e-95
E value
                  164
Match length
% identity
                  99
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  141599
                  LIB3168-001-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                   630
                   1.0e-68
```

E value 160 Match length 82 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana



>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

 Seq. No.
 141600

 Seq. ID
 LIB3168-001-P1-K1-H10

 Method
 BLASTX

 NCBI GI
 g1628583

 BLAST score
 181

E value 2.0e-13
Match length 90
% identity 50

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141601

Seq. ID LIB3168-001-P1-K1-H11

Method BLASTX
NCBI GI g112681
BLAST score 785
E value 6.0e-84
Match length 174
% identity 87

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141602

Seq. ID LIB3168-001-P1-K1-H12

Method BLASTX
NCBI GI g1628583
BLAST score 706
E value 1.0e-74
Match length 168
% identity 82

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141603

Seq. ID LIB3168-001-P1-K1-H2

Method BLASTX
NCBI GI g112682
BLAST score 686
E value 2.0e-72
Match length 150
% identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141604

E value Match length



```
LIB3168-001-P1-K1-H3
Seq. ID
                  BLASTX
Method
                  g112737
NCBI GI ·
                  250
BLAST score
                  3.0e-21
E value
                  86
Match length
                  63
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  141605
Seq. No.
Seq. ID
                  LIB3168-001-P1-K1-H4
                  BLASTX
Method
                  q1628583
NCBI GI
                  316
BLAST score
                  2.0e-29
E value
Match length
                  71
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  141606
Seq. No.
Seq. ID
                  LIB3168-001-P1-K1-H5
                  BLASTX
Method
                  g1628583
NCBI GI
BLAST score
                  338
E value
                  2.0e-32
                  65
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  141607
Seq. No.
Seq. ID
                  LIB3168-001-P1-K1-H6
                  BLASTX
Method
NCBI GI
                  q2651310
                  188
BLAST score
                  7.0e-49
E value
                  102
Match length
% identity
                  (AC002336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  141608
                  LIB3168-001-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
                  625
BLAST score
```

17288

3.0e-65

128



% identity 99
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141609

 Seq. No.
 141609

 Seq. ID
 LIB3168-001-P1-K1-H8

 Method
 BLASTX

 NCBI GI
 g1628583

 BLAST score
 638

 E value
 7.0e-67

 Match longth
 123

Match length 123 % identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141610

Seq. ID LIB3168-001-P1-K1-H9

Method BLASTX
NCBI GI g1628583
BLAST score 496
E value 1.0e-60
Match length 121
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141611

Seq. ID LIB3168-002-P1-K1-A1

Method BLASTX
NCBI GI g1170936
BLAST score 209
E value 9.0e-17
Match length 68

% identity 68

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_1084406_pir__S46538 methionine adenosyltransferase (EC
2.5.1.6) - tomato >gi_429104_emb_CAA80865_ (Z24741)
S-adenosyl-L-methionine synthetase [Lycopersicon

esculentum]

Seq. No. 141612

Seq. ID LIB3168-002-P1-K1-A10

Method BLASTX
NCBI GI g112739
BLAST score 357
E value 5.0e-34
Match length 109
% identity 68

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68854_pir_ NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]



>gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

141613 Seq. No. LIB3168-002-P1-K1-A11 Seq. ID BLASTX Method g112741 NCBI GI 705 BLAST score 1.0e-74 E value 131 Match length

100

% identity 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

141614 Seq. No.

Seq. ID LIB3168-002-P1-K1-A12

Method BLASTX q112681 NCBI GI 511 BLAST score 4.0e-52 E value 121 Match length 83 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604_pir__S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936_emb_CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

141615 Seq. No.

LIB3168-002-P1-K1-A2 Seq. ID

Method BLASTX g1628583 NCBI GI 514 BLAST score 3.0e-52 E value 109 Match length % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

141616 Seq. No.

LIB3168-002-P1-K1-A3 Seq. ID

BLASTX Method NCBI GI g112681 BLAST score 399 5.0e-39 E value Match length 112 67 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493_ (X14312) 12S seed

Seq. No.

Seq. ID

Method



storage protein [Arabidopsis thaliana]

```
141617
Seq. No.
Seq. ID
                  LIB3168-002-P1-K1-A4
                  BLASTX
Method
                  g1628583
NCBI GI
                  554
BLAST score
                  4.0e-57
E value
                  111
Match length
% identity
                  96
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  141618
Seq. No.
                  LIB3168-002-P1-K1-A8
Seq. ID
                  BLASTX
Method
                  g112743
NCBI GI
                  549
BLAST score
                  2.0e-56
E value
                  117
Match length
% identity
                  87
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi 166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_
                   (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >gi 4490713_emb CAB38847.1 (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
                  141619
Seq. No.
Seq. ID
                  LIB3168-002-P1-K1-A9
                  BLASTX
Method
                  g1628583
NCBI GI
                  620
BLAST score
                  1.0e-64
E value
Match length
                  119
                  100
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   141620
                  LIB3168-002-P1-K1-B10
Seq. ID
                   BLASTX
Method
                   q1628583
NCBI GI
BLAST score
                   127
                   4.0e-07
E value
                   53
Match length
                   100
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
```

17291

141621

BLASTX

LIB3168-002-P1-K1-B11



```
g1628583
NCBI GI
                  621
BLAST score
                  5.0e-65
E value
                  119
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  141622
                  LIB3168-002-P1-K1-B12
Seq. ID
Method
                  BLASTN
                  q2264317
NCBI GI
                  55
BLAST score
                  5.0e-22
E value
                  196
Match length
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUG13, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141623
Seq. ID
                  LIB3168-002-P1-K1-B2
Method
                  BLASTX
                  q112741
NCBI GI
                  400
BLAST score
                  3.0e-39
E value
                  79
Match length
% identity
                  96
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  141624
Seq. No.
                  LIB3168-002-P1-K1-B4
Seq. ID
                  BLASTX
Method
                  g112681
NCBI GI
                  544
BLAST score
                  7.0e-56
E value
                  128
Match length
                  83
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir_ S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
```

141625 Seq. No.

Seq. ID LIB3168-002-P1-K1-B5

BLASTX Method q112737 NCBI GI BLAST score 226 E value 1.0e-37 114 Match length



```
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  141626
Seq. No.
                  LIB3168-002-P1-K1-B6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4415905
                  132
BLAST score
                  2.0e-68
E value
                  163
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC F13K3 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  141627
Seq. No.
Seq. ID
                  LIB3168-002-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q1628583
                  619
BLAST score
                  1.0e-64
E value
                  120
Match length
                  99
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  141628
                  LIB3168-002-P1-K1-B8
Seq. ID
                  BLASTX
Method
                  g2129659
NCBI GI
                  524
BLAST score
                  2.0e-53
E value
Match length
                  151
                  73
% identity
                  oleosin, isoform 21K - Arabidopsis thaliana >gi_725260
NCBI Description
                   (L40954) oleosin [Arabidopsis thaliana]
                   141629
Seq. No.
                  LIB3168-002-P1-K1-C1
Seq. ID
                   BLASTX
Method
                   g3236238
NCBI GI
BLAST score
                   141
                   3.0e-53
E value
                   121
Match length
                   88
```

% identity

(AC004684) putative ARF1 GTPase activating protein NCBI Description [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_

(AB017876) Aspl [Arabidopsis thaliana]

Seq. No. 141630

LIB3168-002-P1-K1-C10 Seq. ID

NCBI Description

thaliana]



```
BLASTX
Method
NCBI GI
                  q1628583
                  500
BLAST score
                  6.0e-51
E value
                  99
Match length
                  97
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  141631
Seq. No.
                  LIB3168-002-P1-K1-C11
Seq. ID
Method
                  BLASTX
                  q1628583
NCBI GI
                  621
BLAST score
                  5.0e-65
E value
Match length
                  119
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                   141632
Seq. No.
Seq. ID
                  LIB3168-002-P1-K1-C2
                  BLASTN
Method
                   q3228389
NCBI GI
                   393
BLAST score
                   0.0e + 00
E value
Match length
                   393
                   100
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F17L21,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   141633
Seq. No.
                   LIB3168-002-P1-K1-C3
Seq. ID
                   BLASTX
Method
                   q3334323
NCBI GI
BLAST score
                   656
                   7.0e-69
E value
                   151
Match length
                   86
% identity
                   GTP-BINDING PROTEIN SAR1A >qi 1314860 (U56929) Sar1 homolog
NCBI Description
                   [Arabidopsis thaliana] >gi_2104532_gb_AAC78700.1_
                   (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis
                   thaliana] >gi 2104550 (AF001535) AGAA.4 [Arabidopsis
                   thaliana]
                   141634
Seq. No.
                   LIB3168-002-P1-K1-C4
Seq. ID
                   BLASTX
Method
                   g3924605
NCBI GI
BLAST score
                   509
                   9.0e-52
E value
Match length
                   116
% identity
```

17294

(AF069442) putative inhibitor of apoptosis [Arabidopsis

141635 Seq. No. LIB3168-002-P1-K1-C5 Seq. ID Method BLASTX g1628583 NCBI GI BLAST score 638 6.0e-67 E value 127 Match length 97 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 141636 Seq. No. LIB3168-002-P1-K1-C6 Seq. ID Method BLASTX NCBI GI g1628583 BLAST score 342 3.0e-32 E value Match length 130 57 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 141637 Seq. No. LIB3168-002-P1-K1-C7 Seq. ID Method BLASTX g112682 NCBI GI 717 BLAST score 4.0e-76 E value Match length 159 % identity 84 NCBI Description

12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

141638 Seq. No.

Seq. ID LIB3168-002-P1-K1-C9

Method BLASTX g1628583 NCBI GI 634 BLAST score 2.0e-66 E value 123 Match length % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141639

LIB3168-002-P1-K1-D1 Seq. ID

Method BLASTX NCBI GI g1628583 608 BLAST score E value 2.0e-63



Match length 148
% identity 80
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141640
Seq. ID LIB3168-002-P1-K1-D11
Method BLASTX
NCBI GI g112682

Method BLASTX
NCBI GI g112682
BLAST score 696
E value 1.0e-73
Match length 148
% identity 89

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141641

Seq. ID LIB3168-002-P1-K1-D12

Method BLASTX
NCBI GI g1628583
BLAST score 571
E value 6.0e-59
Match length 123
% identity 89

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141642

Seq. ID LIB3168-002-P1-K1-D2

Method BLASTX
NCBI GI g112681
BLAST score 692
E value 4.0e-73
Match length 167
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141643

Seq. ID LIB3168-002-P1-K1-D4

Method BLASTX
NCBI GI g1628583
BLAST score 313
E value 6.0e-29
Match length 60
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]



```
Seq. No.
                  141644
                  LIB3168-002-P1-K1-D6
Seq. ID
Method
                  BLASTX
                  g2979559
NCBI GI
BLAST score
                  433
                  4.0e-43
E value
Match length
                  91
% identity
                  (AC003680) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  141645
Seq. No.
                  LIB3168-002-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  642
E value
                  3.0e-67
Match length
                  123
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  141646
Seq. No.
                  LIB3168-002-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2623303
BLAST score
                   447
                  1.0e-44
E value
                  88
Match length
                  98
% identity
                  (AC002409) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   141647
                  LIB3168-002-P1-K1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                   q112741
                   725
BLAST score
                   4.0e-77
E value
                   135
Match length
                   100
% identity
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                   Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                   3 precursor [Arabidopsis thaliana] >gi 395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
                   141648
Seq. No.
Seq. ID
                   LIB3168-002-P1-K1-E1
                   BLASTX
Method
                   q1628583
NCBI GI
BLAST score
                   626
E value
                   2.0e-65
```

17297

123

Match length



```
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  141649
Seq. No.
                  LIB3168-002-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
                  450
BLAST score
E value
                  3.0e-50
Match length
                  107
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  141650
                  LIB3168-002-P1-K1-E11
Seq. ID
                  BLASTX
Method
                  q4204299
NCBI GI
                   675
BLAST score
E value
                  4.0e-71
Match length
                   131
% identity
                   100
                   (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   141651
                   LIB3168-002-P1-K1-E12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3256065
BLAST score
                   343
E value
                   0.0e+00
Match length
                   363
% identity
                   99
                  Arabidopsis thaliana mRNA for chloroplast NAD-dependent
NCBI Description
                   malate dehydrogenase
                   141652
Seq. No.
                   LIB3168-002-P1-K1-E2
Seq. ID
                   BLASTX
Method
                   g1107501
NCBI GI
                   385
BLAST score
                   3.0e-37
E value
                   128
Match length
% identity
                   62
                   (X91954) orf [Arabidopsis thaliana] >gi 3367530 (AC004392)
NCBI Description
```

Match to gb X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from

this gene. [Arabidopsis thaliana]

141653 Seq. No.

Seq. ID LIB3168-002-P1-K1-E3

BLASTX Method g514324 NCBI GI BLAST score 226



```
E value 9.0e-31
Match length 107
% identity 76
NCBI Description (L34773)
>qi 24627
```

(L34773) RNA polymerase subunit [Arabidopsis thaliana] >gi_2462755 (AC002292) RNA polymerase subunit (isoform B) [Arabidopsis thaliana] >gi_1586550_prf__2204246B RNA

polymerase [Arabidopsis thaliana]

Seq. No. 141654

Seq. ID LIB3168-002-P1-K1-E4

Method BLASTN
NCBI GI g4539331
BLAST score 205
E value 1.0e-111
Match length 455
% identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13

(ESSA project)

Seq. No. 141655

Seq. ID LIB3168-002-P1-K1-E5

Method BLASTX
NCBI GI g112682
BLAST score 478
E value 3.0e-48
Match length 111
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141656

Seq. ID LIB3168-002-P1-K1-E6

Method BLASTN
NCBI GI g3985950
BLAST score 434
E value 0.0e+00
Match length 488
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MPI10, complete sequence [Arabidopsis thaliana]

Seq. No. 141657

Seq. ID LIB3168-002-P1-K1-E7

Method BLASTN
NCBI GI 94757417
BLAST score 115
E value 7.0e-58
Match length 377
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

T30G6, complete sequence

Seq. No. 141658

Seq. ID LIB3168-002-P1-K1-E8



Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141659

Seq. ID LIB3168-002-P1-K1-F1

Method BLASTN
NCBI GI g2828278
BLAST score 219
E value 1.0e-120
Match length 472
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16

(ESSAII project)

Seq. No. 141660

Seq. ID LIB3168-002-P1-K1-F11

Method BLASTX
NCBI GI g1526424
BLAST score 358
E value 3.0e-34
Match length 83
% identity 84

NCBI Description (D64140) LEA protein in group 3 [Arabidopsis thaliana]

Seq. No. 141661

Seq. ID LIB3168-002-P1-K1-F12

Method BLASTX
NCBI GI g1628583
BLAST score 373
E value 8.0e-36
Match length 87
% identity 86

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141662

Seq. ID LIB3168-002-P1-K1-F2

Method BLASTN
NCBI GI g3068702
BLAST score 95
E value 8.0e-46
Match length 95
% identity 100

NCBI Description Arabidopsis thaliana putative transmembrane protein Glp

(AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), put

Seq. No. 141663



```
LIB3168-002-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112681
                  578
BLAST score
                  8.0e-60
E value
                  138
Match length
% identity
                  82
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  141664
                  LIB3168-002-P1-K1-F4
Seq. ID
Method
                  BLASTX
                  q1628583
NCBI GI
BLAST score
                  599
                  2.0e-62
E value
Match length
                  129
                  91
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  141665
                  LIB3168-002-P1-K1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4204299
                  421
BLAST score
E value
                  1.0e-41
Match length
                  84
% identity
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  141666
                  LIB3168-002-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  642
                  3.0e-67
E value
                  123
Match length
% identity
                  100
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  141667
Seq. ID
                  LIB3168-002-P1-K1-F9
                  BLASTX
Method
                  g112682
NCBI GI
```

BLAST score 672 8.0e-71 E value Match length 152 87 % identity

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510



cruciferin precursor (CRB) - Arabidopsis thaliana >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed storage protein [Arabidopsis thaliana]

 Seq. No.
 141668

 Seq. ID
 LIB3168-002-P1-K1-G1

 Method
 BLASTN

 NCBI GI
 g1628582

 BLAST score
 77

BLAST score 77
E value 5.0e-36
Match length 77
% identity 35

NCBI Description Arabidopsis thaliana 12S cruciferin seed storage protein

(ATCRU3) gene, complete cds

Seq. No. 141669

Seq. ID LIB3168-002-P1-K1-G10

Method BLASTX
NCBI GI g1628583
BLAST score 112
E value 3.0e-05
Match length 66
% identity 94

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141670

Seq. ID LIB3168-002-P1-K1-G11

Method BLASTX
NCBI GI g112681
BLAST score 760
E value 4.0e-81
Match length 144
% identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141671

Seq. ID LIB3168-002-P1-K1-G12

Method BLASTN
NCBI GI g11804
BLAST score 195
E value 1.0e-105
Match length 333
% identity 92

NCBI Description Tobacco chloroplast genes for 4.5S and 5S ribosomal RNA

Seq. No. 141672

Seq. ID LIB3168-002-P1-K1-G3

Method BLASTN
NCBI GI g608672
BLAST score 296

17302



```
1.0e-166
E value
                  319
Match length
% identity
                  99
NCBI Description Arabadopsis thaliana Landsberg AAP5 mRNA
```

141673 Seq. No. LIB3168-002-P1-K1-G4 Seq. ID BLASTX Method g1628583 NCBI GI 624 BLAST score 4.0e-65 E value

121 Match length % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

141674 Seq. No. LIB3168-002-P1-K1-G5 Seq. ID BLASTX Method g1628583 NCBI GI

635 BLAST score 2.0e-66 E value 123 Match length % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

141675 Seq. No.

LIB3168-002-P1-K1-G6 Seq. ID

BLASTX Method q1628583 NCBI GI BLAST score 642 3.0e-67 E value Match length 123 % identity 100

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

141676 Seq. No.

LIB3168-002-P1-K1-G7 Seq. ID

Method BLASTX q1628583 NCBI GI 510 BLAST score E value 4.0e-52 Match length 99 99 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

141677 Seq. No.

Seq. ID LIB3168-002-P1-K1-G8

BLASTX Method NCBI GI g112737



E value 5.0e-60
Match length 81
NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_(AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

 Seq. No.
 141678

 Seq. ID
 LIB3168-002-P1-K1-G9

 Method
 BLASTX

 NCBI GI
 g1628583

 BLAST score
 212

BLAST score 212 E value 6.0e-17 Match length 69 % identity 99

BLAST score

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141679

Seq. ID LIB3168-002-P1-K1-H1

Method BLASTX
NCBI GI g1628583
BLAST score 578
E value 8.0e-60
Match length 120
% identity 95

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141680

Seq. ID LIB3168-002-P1-K1-H10

Method BLASTN
NCBI GI g2618604
BLAST score 197
E value 1.0e-107
Match length 201
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTG13, complete sequence [Arabidopsis thaliana]

Seq. No. 141681

Seq. ID LIB3168-002-P1-K1-H12

Method BLASTX
NCBI GI g112682
BLAST score 549
E value 2.0e-56
Match length 131
% identity 80

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana



>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
storage protein [Arabidopsis thaliana]

Seq. No. 141682

Seq. ID LIB3168-002-P1-K1-H2

Method BLASTN
NCBI GI g1628582
BLAST score 33
E value 5.0e-09
Match length 144
% identity 89

NCBI Description Arabidopsis thaliana 12S cruciferin seed storage protein

(ATCRU3) gene, complete cds

Seq. No. 141683

Seq. ID LIB3168-002-P1-K1-H3

Method BLASTX
NCBI GI g1628583
BLAST score 594
E value 1.0e-61
Match length 120
% identity 96

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141684

Seq. ID LIB3168-002-P1-K1-H5

Method BLASTX
NCBI GI g2129657
BLAST score 480
E value 3.0e-48
Match length 125
% identity 80

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
thaliana] >gi 987016 emb CAA90878_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 141685

Seq. ID LIB3168-002-P1-K1-H6

Method BLASTX
NCBI GI g81546
BLAST score 244
E value 1.0e-20
Match length 154
% identity 37

NCBI Description alpha-globulin type B precursor (tandem 1) - upland cotton

(fragment)

Seq. No. 141686

Seq. ID LIB3168-002-P1-K1-H7

Method BLASTN
NCBI GI g2842474
BLAST score 266
E value 1.0e-148

17305



Match length 266 % identity 100 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No. 141687

Seq. ID LIB3168-002-P1-K1-H8

Method BLASTX
NCBI GI g112682
BLAST score 697
E value 1.0e-73
Match length 159
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141688

Seq. ID LIB3168-002-P1-K1-H9

Method BLASTX
NCBI GI g2583108
BLAST score 413
E value 1.0e-40
Match length 103
% identity 83

NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No. 141689

Seq. ID LIB3168-003-P1-K1-A1

Method BLASTN
NCBI GI g2281081
BLAST score 173
E value 2.0e-92
Match length 394
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F18019 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 141690

Seq. ID LIB3168-003-P1-K1-A7

Method BLASTX
NCBI GI g112681
BLAST score 291
E value 2.0e-26
Match length 97
% identity 61

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__\$08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141691

Seq. ID LIB3168-003-P1-K1-A8

Method BLASTX



q1628583 NCBI GI 650 BLAST score 2.0e-68 E value 127 Match length 98 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

141692 Seq. No.

LIB3168-003-P1-K1-A9 Seq. ID

BLASTX Method g112682 NCBI GI BLAST score 580 3.0e-60 E value 110 Match length 100 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

141693 Seq. No.

LIB3168-003-P1-K1-B1 Seq. ID

Method BLASTX q1628583 NCBI GI 625 BLAST score 3.0e-65 E value 120 Match length 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141694

LIB3168-003-P1-K1-B2 Seq. ID

Method BLASTX q1628583 NCBI GI BLAST score 619 1.0e-64 E value 120 Match length 99 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

141695 Seq. No.

LIB3168-003-P1-K1-B7 Seq. ID

Method BLASTN q2673901 NCBI GI 382 BLAST score 0.0e+00E value 382 Match length 100 % identity

Arabidopsis thaliana chromosome II BAC T24P15 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]



Seq. No. 141696

Seq. ID LIB3168-003-P1-K1-B9

Method BLASTX
NCBI GI g1345973
BLAST score 522
E value 3.0e-53
Match length 114

% identity 83

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC

1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 141697

Seq. ID LIB3168-003-P1-K1-C1

Method BLASTX
NCBI GI g112682
BLAST score 646
E value 1.0e-67
Match length 153
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141698

Seq. ID LIB3168-003-P1-K1-C3

Method BLASTX
NCBI GI g1628583
BLAST score 538
E value 5.0e-55
Match length 101
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141699

Seq. ID LIB3168-003-P1-K1-C7

Method BLASTX
NCBI GI g4455200
BLAST score 393
E value 3.0e-38
Match length 87
% identity 95

NCBI Description (AL035440) putative CDP-diacylglycerol synthetase

[Arabidopsis thaliana]

Seq. No. 141700



LIB3168-003-P1-K1-C8 Seq. ID BLASTX Method g112741 NCBI GI 770 BLAST score 3.0e-82 E value 144 Match length 99 % identity 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana] 141701 Seq. No. LIB3168-003-P1-K1-C9 Seq. ID BLASTN Method g4662609 NCBI GI 278 BLAST score 1.0e-155 E value 383 Match length % identity NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence 141702 Seq. No. LIB3168-003-P1-K1-D1 Seq. ID BLASTX Method g1628583 NCBI GI BLAST score 663 E value 8.0e-70 139 Match length % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 141703 Seq. No. LIB3168-003-P1-K1-D2 Seq. ID Method BLASTX NCBI GI g1628583 BLAST score 233 1.0e-19 E value Match length 46 96 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 141704 Seq. No. LIB3168-003-P1-K1-D3 Seq. ID

BLASTX Method g1703220 NCBI GI 717 BLAST score 5.0e-76E value 153 Match length



% identity 86
NCBI Description AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [Arabidopsis thaliana]

 Seq. No.
 141705

 Seq. ID
 LIB3168-003-P1-K1-D7

 Method
 BLASTX

 NCBI GI
 g112741

BLAST score 850 E value 1.0e-91 Match length 161 % identity 98

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -

Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 141706

Seq. ID LIB3168-003-P1-K1-D9

Method BLASTX
NCBI GI g112681
BLAST score 637
E value 1.0e-66
Match length 146
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141707

Seq. ID LIB3168-003-P1-K1-E1

Method BLASTX
NCBI GI g112737
BLAST score 375
E value 3.0e-36
Match length 100
% identity 74

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 141708

Seg. ID LIB3168-003-P1-K1-E7

Method BLASTN
NCBI GI g3402671
BLAST score 431
E value 0.0e+00
Match length 470



% identity NCBI Description Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana] 141709 Seq. No. LIB3168-004-P1-K1-A1 Seq. ID BLASTN Method g2351064 NCBI GI BLAST score 40 5.0e-14 E value 56 Match length 95 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana] 141710 Seq. No. LIB3168-004-P1-K1-A11 Seq. ID BLASTX Method g1730560 NCBI GI 374 BLAST score 4.0e-36 E value 111 Match length 67 % identity ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE NCBI Description H) >gi_510932_emb_CAA84494_ (Z35117) alpha 1,4-glucan phosphorylase type H [Vicia faba] 141711 Seq. No. LIB3168-004-P1-K1-A2 Seq. ID BLASTN Method g4468103 NCBI GI 181 BLAST score 2.0e-97 E value 235 Match length % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 . (ESSA project) 141712 Seq. No. Seq. ID LIB3168-004-P1-K1-A5 BLASTX Method q112681 NCBI GI 700 BLAST score

4.0e-74 E value Match length 137 99 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

141713 Seq. No.

Seq. ID LIB3168-004-P1-K1-A6

BLASTX Method g112681 NCBI GI 613 BLAST score



E value 5.0e-64 Match length 121 % identity 98

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141714

Seq. ID LIB3168-004-P1-K1-A7

Method BLASTN
NCBI GI g2828181
BLAST score 269
E value 1.0e-150
Match length 373
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MLE8, complete sequence [Arabidopsis thaliana]

Seq. No. 141715

Seq. ID LIB3168-004-P1-K1-A8

Method BLASTX
NCBI GI g112682
BLAST score 595
E value 7.0e-62
Match length 138
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141716

Seq. ID LIB3168-004-P1-K1-B1

Method BLASTN
NCBI GI g1777655
BLAST score 126
E value 1.0e-64
Match length 158
% identity 95

NCBI Description Crossosoma californicum 18S ribosomal RNA gene, partial

sequence

Seq. No. 141717

Seq. ID LIB3168-004-P1-K1-B10

Method BLASTN
NCBI GI g3335331
BLAST score 404
E value 0.0e+00
Match length 428
% identity 99

NCBI Description Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 141718

NCBI Description



```
LIB3168-004-P1-K1-B12
Seq. ID
                  BLASTN
Method
                  g16472
NCBI GI
                  305
BLAST score
                  1.0e-171
E value
Match length
                  313
% identity
NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type
                  141719
Seq. No.
                  LIB3168-004-P1-K1-B3
Seq. ID
                  BLASTN
Method
                  q1628582
NCBI GI
                  81
BLAST score
                  7.0e-38
E value
Match length
                  144
% identity
NCBI Description Arabidopsis thaliana 12S cruciferin seed storage protein
                   (ATCRU3) gene, complete cds
                  141720
Seq. No.
                  LIB3168-004-P1-K1-B4
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3023848
BLAST score
                   365
                   1.0e-38
E value
Match length
                   93
% identity
                   GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                   PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA)
                   >gi 2289095 (U77381) WD-40 repeat protein [Arabidopsis
                   thaliana]
                   141721
Seq. No.
                   LIB3168-004-P1-K1-B5
Seq. ID
                   BLASTX
Method
                   g112681
NCBI GI
                   474
BLAST score
                   9.0e-48
E value
                   115
Match length
                   81
% identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
                   141722
Seq. No.
                   LIB3168-004-P1-K1-B6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q112681
                   517
BLAST score
                   9.0e-53
E value
                   124
Match length
                   81
 % identity
```

17313

12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

BLAST score

Match length

E value

363 0.0e+00

431



>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
storage protein [Arabidopsis thaliana]

141723 Seq. No. LIB3168-004-P1-K1-B8 Seq. ID BLASTX Method g3582436 NCBI GI 247 BLAST score 5.0e-23 E value 99 Match length 58 % identity NCBI Description (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum] Seq. No. 141724 LIB3168-004-P1-K1-C1 Seq. ID BLASTX Method q266693 NCBI GI 270 BLAST score 3.0e-24E value 74 Match length 74 % identity OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis NCBI Description thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_(AL035523) oleosin, 18.5K [Arabidopsis thaliana] Seq. No. 141725 LIB3168-004-P1-K1-C11 Seq. ID Method BLASTX g1628583 NCBI GI 705 BLAST score 9.0e-75 E value Match length 135 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 141726 LIB3168-004-P1-K1-C12 Seq. ID Method BLASTN NCBI GI g3063690 BLAST score 403 0.0e+00E value 422 Match length % identity 99 Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 NCBI Description (ESSAII project) 141727 Seq. No. LIB3168-004-P1-K1-C3 Seq. ID BLASTN Method g3108025 NCBI GI

17314



% identity 96
NCBI Description Arabidopsis thaliana chromosome 1 BAC T13D8, complete
sequence [Arabidopsis thaliana]

Seq. No. 141728

Seq. ID LIB3168-004-P1-K1-C7

Method BLASTX
NCBI GI g112737
BLAST score 580
E value 4.0e-60
Match length 139
% identity 81

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__ NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 141729

Seq. ID LIB3168-004-P1-K1-C8

Method BLASTX
NCBI GI g2160151
BLAST score 291
E value 2.0e-26
Match length 93
% identity 63

NCBI Description (AC000375) Strong similarity to Brassica aspartic protease

(gb X77260). [Arabidopsis thaliana]

Seq. No. 141730

Seq. ID LIB3168-004-P1-K1-D1

Method BLASTX
NCBI GI g2326363
BLAST score 648
E value 5.0e-68
Match length 142
% identity 90

NCBI Description (AJ001037) DNA-directed RNA polymerase [Arabidopsis

thaliana]

Seq. No. 141731

Seq. ID LIB3168-004-P1-K1-D10

Method BLASTX
NCBI GI g1109699
BLAST score 597
E value 4.0e-62
Match length 114
% identity 100

NCBI Description (X83381) gibberellin 20-oxidase [Arabidopsis thaliana]

Seq. No. 141732

Seq. ID LIB3168-004-P1-K1-D11

Method BLASTX
NCBI GI g1628583
BLAST score 421

17315



E value 2.0e-41 Match length 102 % identity 84

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141733

Seq. ID LIB3168-004-P1-K1-D12

Method BLASTX
NCBI GI g1628583
BLAST score 729
E value 1.0e-77
Match length 139
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141734

Seq. ID LIB3168-004-P1-K1-D2

Method BLASTX
NCBI GI g3170525
BLAST score 446
E value 2.0e-44
Match length 114
% identity 75

NCBI Description (AF054615) cellulase [Fragaria x ananassa]

Seq. No. 141735

Seq. ID LIB3168-004-P1-K1-D4

Method BLASTX
NCBI GI g1345973
BLAST score 360
E value 3.0e-34
Match length 114
% identity 68

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 141736

Seq. ID LIB3168-004-P1-K1-D5

Method BLASTX
NCBI GI g1628583
BLAST score 464
E value 1.0e-46
Match length 122
% identity 75

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

E value

Match length

% identity



cruciferin seed storage protein [Arabidopsis thaliana]

```
Seq. No.
                  141737
                  LIB3168-004-P1-K1-D6
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  343
E value
                  8.0e-33
                  76
Match length
                  87
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  141738
                  LIB3168-004-P1-K1-D7
Seq. ID
                  BLASTX
Method
                  g1173187
NCBI GI
BLAST score
                   605
                  5.0e-63
E value
                  122
Match length
                   95
% identity
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
NCBI Description
                   ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                   strawberry >gi_643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
                   141739
Seq. No.
                  LIB3168-004-P1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   625
E value
                   2.0e-65
Match length
                   120
% identity
                   100
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   141740
                   LIB3168-004-P1-K1-D9
Seq. ID
                   BLASTX
Method
                   q3426039
NCBI GI
BLAST score
                   296
E value
                   9.0e-27
Match length
                   120
% identity
NCBI Description
                   (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                   141741
                   LIB3168-004-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2062164
                   94
BLAST score
```

17317

4.0e-03

130

11



NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No. 141742

Seq. ID LIB3168-004-P1-K1-E11

Method BLASTX
NCBI GI g112682
BLAST score 653
E value 1.0e-68
Match length 143
% identity 87

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141743

Seq. ID LIB3168-004-P1-K1-E12

Method BLASTX
NCBI GI g112682
BLAST score 595
E value 8.0e-62
Match length 138
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141744

Seq. ID LIB3168-004-P1-K1-E2

Method BLASTX
NCBI GI g2501188
BLAST score 208
E value 2.0e-16
Match length 59
% identity 75

NCBI Description THIAZOLE BIOSYNTHETIC ENZYME >gi_2129750_pir_S71191 TH14

protein homolog - Arabidopsis thaliana >gi_1113783 (U17589)

Thil protein [Arabidopsis thaliana]

Seq. No. 141745

Seq. ID LIB3168-004-P1-K1-E3

Method BLASTX
NCBI GI g114654
BLAST score 266
E value 3.0e-23
Match length 77
% identity 78

NCBI Description ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III)

>gi_67898_pir__LWNTA H+-transporting ATP synthase (EC

3.6.1.34) lipid-binding protein - common tobacco

chloroplast >gi_11812_emb_CAA77343_ (Z00044) ATPase III subunit [Nicotiana tabacum] >gi_343484 (M10124) ATPase subunit III [Nicotiana tabacum] >gi_224347_prf__1102209A



ATPase III, H translocating [Nicotiana sp.] >gi 225272 prf__1211235G ATPase III [Nicotiana tabacum]

Seq. No. 141746 LIB3168-004-P1-K1-E5 Seq. ID Method BLASTN q2244991 NCBI GI BLAST score 247 E value 1.0e-136 Match length 376 97 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No Seq. No. 141747 LIB3168-004-P1-K1-E6 Seq. ID BLASTN Method NCBI GI g2244991 179 BLAST score E value 4.0e-96 274 Match length 96 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No 141748 Seq. No. LIB3168-004-P1-K1-E7 Seq. ID BLASTN Method g2264306 NCBI GI BLAST score 112 5.0e-56 E value Match length 375 100 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MBK5, complete sequence [Arabidopsis thaliana] 141749 Seq. No. Seq. ID LIB3168-004-P1-K1-E8 Method BLASTX NCBI GI g112741 BLAST score 729 1.0e-77 E value Match length 136 100 % identity NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No. 141750

Seq. ID LIB3168-004-P1-K1-E9

Method BLASTX
NCBI GI g1628583
BLAST score 622



E value 5.0e-65 120 Match length % identity 99

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

141751 Seq. No.

LIB3168-004-P1-K1-F1 Seq. ID

Method BLASTX g114661 NCBI GI BLAST score 616 E value 2.0e-64 Match length 137 % identity 87

ATP SYNTHASE A CHAIN PRECURSOR (SUBUNIT IV) NCBI Description

>gi 67924 pir LWNT6 H+-transporting ATP synthase (EC

3.6.1.34) chain a - common tobacco chloroplast

>gi_11813_emb_CAA77344_ (Z00044) ATPase sunthase IV subunit
[Nicotiana tabacum] >gi_225273_prf__1211235H ATPase a

[Nicotiana tabacum]

Seq. No. 141752

LIB3168-004-P1-K1-F10 Seq. ID

Method BLASTX NCBI GI g112681 BLAST score 634 2.0e-66 E value 131 Match length 93 % identity

12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141753

LIB3168-004-P1-K1-F12 Seq. ID

Method BLASTX g3421384 NCBI GI BLAST score 678 1.0e-71 E value Match length 142 % identity

NCBI Description (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase

[Arabidopsis thaliana]

Seq. No. 141754

Seq. ID LIB3168-004-P1-K1-F7

Method BLASTX NCBI GI g3287691 BLAST score 194 E value 8.0e-15 Match length 134 % identity 39

(AC003979) Contains similarity to RING zinc finger protein NCBI Description

gb X95455 from Gallus gallus. [Arabidopsis thaliana]

NCBI Description

MNF13



```
Seq. No.
                  141755
Seq. ID
                  LIB3168-004-P1-K1-F8
Method
                  BLASTX
                  g2160151
NCBI GI
BLAST score
                  538
                  4.0e-55
E value
Match length
                  121
% identity
                  87
                  (AC000375) Strong similarity to Brassica aspartic protease
NCBI Description
                  (gb X77260). [Arabidopsis thaliana]
                  141756
Seq. No.
Seq. ID
                  LIB3168-004-P1-K1-F9
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  688
                  1.0e-72
E value
Match length
                  143
% identity
                  93
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  141757
                  LIB3168-004-P1-K1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2842474
BLAST score
                  174
E value
                  2.0e-93
                  174
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
                   (ESSAII project)
Seq. No.
                  141758
Seq. ID
                  LIB3168-004-P1-K1-G10
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  618
                  2.0e-64
E value
Match length
                  120
% identity
                  99
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  141759
Seq. ID
                  LIB3168-004-P1-K1-G3
Method
                  BLASTN
NCBI GI
                  g2656028
BLAST score
                  335
E value
                  0.0e + 00
Match length
                  417
% identity
                  97
```

17321

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:



```
141760
Seq. No.
                  LIB3168-004-P1-K1-G5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q112681
                  499
BLAST score
                  1.0e-50
E value
                  95
Match length
                  99
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  141761
                  LIB3168-004-P1-K1-G6
Seq. ID
                  BLASTX
Method
                  g112681
NCBI GI
BLAST score
                  126
                  4.0e-45
E value
                  132
Match length
% identity
                  68
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir __S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  141762
                  LIB3168-004-P1-K1-G8
Seq. ID
                  BLASTX
Method
                  g2213586
NCBI GI
BLAST score
                  555
E value
                  4.0e-57
Match length
                  135
                  84
% identity
NCBI Description
                  (AC000348) T7N9.6 [Arabidopsis thaliana]
Seq. No.
                  141763
                  LIB3168-004-P1-K1-G9
Seq. ID
Method
                  BLASTN
                  g4106339
NCBI GI
                  327
BLAST score
E value
                  0.0e + 00
                  354
Match length
% identity
                  Arabidopsis thaliana protein phosphatase 2A regulatory
NCBI Description
                  subunit isoform B' delta mRNA, complete cds
Seq. No.
                  141764
```

Seq. ID LIB3168-004-P1-K1-H1

Method BLASTX NCBI GI g1628583 BLAST score 386 E value 2.0e-58 Match length 119



% identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141765

LIB3168-004-P1-K1-H10 Seq. ID

Method BLASTX NCBI GI g112740 BLAST score 260 E value 1.0e-22 Match length 117 % identity 51

NAPIN 2 PRECURSOR (1.7S SEED STORAGE PROTEIN) NCBI Description

>gi 81691 pir A25997 napin precursor (napA) - rape

>gi 167153 (J02586) prepronapin [Brassica napus] >gi_167155

(J02798) napin [Brassica napus]

Seq. No. 141766

LIB3168-004-P1-K1-H11 Seq. ID

Method BLASTN NCBI GI q1628582 BLAST score 52 2.0e-20 E value Match length 112 % identity 87

Arabidopsis thaliana 12S cruciferin seed storage protein NCBI Description

(ATCRU3) gene, complete cds

141767 Seq. No.

LIB3168-004-P1-K1-H12 Seq. ID

BLASTX Method q112681 NCBI GI BLAST score 630 6.0e-66 E value 143 Match length 85 % identity

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

141768 Seq. No.

Seq. ID LIB3168-004-P1-K1-H3

Method BLASTX NCBI GI g1628583 BLAST score 208 E value 4.0e-17 Match length 56 % identity 82

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141769

Seq. ID LIB3168-004-P1-K1-H5



```
Method
                  BLASTX
NCBI GI
                  g1742961
BLAST score
                  480
E value
                  2.0e-48
Match length
                  96
% identity
                  98
NCBI Description
                  (X94756) cystathionine gamma-synthase [Arabidopsis
                  thaliana]
Seq. No.
                  141770
Seq. ID
                  LIB3168-004-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g1742961
BLAST score
                  483
E value
                  8.0e-49
Match length
                  97
                  98
% identity
NCBI Description
                  (X94756) cystathionine gamma-synthase [Arabidopsis
                  thaliana]
Seq. No.
                  141771
Seq. ID
                  LIB3168-004-P1-K1-H8
Method
                  BLASTN
NCBI GI
                  g4206762
BLAST score
                  251
                  1.0e-139
E value
Match length
                  347
                  97
% identity
NCBI Description
                  Arabidopsis thaliana cell wall-plasma membrane linker
                  protein homolog (CWLP) mRNA, complete cds
Seq. No.
                  141772
Seq. ID
                  LIB3168-004-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  738
E value
                  1.0e-78
Match length
                  139
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936_emb_CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  141773
Seq. ID
                  LIB3168-005-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  380
E value
```

1.0e-36 Match length 97 78 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]



```
Seq. No.
                  LIB3168-005-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  755
E value
                  1.0e-80
Match length
                  143
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  141775
Seq. ID
                  LIB3168-005-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  q4512656
BLAST score
                  160
E value
                  1.0e-84
Match length
                  376
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic
                  sequence, complete sequence
Seq. No.
                  141776
                  LIB3168-005-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  628
                  1.0e-65
E value
                  134
Match length
                  92
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  141777
Seq. No.
Seq. ID
                  LIB3168-005-P1-K1-A5
                  BLASTX
Method
                  g1351272
NCBI GI
BLAST score
                  479
                  3.0e-48
E value
Match length
                  112
                  85
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi 414550
NCBI Description
                  (U02949) cytosolic triose phosphate isomerase [Arabidopsis
                  thaliana] >gi 742408 prf 2009415A triose phosphate
                  isomerase [Arabidopsis thaliana]
                  141778
Seq. No.
                  LIB3168-005-P1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q112682
BLAST score
                  703
                  2.0e-74
E value
Match length
                  144
% identity
                  92
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir__S08510
```



cruciferin precursor (CRB) - Arabidopsis thaliana >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 141779

Seq. ID LIB3168-005-P1-K1-B1

Method BLASTX NCBI GI g4104058 BLAST score 248 E value 3.0e-21 Match length 106 % identity 47

(AF031195) blue copper-binding protein homolog [Triticum NCBI Description

aestivum]

Seq. No. 141780

Seq. ID LIB3168-005-P1-K1-B10

Method BLASTX NCBI GI g112741 BLAST score 705 E value 9.0e-75 Match length 131 100 % identity

2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >qi 166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 141781

LIB3168-005-P1-K1-B11 Seq. ID

BLASTX Method NCBI GI g1628583 BLAST score 440 1.0e-43 E value 83 Match length 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141782

LIB3168-005-P1-K1-B12 Seq. ID

Method BLASTX q1628583 NCBI GI 674 BLAST score 4.0e-71 E value Match length 142 % identity 92

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141783



```
LIB3168-005-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  314
E value
                  7.0e-29
Match length
                  60
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  141784
Seq. No.
Seq. ID
                  LIB3168-005-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  g4512656
BLAST score
                  165
E value
                  1.0e-87
Match length
                  357
% identity
                  83
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                  sequence, complete sequence
                  141785
Seq. No.
Seq. ID
                  LIB3168-005-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  641
E value
                  3.0e-67
Match length
                  133
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  141786
                  LIB3168-005-P1-K1-B6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4455348
BLAST score
                  404
E value
                  0.0e + 00
Match length
                  419
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8
NCBI Description
                  (ESSAII project)
                  141787
Seq. No.
                  LIB3168-005-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
                  2.0e-65
E value
Match length
                  120
```

% identity 100
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis



141788 Seq. No. Seq. ID LIB3168-005-P1-K1-B8 Method BLASTX NCBI GI g112741 BLAST score 741 6.0e-79 E value 138 Match length 100 % identity

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit

3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 141789

Seq. ID LIB3168-005-P1-K1-C1

Method BLASTN
NCBI GI g3790586
BLAST score 109
E value 3.0e-54
Match length 175
% identity 100

NCBI Description Arabidopsis thaliana RING-H2 finger protein RHF2a mRNA,

complete cds

Seq. No. 141790

Seq. ID LIB3168-005-P1-K1-C10

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141791

Seq. ID LIB3168-005-P1-K1-C12

Method BLASTX
NCBI GI g3695378
BLAST score 404
E value 2.0e-39
Match length 106
% identity 76

NCBI Description (AF096370) contains similarity to NAM (no apical meristem)

-like proteins [Arabidopsis thaliana]

Seq. No. 141792

Seq. ID LIB3168-005-P1-K1-C2

Method BLASTX
NCBI GI g1628583
BLAST score 351
E value 3.0e-33
Match length 81



% identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

141793 Seq. No.

LIB3168-005-P1-K1-C3 Seq. ID

Method BLASTX NCBI GI q1628583 BLAST score 599 E value 3.0e-62 Match length 120 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141794

LIB3168-005-P1-K1-C5 Seq. ID

Method BLASTX NCBI GI g112682 BLAST score 595 E value 8.0e-62 Match length 138 % identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

141795 Seq. No.

LIB3168-005-P1-K1-C6 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 767 5.0e-82 E value Match length 145 100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

141796 Seq. No.

Seq. ID LIB3168-005-P1-K1-C8

Method BLASTX g1628583 NCBI GI BLAST score 704 E value 1.0e-74 Match length 137 % identity 99

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141797

Seq. ID LIB3168-005-P1-K1-D1



BLASTX Method .g1628583 NCBI GI BLAST score 627 1.0e-65 E value 123 Match length 98 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

141798 Seq. No.

LIB3168-005-P1-K1-D10 Seq. ID

BLASTX Method NCBI GI g1628583 BLAST score 622 5.0e-65 E value 120 Match length 99 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

141799 Seq. No.

LIB3168-005-P1-K1-D11 Seq. ID

Method BLASTX g1703108 NCBI GI BLAST score 638 7.0e-67 E value 118 Match length 100 % identity

NCBI Description

ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis

thaliana]

Seq. No. 141800

LIB3168-005-P1-K1-D2 Seq. ID

Method BLASTX NCBI GI q112681 600 BLAST score 2.0e-62 E value 115 Match length 97 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936 emb_CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141801

LIB3168-005-P1-K1-D3 Seq. ID

Method BLASTX g1628583 NCBI GI BLAST score 684 3.0e-72E value 147 Match length



% identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 141802 Seq. No. LIB3168-005-P1-K1-D5 Seq. ID Method BLASTX g2244906 NCBI GI BLAST score 392 5.0e-38 E value Match length 116 69 % identity NCBI Description (Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana] 141803 Seq. No. LIB3168-005-P1-K1-D6 Seq. ID Method BLASTX g112739 NCBI GI BLAST score 184 7.0e-14 E value 35 Match length 97 % identity NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana] 141804 Seq. No. LIB3168-005-P1-K1-D7 Seq. ID Method BLASTX NCBI GI g1628583 BLAST score 595 5.0e-62 E value Match length 116 % identity 98 (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 141805 Seq. ID LIB3168-005-P1-K1-D8 Method BLASTX NCBI GI q1628583 BLAST score 625 E value 2.0e-65

Match length 120 % identity 100

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141806

17331



LIB3168-005-P1-K1-E1 Seq. ID Method BLASTX g1628583 NCBI GI BLAST score 625 2.0e-65 E value 120 Match length 100 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 141807 LIB3168-005-P1-K1-E10 Seq. ID Method BLASTX NCBI GI g112681 BLAST score 620 9.0e-65 E value 143 Match length % identity 84 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] 141808 Seq. No. LIB3168-005-P1-K1-E11 Seq. ID Method BLASTX g1628583 NCBI GI BLAST score 575 E value 2.0e-59 Match length 143 80 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 141809 Seq. No. LIB3168-005-P1-K1-E12 Seq. ID Method BLASTN NCBI GI a16231 BLAST score 78 E value 3.0e-36 Match length 109 % identity 93 Arabidopsis CRA1 gene for 12S seed storage protein NCBI Description >gi 166675 gb M37247 ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4 Seq. No. 141810 Seq. ID LIB3168-005-P1-K1-E2

Method BLASTX
NCBI GI g112741
BLAST score 728
E value 2.0e-77
Match length 137
% identity 99

17332



NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -

Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 141811

Seq. ID LIB3168-005-P1-K1-E3

Method BLASTX
NCBI GI g112737
BLAST score 566
E value 2.0e-58
Match length 137
% identity 80

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 141812

Seq. ID LIB3168-005-P1-K1-E5

Method BLASTX
NCBI GI g112682
BLAST score 620
E value 9.0e-65
Match length 143
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141813

Seq. ID LIB3168-005-P1-K1-E7

Method BLASTX
NCBI GI g1628583
BLAST score 593
E value 9.0e-62
Match length 116
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141814

Seq. ID LIB3168-005-P1-K1-E8

Method BLASTX
NCBI GI 94263523
BLAST score 176
E value 2.0e-34
Match length 136



```
% identity
NCBI Description
                  (AC004044) hypothetical protein [Arabidopsis thaliana]
                  141815
Seq. No.
                  LIB3168-005-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129659
BLAST score
                  378
E value
                  2.0e-36
Match length
                  120
% identity
                  68
                  oleosin, isoform 21K - Arabidopsis thaliana >gi_725260
NCBI Description
                  (L40954) oleosin [Arabidopsis thaliana]
Seq. No.
                  141816
                  LIB3168-005-P1-K1-F10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2864607
BLAST score
                  414
                  0.0e+00
E value
Match length
                  418
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
NCBI Description
                  (ESSAII project)
Seq. No.
                  141817
                  LIB3168-005-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129657
BLAST score
                  433
                  8.0e-43
E value
Match length
                  116
                  78
% identity
NCBI Description
                  oleosin isoform - Arabidopsis thaliana
                  >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
                  thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin
                  [Arabidopsis thaliana]
Seq. No.
                  141818
Seq. ID
                  LIB3168-005-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  611
E value
                  1.0e-63
Match length
                  117
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
```

Seq. No. 141819 Seq. ID LIB3168-005-P1-K1-F2

Method BLASTX
NCBI GI g112681
BLAST score 492
E value 8.0e-50
Match length 121



% identity

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141820

LIB3168-005-P1-K1-F3 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 411 3.0e-40 E value Match length 113 % identity 73

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141821

Seq. ID LIB3168-005-P1-K1-F5

Method BLASTX NCBI GI g116527 BLAST score 642 E value 2.0e-67 Match length 137 % identity 88

NCBI Description PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 196)

> >gi_1143166 (U32397) ClpP protease [Nicotiana tabacum] >gi 2924270 emb CAA77422 (Z00044) ATP-dependent protease

proteolytic subuni [Nicotiana tabacum]

Seq. No. 141822

LIB3168-005-P1-K1-F6 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 171 E value 4.0e-12 81 Match length 96 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141823

Seq. ID LIB3168-005-P1-K1-F7

Method BLASTX NCBI GI g112682 BLAST score 580 3.0e-60 E value Match length 110 % identity 99

12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]



Seq. No. 141824

Seq. ID LIB3168-005-P1-K1-F8

Method BLASTX
NCBI GI g2194142
BLAST score 164
E value 7.0e-43
Match length 104
% identity 92

NCBI Description (AC002062) ESTs gb_N38288,gb_T43486,gb_AA395242 come from

this gene. [Arabidopsis thaliana]

Seq. No. 141825

Seq. ID LIB3168-005-P1-K1-F9

Method BLASTN
NCBI GI g2182286
BLAST score 71
E value 9.0e-32
Match length 115
% identity 90

NCBI Description Sequence of BAC F20P5 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 141826

Seq. ID LIB3168-005-P1-K1-G1

Method BLASTN
NCBI GI 94490717
BLAST score 253
E value 1.0e-140
Match length 395
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA

project)

Seq. No. 141827

Seq. ID LIB3168-005-P1-K1-G10

Method BLASTX
NCBI GI g112739
BLAST score 471
E value 3.0e-47
Match length 131
% identity 73

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 141828

Seq. ID LIB3168-005-P1-K1-G12

Method BLASTN
NCBI GI g3449330
BLAST score 415
E value 0.0e+00
Match length 430

Contraction of the second



Seq. No. 141829

Seq. ID LIB3168-005-P1-K1-G2

Method BLASTX
NCBI GI g112682
BLAST score 574
E value 2.0e-59
Match length 119
% identity 89

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141830

Seq. ID LIB3168-005-P1-K1-G3

Method BLASTN
NCBI GI g903687
BLAST score 60
E value 5.0e-25
Match length 170
% identity 90

NCBI Description Arabidopsis thaliana leucine zipper mRNA, complete cds

Seq. No. 141831

Seq. ID LIB3168-005-P1-K1-G5

Method BLASTX
NCBI GI 94510377
BLAST score 322
E value 5.0e-32
Match length 142
% identity 56

NCBI Description (AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No. 141832

Seq. ID LIB3168-005-P1-K1-G6

Method BLASTX
NCBI GI g1628583
BLAST score 404
E value 8.0e-40
Match length 83
% identity 96

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141833

Seq. ID LIB3168-005-P1-K1-G7

Method BLASTX
NCBI GI g1628583
BLAST score 316
E value 4.0e-29
Match length 60



% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141834

Seq. ID LIB3168-005-P1-K1-G8

Method BLASTX
NCBI GI g112681
BLAST score 603
E value 8.0e-63
Match length 121
% identity 98

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141835

Seq. ID LIB3168-005-P1-K1-H1

Method BLASTX
NCBI GI g112681
BLAST score 577
E value 1.0e-59
Match length 140
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141836

Seq. ID LIB3168-005-P1-K1-H11

Method BLASTN NCBI GI g2760164

BLAST score 42 E value 3.0e-14 Match length 295 % identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18P6, complete sequence [Arabidopsis thaliana]

Seq. No. 141837

Seq. ID LIB3168-005-P1-K1-H12

Method BLASTX
NCBI GI g1628583
BLAST score 482
E value 1.0e-48
Match length 124
% identity 77

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141838



```
LIB3168-005-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3335171
BLAST score
                  607
                  3.0e-63
E value
Match length
                  132
                  90
% identity
NCBI Description (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]
                  141839
Seq. No.
                  LIB3168-005-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  335
                  1.0e-71
E value
Match length
                  140
                  97
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq No.
                  141840
                  LIB3168-005-P1-K1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3063690
BLAST score
                  307
                  1.0e-172
E value
                  347
Match length
                  97
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11
                  (ESSAII project)
Seq. No.
                  141841
Seq. ID
                  LIB3168-005-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q3176874
BLAST score
                  597
                  4.0e-62
E value
Match length
                  115
% identity
                  98
                  (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  141842
Seq. ID
                  LIB3168-005-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q3063460
BLAST score
                  99
E value
                  3.0e-30
Match length
                  80
% identity
                  97
NCBI Description (AC003981) F22013.22 [Arabidopsis thaliana]
```

Seq. No. 141843

Seq. ID LIB3168-006-P1-K1-A1

Method BLASTX NCBI GI g1628583



BLAST score 636 E value 1.0e-66 Match length 123 % identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141844

Seq. ID LIB3168-006-P1-K1-A10

Method BLASTX
NCBI GI g2129657
BLAST score 535
E value 1.0e-54
Match length 137
% identity 81

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 141845

Seq. ID LIB3168-006-P1-K1-A11

Method BLASTX
NCBI GI g2129657
BLAST score 300
E value 3.0e-27
Match length 126
% identity 54

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 141846

Seq. ID LIB3168-006-P1-K1-A12

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141847

Seq. ID LIB3168-006-P1-K1-A2

Method BLASTX
NCBI GI g112682
BLAST score 676
E value 3.0e-71
Match length 138
% identity 91

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis



thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

141848 Seq. No. LIB3168-006-P1-K1-A3 Seq. ID Method BLASTX NCBI GI q1628583 BLAST score 386 3.0e-37 E value Match length 96 79 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 141849 Seq. No. LIB3168-006-P1-K1-A4 Seq. ID BLASTN Method g3482964 NCBI GI BLAST score 191 1.0e-103 E value 374 Match length 98 % identity Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4 NCBI Description (ESSAII project) Seq. No. 141850 LIB3168-006-P1-K1-A5 Seq. ID Method BLASTX NCBI GI q1628583 BLAST score 645 E value 1.0e-67 Match length 146 86 % identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 141851 Seq. ID LIB3168-006-P1-K1-A6 Method BLASTX NCBI GI g112681 BLAST score 696 E value 1.0e-73 Match length 142 94 % identity NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir \$08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141852

Seq. ID LIB3168-006-P1-K1-A8

Method BLASTX g112682 NCBI GI BLAST score 526



E value 7.0e-54 Match length 117 % identity 85

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141853

Seq. ID LIB3168-006-P1-K1-A9

Method BLASTX
NCBI GI g112681
BLAST score 705
E value 9.0e-75
Match length 134
% identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141854

Seq. ID LIB3168-006-P1-K1-B10

Method BLASTX
NCBI GI 94455276
BLAST score 505
E value 3.0e-51
Match length 117
% identity 86

NCBI Description (AL035527) peptide transporter-like protein [Arabidopsis

thaliana]

Seq. No. 141855

Seq. ID LIB3168-006-P1-K1-B11

Method BLASTX
NCBI GI g1628583
BLAST score 216
E value 1.0e-17
Match length 45
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141856

Seq. ID LIB3168-006-P1-K1-B12

Method BLASTN
NCBI GI 94490734
BLAST score 459
E value 0.0e+00
Match length 482
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA

project)



Seq. No. 141857 Seq. ID LIB316

LIB3168-006-P1-K1-B2

Method BLASTX
NCBI GI g4454026
BLAST score 390
E value 9.0e-38
Match length 90
% identity 82

NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No.

141858

Seq. ID

LIB3168-006-P1-K1-B3

Method BLASTX
NCBI GI g3080400
BLAST score 576
E value 1.0e-60
Match length 150
% identity 82

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

>gi_4455264_emb_CAB36800.1_ (AL035527) putative protein

[Arabidopsis thaliana]

Seq. No.

141859

Seq. ID LIB3168-006-P1-K1-B4

Method BLASTX
NCBI GI g2887500
BLAST score 294
E value 2.0e-26
Match length 61
% identity 87

NCBI Description (AC002339) putative AP2 domain-containing protein

[Arabidopsis thaliana]

Seq. No.

141860

Seq. ID LIB3168-006-P1-K1-B5

Method BLASTX
NCBI GI g1628583
BLAST score 667
E value 3.0e-70
Match length 129
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141861

Seq. ID LIB3168-006-P1-K1-B8

Method BLASTX
NCBI GI g1628583
BLAST score 642
E value 3.0e-67
Match length 123
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]



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Seq. No.
                  141862
                  LIB3168-006-P1-K1-B9
Seq. ID
Method
                  BLASTN
                  g2182289
NCBI GI
                  59
BLAST score
                  2.0e-24
E value
Match length
                  358
                  89
% identity
NCBI Description Arabidopsis thaliana chromosome I BAC F11P17 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  141863
Seq. No.
                  LIB3168-006-P1-K1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2264311
                  98
BLAST score
                  1.0e-47
E value
Match length
                  428
                  87
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MLN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  141864
                  LIB3168-006-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  614
                  4.0e-64
E value
Match length
                  129
                  91
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  141865
                  LIB3168-006-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  625
                  2.0e-65
E value
                  120
Match length
                  100
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  141866
Seq. ID
                  LIB3168-006-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g112737
```

BLAST score 715 9.0e-76 E value Match length 164 % identity 84

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE



PROTEIN) >qi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No. 141867 LIB3168-006-P1-K1-C3 Seq. ID Method BLASTX NCBI GI g2129657 BLAST score 596 7.0e-62 E value Match length 156

% identity NCBI Description oleosin isoform - Arabidopsis thaliana

>qi 987014 emb CAA90877 (Z54164) oleosin [Arabidopsis thaliana] >qi 987016 emb CAA90878 (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 141868

LIB3168-006-P1-K1-C4 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 525 E value 1.0e-53 Match length 133 78 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141869

LIB3168-006-P1-K1-C5 Seq. ID

BLASTX Method NCBI GI g112681 BLAST score 783 7.0e-84 E value Match length 148 % identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir \$08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141870

LIB3168-006-P1-K1-C6 Seq. ID

Method BLASTX g1628583 NCBI GI BLAST score 642 E value 3.0e-68 Match length 133 % identity NCBI Description

(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]



Seq. No. 141871

Seq. ID LIB3168-006-P1-K1-C7

Method BLASTX NCBI GI g1628583 BLAST score 411 4.0e-40 E value 117 Match length 72 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

141872 Seq. No.

Seq. ID LIB3168-006-P1-K1-C8

Method BLASTX NCBI GI q112737 571 BLAST score 5.0e-59 E value 137 Match length % identity 81

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

> PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 141873

LIB3168-006-P1-K1-C9 Seq. ID

Method BLASTX NCBI GI g112681 BLAST score 650 E value 3.0e-68 Match length 159 81 % identity

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141874

Seq. ID LIB3168-006-P1-K1-D1

Method BLASTX NCBI GI q1628583 BLAST score 521 E value 3.0e-53 Match length 110 % identity 91

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

141875 Seq. No.

Seq. ID LIB3168-006-P1-K1-D10



Method BLASTX
NCBI GI g1628583
BLAST score 642
E value 3.0e-67
Match length 123
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141876

Seq. ID LIB3168-006-P1-K1-D11

Method BLASTX
NCBI GI g119143
BLAST score 766
E value 9.0e-82
Match length 149
% identity 99

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_81606_pir__S06724 translation elongation factor eEF-1
alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
(X16430) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1369927_emb_CAA34454_ (X16431) elongation factor
1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_
(X16431) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana]
>gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana]
>gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No. 141877

Seq. ID LIB3168-006-P1-K1-D12

Method BLASTX
NCBI GI 94406820
BLAST score 453
E value 3.0e-45
Match length 86
% identity 100

NCBI Description (AC006201) putative ras superfamily member [Arabidopsis

thaliana]

Seq. No. 141878

Seq. ID LIB3168-006-P1-K1-D2

Method BLASTN
NCBI GI g4589411
BLAST score 71
E value 2.0e-31
Match length 209
% identity 61

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F5H8, complete sequence

Seq. No. 141879

Seq. ID LIB3168-006-P1-K1-D3

Method BLASTX
NCBI GI g1628583
BLAST score 358
E value 5.0e-34



Match length 89 % identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141880

Seq. ID LIB3168-006-P1-K1-D5

Method BLASTX
NCBI GI g112682
BLAST score 661
E value 2.0e-69
Match length 153
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141881

Seq. ID LIB3168-006-P1-K1-D6

Method BLASTX
NCBI GI g1628583
BLAST score 568
E value 2.0e-58
Match length 140
% identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141882

Seq. ID LIB3168-006-P1-K1-D7

Method BLASTX
NCBI GI g112682
BLAST score 693
E value 3.0e-73
Match length 157
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937 emb_CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141883

Seq. ID LIB3168-006-P1-K1-D8

Method BLASTX
NCBI GI g112741
BLAST score 866
E value 2.0e-93
Match length 164
% identity 98

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -

Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit



3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No. 141884

Seq. ID LIB3168-006-P1-K1-D9

Method BLASTX
NCBI GI g1531762
BLAST score 195
E value 8.0e-15
Match length 51
% identity 75

NCBI Description (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis

thaliana]

Seq. No. 141885

Seq. ID LIB3168-006-P1-K1-E1

Method BLASTX
NCBI GI g131332
BLAST score 307
E value 5.0e-28
Match length 70
% identity 90

NCBI Description PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_72716_pir__F2RZ0P

photosystem II phosphoprotein psbH - rice chloroplast

>gi_11953_emb_CAA31204_ (X12695) 10 kD phosphoprotein (AA 1
- 73) [Oryza sativa] >gi_12016_emb_CAA33976_ (X15901) PSII

10kDa phosphoprotein [Oryza sativa]

>gi_226635_prf__1603356BJ photosystem II 10kD

phosphoprotein [Oryza sativa]

Seq. No. 141886

Seq. ID LIB3168-006-P1-K1-E10

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141887

Seq. ID LIB3168-006-P1-K1-E11

Method BLASTX
NCBI GI g114330
BLAST score 530
E value 4.0e-54
Match length 142
% identity 73

NCBI Description PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)

>gi_67972_pir__PXMUP1 H+-transporting ATPase (EC 3.6.1.35)
type 1, plasma membrane - Arabidopsis thaliana >gi_166746
(M24107) plasma membrane proton pump H+ ATPase [Arabidopsis

thaliana]



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Seq. No.
                   141888
                   LIB3168-006-P1-K1-E2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4753645
BLAST score
                   114
                   1.0e-57
E value
Match length
                   152
% identity
                   92
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18
NCBI Description
                   (ESSA project)
Seq. No.
                   141889
Seq. ID
                   LIB3168-006-P1-K1-E3
Method
                   BLASTN
NCBI GI
                   g2842474
                   138
BLAST score
                   4.0e-72
E value
Match length
                   138
% identity
                   100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
                   (ESSAII project)
                   141890
Seq. No.
                   LIB3168-006-P1-K1-E4
Seq. ID
Method
                   BLASTX
                   g1791307
NCBI GI
BLAST score
                   710
E value
                   1.0e-77
Match length
                   156
                   96
% identity
NCBI Description (U83501) permease homolog [Arabidopsis thaliana]
Seq. No.
                   141891
                   LIB3168-006-P1-K1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q112737
BLAST score
                   545
E value
                   5.0e-56
Match length
                   135
                   79
% identity
                   2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68853_pir__ NWMU1 2S albumin 1 precursor -
Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                   1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                   >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                   precursor [Arabidopsis thaliana]
```

Seq. No. 141892

Seq. ID LIB3168-006-P1-K1-E6

Method BLASTX
NCBI GI g2088652
BLAST score 716
E value 6.0e-76
Match length 150
% identity 91



NCBI Description (AF002109) 26S proteasome regulatory subunit S12 isolog [Arabidopsis thaliana] >gi_2351376 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis thaliana]

Seq. No. 141893

Seq. ID LIB3168-006-P1-K1-E7

Method BLASTX
NCBI GI g3540206
BLAST score 191
E value 2.0e-14
Match length 104
% identity 18

NCBI Description (AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 141894

Seq. ID LIB3168-006-P1-K1-E8

Method BLASTX
NCBI GI g3367515
BLAST score 491
E value 1.0e-49
Match length 103
% identity 92

NCBI Description (AC004392) Similar to

glucose-6-phosphate/phosphate-translocator (GPT)

gb_AF020814 from Pisum sativum. [Arabidopsis thaliana]

Seq. No. 141895

Seq. ID LIB3168-006-P1-K1-E9

Method BLASTX
NCBI GI g3335169
BLAST score 907
E value 3.0e-98
Match length 169
% identity 99

NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No. 141896

Seq. ID LIB3168-006-P1-K1-F1

Method BLASTN
NCBI GI g2828182
BLAST score 397
E value 0.0e+00
Match length 397
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No. 141897

Seq. ID LIB3168-006-P1-K1-F11

Method BLASTX
NCBI GI g112682
BLAST score 748
E value 1.0e-79
Match length 161

17351



% identity 8

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141898

Seq. ID LIB3168-006-P1-K1-F12

Method BLASTN
NCBI GI g3128140
BLAST score 219
E value 1.0e-120
Match length 438
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJE4, complete sequence [Arabidopsis thaliana]

Seq. No. 141899

Seq. ID LIB3168-006-P1-K1-F2

Method BLASTX
NCBI GI g1169476
BLAST score 613
E value 6.0e-64
Match length 117
% identity 100

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE

ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632)

vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No. 141900

Seq. ID LIB3168-006-P1-K1-F3

Method BLASTN
NCBI GI g3402745
BLAST score 265
E value 1.0e-147
Match length 269
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5

(ESSAII project)

Seq. No. 141901

Seq. ID LIB3168-006-P1-K1-F4

Method BLASTX
NCBI GI g112682
BLAST score 799
E value 1.0e-85
Match length 165
% identity 92

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidops $\overline{\mathrm{i}}\mathrm{s}$ thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141902

Seq. ID LIB3168-006-P1-K1-F5



Method BLASTX
NCBI GI g1628583
BLAST score 667
E value 3.0e-70
Match length 141
% identity 91

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141903

Seq. ID LIB3168-006-P1-K1-F6

Method BLASTX
NCBI GI g231536
BLAST score 344
E value 2.0e-32
Match length 105
% identity 67

NCBI Description CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)
(LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL

AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase

(EC 3.4.11.1) - Arabidopsis thaliana

>gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase
[Arabidopsis thaliana] >gi_4115380 (AC005967) putative

leucine aminopeptidase [Arabidopsis thaliana]

Seq. No. 141904

Seq. ID LIB3168-006-P1-K1-F7

Method BLASTX
NCBI GI g4490339
BLAST score 86
E value 3.0e-14
Match length 141
% identity 45

NCBI Description (AL035656) putative protein [Arabidopsis thaliana]

Seq. No. 141905

Seq. ID LIB3168-006-P1-K1-F8

Method BLASTX
NCBI GI g112741
BLAST score 846
E value 4.0e-91
Match length 160
% identity 98

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 141906

Seq. ID LIB3168-006-P1-K1-F9

Method BLASTX NCBI GI g629528 BLAST score 546



```
4.0e-56
E value
Match length
                  116
                  99
% identity
                  hypothetical protein - Arabidopsis thaliana
NCBI Description
                  >gi 1076335 pir S51580 hypothetical protein 1 -
                  Arabidopsis thaliana >gi_499167_emb_CAA56144_ (X79707) ORF
                  [Arabidopsis thaliana]
Seq. No.
                  141907
                  LIB3168-006-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220477
BLAST score
                  521
E value
                  3.0e-53
Match length
                  104
                  100
% identity
                  (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                  141908
Seq. No.
                  LIB3168-006-P1-K1-G10
Seq. ID
Method
                  BLASTX
                  g231536
NCBI GI
BLAST score
                  714
                  1.0e-75
E value
                  166
Match length
% identity
                  89
                  CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)
NCBI Description
                  (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL
                  AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase
                  (EC 3.4.11.1) - Arabidopsis thaliana
                  >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase
                  [Arabidopsis thaliana] >gi 4115380 (AC005967) putative
                  leucine aminopeptidase [Arabidopsis thaliana]
Seq. No.
                  141909
                  LIB3168-006-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  408
E value
                  1.0e-39
                  78
Match length
                  97
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
```

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141910

Seq. ID LIB3168-006-P1-K1-G2

Method BLASTX NCBI GI g4204298 BLAST score 634 E value 2.0e-66 Match length 157 % identity 80

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]



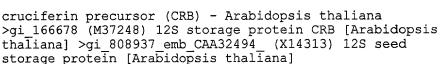
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Seq. No.
                  141911
Seq. ID
                  LIB3168-006-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q633890
BLAST score
                  422
E value
                  2.0e-41
Match length
                  146
% identity
                  60
                  (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
NCBI Description
                  vulgare]
Seq. No.
                  141912
                  LIB3168-006-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4432839
BLAST score
                  664
                  8.0e-70
E value
Match length
                  130
                  98
% identity
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                  141913
                  LIB3168-006-P1-K1-G5
Seq. ID
Method
                  BLASTX
                  g3157930
NCBI GI
BLAST score
                  707
E value
                  7.0e-75
Match length
                  152
% identity
                  91
NCBI Description
                  (AC002131) Strong similarity to
                  amino-cyclopropane-carboxylic acid oxidase gb L27664 from
                  Brassica napus. ESTs gb Z48548 and gb Z48549 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  141914
Seq. ID
                  LIB3168-006-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  643
E value
                  2.0e-67
Match length
                  170
% identity
                  79
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  141915
Seq. No.
Seq. ID
                  LIB3168-006-P1-K1-G8
                  BLASTX
Method
                  g112682
NCBI GI
BLAST score
                  685
                  3.0e-72
E value
                  139
Match length
```

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

91

% identity





```
141916
Seq. No.
Seq. ID
                  LIB3168-006-P1-K1-G9
Method
                  BLASTX
                  q4586249
NCBI GI
BLAST score
                  369
E value
                  2.0e-35
Match length
                  119
% identity
                  (AL049640) putative pollen surface protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  141917
Seq. ID
                  LIB3168-006-P1-K1-H1
Method
                  BLASTX
                  g1628583
NCBI GI
                  394
BLAST score
                  3.0e-38
E value
Match length
                  97
% identity
                  80
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  141918
                  LIB3168-006-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                   635
E value
                   2.0e-66
Match length
                   123
% identity
                   99
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   141919
                  LIB3168-006-P1-K1-H11
Seq. ID
                  BLASTN
Method
                  g4757399
NCBI GI
BLAST score
                   163
E value
                   1.0e-86
                   355
Match length
% identity
                   86
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MEE13, complete sequence
                   141920
Seq. No.
```

Seq. ID LIB3168-006-P1-K1-H12

Method BLASTN NCBI GI g16231 BLAST score 48 E value 6.0e-18



Match length 120 % identity 92

NCBI Description Arabidopsis CRA1 gene for 12S seed storage protein

>gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage

protein CRA1 gene, exons 1-4

Seq. No. 141921

Seq. ID LIB3168-006-P1-K1-H2

Method BLASTX
NCBI GI g112681
BLAST score 571
E value 5.0e-59
Match length 149
% identity 79

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141922

Seq. ID LIB3168-006-P1-K1-H5

Method BLASTX
NCBI GI g112737
BLAST score 651
E value 1.0e-69
Match length 146
% identity 91

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit

1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 141923

Seq. ID LIB3168-006-P1-K1-H6

Method BLASTX
NCBI GI g112681
BLAST score 655
E value 9.0e-69
Match length 166
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141924

Seq. ID LIB3168-006-P1-K1-H7

Method BLASTX
NCBI GI g112682
BLAST score 175
E value 7.0e-15
Match length 92



 Seq. No.
 141925

 Seq. ID
 LIB3168-006-P1-K1-H8

 Method
 BLASTX

 NCBI GI
 g2827635

 BLAST score
 639

BLAST score 639
E value 6.0e-67
Match length 138
% identity 93

NCBI Description (AL021636) predicted protein [Arabidopsis thaliana]

Seq. No. 141926

Seq. ID LIB3168-006-P1-K1-H9

Method BLASTX
NCBI GI g1628583
BLAST score 620
E value 8.0e-65
Match length 119
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141927

Seq. ID LIB3168-007-P1-K1-A1

Method BLASTX
NCBI GI g112737
BLAST score 679
E value 1.0e-71
Match length 142
% identity 89

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 141928

Seq. ID LIB3168-007-P1-K1-A11

Method BLASTN
NCBI GI g3869075
BLAST score 371
E value 0.0e+00
Match length 379
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXK3, complete sequence [Arabidopsis thaliana]

Seq. No. 141929



```
LIB3168-007-P1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2894604
BLAST score
                   369
                   3.0e - 35
E value
                   92
Match length
                   80
% identity
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   141930
Seq. No.
                   LIB3168-007-P1-K1-A2
Seq. ID
Method
                   BLASTX
                   g1628583
NCBI GI
BLAST score
                   423
                   2.0e-41
E value
                   107
Match length
                   82
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   141931
Seq. No.
                   LIB3168-007-P1-K1-A3
Seq. ID
Method
                   BLASTN
                   g2842474
NCBI GI
BLAST score
                   136
                   2.0e-70
E value
Match length
                   285
% identity
                   61
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
                   (ESSAII project)
                   141932
Seq. No.
                   LIB3168-007-P1-K1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   666
                   5.0e-70
E value
                   167
Match length
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   141933
Seq. ID
                   LIB3168-007-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   q112737
BLAST score
                   755
E value
                   2.0e-80
Match length
                   153
                   92
% identity
                   2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
```

1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]



>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
precursor [Arabidopsis thaliana]

Seq. No. 141934

Seq. ID LIB3168-007-P1-K1-A7

Method BLASTX
NCBI GI g1628583
BLAST score 221
E value 3.0e-18
Match length 49
% identity 94

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141935

Seq. ID LIB3168-007-P1-K1-A8

Method BLASTX
NCBI GI g112682
BLAST score 713
E value 1.0e-75
Match length 160
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141936

Seq. ID LIB3168-007-P1-K1-A9

Method BLASTX
NCBI GI g1628583
BLAST score 728
E value 3.0e-77
Match length 175
% identity 83

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141937

Seq. ID LIB3168-007-P1-K1-B10

Method BLASTX
NCBI GI g1332579
BLAST score 445
E value 2.0e-44
Match length 108
% identity 9

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 141938

Seq. ID LIB3168-007-P1-K1-B11

Method BLASTX
NCBI GI g2129657
BLAST score 377
E value 3.0e-36

17360



Match length 76 % identity

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi 987014 emb CAA90877 (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 141939

LIB3168-007-P1-K1-B2 Seq. ID

Method BLASTN g4589428 NCBI GI 365 BLAST score E value 0.0e + 00Match length 453 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MFH8, complete sequence

141940 Seq. No.

LIB3168-007-P1-K1-B4 Seq. ID

BLASTX Method g2129657 NCBI GI BLAST score 545 E value 8.0e-56 Match length 140 81 % identity

oleosin isoform - Arabidopsis thaliana NCBI Description

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi 987016 emb CAA90878_ (Z54165) oleosin

[Arabidopsis thaliana]

141941 Seq. No.

LIB3168-007-P1-K1-B5 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 158 E value 5.0e-11 47 Match length % identity 66

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

141942 Seq. No.

Seq. ID LIB3168-007-P1-K1-B6

Method BLASTX NCBI GI g113026 BLAST score 638 E value 7.0e-67 Match length 127 % identity

ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) NCBI Description

>gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape
>gi_255220_bbs_112862 isocitrate lyase, threo-D

S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A

E value

Match length



isocitrate lyase [Brassica napus]

```
Seq. No.
                  141943
                  LIB3168-007-P1-K1-B7
Seq. ID
Method
                  BLASTN
                  g3309276
NCBI GI
BLAST score
                  203
E value
                  1.0e-110
Match length
                  414
                  99
% identity
                  Arabidopsis thaliana BAC T26N6 from chromosome IV at 19.3
NCBI Description
                  cM, complete sequence
Seq. No.
                  141944
Seq. ID
                  LIB3168-007-P1-K1-B8
Method
                  BLASTX
                  g4204298
NCBI GI
                  233
BLAST score
E value
                  2.0e-19
                  109
Match length
                  49
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  141945
Seq. No.
                  LIB3168-007-P1-K1-C1
Seq. ID
                  BLASTX
Method
                  g112682
NCBI GI
BLAST score
                   581
                   3.0e-60
E value
                  107
Match length
                  100
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi 808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   141946
Sea. ID
                  LIB3168-007-P1-K1-C10
Method
                  BLASTX
NCBI GI
                   g1628583
BLAST score
                   642
E value
                   3.0e-67
Match length
                   123
                   100
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   141947
Seq. No.
Seq. ID
                  LIB3168-007-P1-K1-C11
                  BLASTX
Method
NCBI GI
                   g112737
BLAST score
                   715
```

17362

9.0e-76

164



% identity 83
NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_(AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No. 141948

Seq. ID LIB3168-007-P1-K1-C12

Method BLASTX
NCBI GI g112682
BLAST score 596
E value 6.0e-62
Match length 141
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141949

Seq. ID LIB3168-007-P1-K1-C3

Method BLASTX
NCBI GI g1628583
BLAST score 450
E value 1.0e-44
Match length 103
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141950

Seq. ID LIB3168-007-P1-K1-C4

Method BLASTN
NCBI GI g4454004
BLAST score 42
E value 3.0e-15
Match length 63
% identity 89

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6

(ESSAII project)

Seq. No. 141951

Seq. ID LIB3168-007-P1-K1-C5

Method BLASTX
NCBI GI g112682
BLAST score 466
E value 1.0e-46
Match length 105
% identity 85

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis



thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 141952

Seq. ID LIB3168-007-P1-K1-C6

Method BLASTX
NCBI GI g4510362
BLAST score 110
E value 7.0e-50
Match length 106
% identity 94

NCBI Description (AC007017) hypothetical protein [Arabidopsis thaliana]

Seq. No. 141953

Seg. ID LIB3168-007-P1-K1-C7

Method BLASTX
NCBI GI g1628583
BLAST score 223
E value 2.0e-43
Match length 123
% identity 77

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141954

Seq. ID LIB3168-007-P1-K1-C8

Method BLASTX
NCBI GI g1628583
BLAST score 796
E value 3.0e-85
Match length 164
% identity 93

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141955

Seq. ID LIB3168-007-P1-K1-C9

Method BLASTX
NCBI GI g2129767
BLAST score 73
E value 5.0e-41
Match length 131
% identity 65

NCBI Description vacuolar processing enzyme (EC 3.4.22.-) isozyme beta

precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_

(D61394) beta-VPE [Arabidopsis thaliana]

Seq. No. 141956

Seq. ID LIB3168-007-P1-K1-D1

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

17364



NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141957

Seq. ID LIB3168-007-P1-K1-D10

Method BLASTX
NCBI GI g1628583
BLAST score 648
E value 5.0e-68
Match length 150
% identity 85

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141958

Seq. ID LIB3168-007-P1-K1-D11

Method BLASTX
NCBI GI g3367534
BLAST score 824
E value 1.0e-88
Match length 165
% identity 98

NCBI Description (AC004392) Strong similarity to coatamer alpha subunit

(HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis

thaliana]

Seq. No. 141959

Seq. ID LIB3168-007-P1-K1-D12

Method BLASTX
NCBI GI g456568
BLAST score 697
E value 1.0e-73
Match length 141
% identity 89

NCBI Description (L29077) ubiquitin conjugating enzyme [Pisum sativum]

Seq. No. 141960

Seq. ID LIB3168-007-P1-K1-D2

Method BLASTX
NCBI GI g112737
BLAST score 724
E value 8.0e-77
Match length 164
% identity 84

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 141961

Seq. ID LIB3168-007-P1-K1-D3

Method BLASTX

17365



NCBI GI g112682 BLAST score 775 E value 8.0e-83 Match length 171 % identity 86

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141962

Seq. ID LIB3168-007-P1-K1-D4

Method BLASTX
NCBI GI g1628583
BLAST score 642
E value 3.0e-67
Match length 123
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141963

Seq. ID LIB3168-007-P1-K1-D5

Method BLASTX
NCBI GI g112682
BLAST score 705
E value 1.0e-74
Match length 160
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141964

Seq. ID LIB3168-007-P1-K1-D6

Method BLASTX
NCBI GI g112681
BLAST score 757
E value 1.0e-80
Match length 167
% identity 87

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141965

Seq. ID LIB3168-007-P1-K1-D7

Method BLASTX
NCBI GI g112737
BLAST score 727
E value 3.0e-77



Seq. No. 141966
Seq. ID LIB3168-007-P1-K1-D8
Method BLASTX
NCBI GI g1628583
BLAST score 841
E value 1.0e-90
Match length 173
% identity 94

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

 Seq. No.
 141967

 Seq. ID
 LIB3168-007-P1-K1-D9

 Method
 BLASTX

 NCBI GI
 q112682

NCBI GI g112682
BLAST score 622
E value 6.0e-65
Match length 145
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141968

Seq. ID LIB3168-007-P1-K1-E10

Method BLASTN
NCBI GI g3228389
BLAST score 378
E value 0.0e+00
Match length 402
% identity 99

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17L21,

complete sequence [Arabidopsis thaliana]

Seq. No. 141969

Seq. ID LIB3168-007-P1-K1-E11

Method BLASTX
NCBI GI g112681
BLAST score 594
E value 1.0e-61
Match length 144
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana



>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
storage protein [Arabidopsis thaliana]

Seq. No. 141970

Seq. ID LIB3168-007-P1-K1-E12

Method BLASTX
NCBI GI g112739
BLAST score 286
E value 4.0e-26
Match length 70
% identity 79

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi 4490711 emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 141971

Seq. ID LIB3168-007-P1-K1-E2

Method BLASTN
NCBI GI g2477521
BLAST score 386
E value 0.0e+00
Match length 386
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 141972

Seq. ID LIB3168-007-P1-K1-E3

Method BLASTX
NCBI GI g1628583
BLAST score 618
E value 1.0e-64
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141973

Seq. ID LIB3168-007-P1-K1-E4

Method BLASTX
NCBI GI g1628583
BLAST score 635
E value 2.0e-66
Match length 123
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141974

Seq. ID LIB3168-007-P1-K1-E5

17368



```
Method
                  BLASTX
NCBI GI
                  q3915961
BLAST score
                  149
                  4.0e-10
E value
                  61
Match length
                  54
% identity
NCBI Description HYPOTHETICAL 267 KD PROTEIN (ORF 2280)
                  >gi 2924274 emb CAA77427 (Z00044) Ycf2 protein [Nicotiana
                  tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical
                  protein [Nicotiana tabacum]
                  141975
Seq. No.
Seq. ID
                  LIB3168-007-P1-K1-E6
Method
                  BLASTX
                  g112681
NCBI GI
                  763
BLAST score
                  2.0e-81
E value
                  152
Match length
% identity
                  99
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  141976
                  LIB3168-007-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
                  836
BLAST score
                  6.0e-90
E value
                  173
Match length
                   94
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   141977
Seq. ID
                  LIB3168-007-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q384341
BLAST score
                   206
E value
                   4.0e-16
Match length
                   109
% identity
                   40
NCBI Description major storage protein [Theobroma cacao]
Seq. No.
                  141978
Seq. ID
                  LIB3168-007-P1-K1-F1
Method
                  BLASTX
                   q112681
NCBI GI
                   655
BLAST score
                   8.0e-69
E value
Match length
                   150
```

cruciferin precursor (CRA1) - Arabidopsis thaliana

85

% identity

NCBI Description

12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509



>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
storage protein [Arabidopsis thaliana]

 Seq. No.
 141979

 Seq. ID
 LIB3168-007-P1-K1-F10

 Method
 BLASTX

Method BLASTX
NCBI GI g112682
BLAST score 556
E value 3.0e-57
Match length 131
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 141980

Seq. ID LIB3168-007-P1-K1-F11

Method BLASTX
NCBI GI g112741
BLAST score 887
E value 6.0e-96
Match length 164
% identity 99

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 141981

Seq. ID LIB3168-007-P1-K1-F3

Method BLASTX
NCBI GI g1628583
BLAST score 364
E value 8.0e-35
Match length 67
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141982

Seq. ID LIB3168-007-P1-K1-F4

Method BLASTX
NCBI GI g1628583
BLAST score 736
E value 2.0e-78
Match length 145
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]



Seq. No. 141983 LIB3168-007-P1-K1-F5 Seq. ID Method BLASTN g2583106 NCBI GI 185 BLAST score 1.0e-99 E value

270

73 % identity Arabidopsis thaliana chromosome II BAC F4L23 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

141984 Seq. No.

Match length

LIB3168-007-P1-K1-F6 Seq. ID

Method BLASTX g1170373 NCBI GI BLAST score 682 6.0e-72 E value 133 Match length 99 % identity

HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 NCBI Description heat shock cognate protein 70-1 - Arabidopsis thaliana

>gi 397482 emb CAA52684 (X74604) heat shock protein 70

cognate [Arabidopsis thaliana]

141985 Seq. No.

LIB3168-007-P1-K1-F7 Seq. ID

Method BLASTX g1628583 NCBI GI 620 BLAST score 1.0e-64 E value 119 Match length 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 141986

Seq. ID LIB3168-007-P1-K1-F8

Method BLASTX q1628583 NCBI GI 769 BLAST score 3.0e-82 E value 146 Match length % identity 100

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

141987 Seq. No.

LIB3168-007-P1-K1-F9 Seq. ID

Method BLASTX NCBI GI g112741 BLAST score 461 E value 3.0e-46 102 Match length 85 % identity

17371



```
2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir_NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  141988
Seq. No.
                  LIB3168-007-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  588
                  5.0e-61
E value
Match length
                  140
% identity
                  81
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >qi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi_4490710_emb_CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  141989
Seq. ID
                  LIB3168-007-P1-K1-G11
Method
                  BLASTX
                  g2129657
NCBI GI
BLAST score
                  509
                  1.0e-51
E value
                  131
Match length
% identity
                  81
                  oleosin isoform - Arabidopsis thaliana
NCBI Description
                  >gi 987014 emb CAA90877 (Z54164) oleosin [Arabidopsis
                  thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin
                  [Arabidopsis thaliana]
                  141990
Seq. No.
                  LIB3168-007-P1-K1-G12
Seq. ID
Method
                  BLASTX
                  g1619602
NCBI GI
                  385
BLAST score
                  3.0e-37
E value
                  96
Match length
                  75
% identity
NCBI Description
                 (Y08726) MtN3 [Medicago truncatula]
                  141991
Seq. No.
                  LIB3168-007-P1-K1-G2
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g4263704
BLAST score 262
E value 6.0e-23
Match length 86
% identity 56

NCBI Description (AC006223) putative sugar starvation-induced protein

[Arabidopsis thaliana]



Seq. No. 141992

LIB3168-007-P1-K1-G3 Seq. ID

Method BLASTX NCBI GI g112737 BLAST score 624 3.0e-65 E value 129 Match length % identity 89

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 141993

LIB3168-007-P1-K1-G4 Seq. ID

Method BLASTX g1628583 NCBI GI BLAST score 769 4.0e-82 E value 159 Match length 94 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

141994 Seq. No.

LIB3168-007-P1-K1-G5 Seq. ID

BLASTX Method g1628583 NCBI GI BLAST score 561 E value 1.0e-57 118 Match length 93 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

141995 Seq. No.

LIB3168-007-P1-K1-G8 Seq. ID

BLASTX Method NCBI GI q112682 BLAST score 626 E value 2.0e-65 Match length 143 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605_pir__S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>qi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >qi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

141996 Seq. No.

LIB3168-007-P1-K1-G9 Seq. ID



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BLASTX
Method
NCBI GI
                  q3142289
BLAST score
                  430
E value
                  2.0e-42
Match length
                  126
% identity
                  67
                  (AC002411) Strong similarity to beta-keto-Coa synthase
NCBI Description
                  gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
Seq. No.
                  141997
                  LIB3168-007-P1-K1-H1
Seq. ID
Method
                  BLASTX
                  g1531762
NCBI GI
BLAST score
                  197
E value
                  2.0e-15
Match length
                  44
% identity
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  141998
                  LIB3168-007-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1773330
BLAST score
                  489
E value
                  2.0e-49
                  109
Match length
% identity
                  85
                  (U80071) glycolate oxidase [Mesembryanthemum crystallinum]
NCBI Description
Seq. No.
                  141999
                  LIB3168-007-P1-K1-H11
Seq. ID
                   BLASTX
Method
                   g4704766
NCBI GI
BLAST score
                   405
                   1.0e-39
E value
Match length
                   115
                   44
% identity
                   (AF131223) protein disulfide isomerase homolog; PDI
NCBI Description
                   [Datisca glomerata]
                   142000
Seq. No.
                   LIB3168-007-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   537
                   3.0e-55
E value
Match length
                   104
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
```

Seq. No. 142001

Seq. ID LIB3168-007-P1-K1-H3

Method BLASTX NCBI GI g1628583



BLAST score 321 E value 1.0e-29 Match length 61 % identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142002

Seq. ID LIB3168-007-P1-K1-H4

Method BLASTX
NCBI GI g2129545
BLAST score 733
E value 6.0e-78
Match length 136
% identity 99

NCBI Description beta-glucanase - Arabidopsis thaliana (fragment) >gi_600857

(U17888) beta-glucanase [Arabidopsis thaliana]

Seq. No. 142003

Seq. ID LIB3168-007-P1-K1-H5

Method BLASTX
NCBI GI g1709007
BLAST score 168
E value 1.0e-11
Match length 99
% identity 39

NCBI Description O-SUCCINYLHOMOSERINE SULFHYDRYLASE (OSH SULFHYDRYLASE)

>gi 607830 (U10904) O-succinylhomoserine sulfhydrylase

[Pseudomonas aeruginosa]

Seq. No. 142004

Seq. ID LIB3168-007-P1-K1-H7

Method BLASTX
NCBI GI g112682
BLAST score 705
E value 1.0e-74
Match length 157
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142005

Seq. ID LIB3168-007-P1-K1-H8

Method BLASTX
NCBI GI g4204299
BLAST score 788
E value 2.0e-84
Match length 168
% identity 90

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 142006



Seq. ID LIB3168-007-P1-K1-H9 Method BLASTX NCBI GI g112737

BLAST score 571 E value 5.0e-59 Match length 137 % identity 81

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142007

Seq. ID LIB3168-009-P1-K1-A1

Method BLASTX
NCBI GI g131289
BLAST score 495
E value 5.0e-61
Match length 125
% identity 95

NCBI Description PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN)

(CP43) >gi_72709_pir__F2NT44 photosystem II chlorophyll a-binding protein psbC - common tobacco chloroplast >gi_225285_prf__1211235W photosystem II 44kD protein

[Nicotiana tabacum]

Seq. No. 142008

Seq. ID LIB3168-009-P1-K1-A10

Method BLASTX
NCBI GI g1628583
BLAST score 412
E value 2.0e-40
Match length 112
% identity 74

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142009

Seq. ID LIB3168-009-P1-K1-A11

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142010

Seq. ID LIB3168-009-P1-K1-A12

Method BLASTX NCBI GI g1628583



BLAST score 778
E value 3.0e-83
Match length 154
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142011

Seq. ID LIB3168-009-P1-K1-A3

Method BLASTX
NCBI GI g1628583
BLAST score 621
E value 8.0e-65
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142012

Seq. ID LIB3168-009-P1-K1-A4

Method BLASTX
NCBI GI g112681
BLAST score 444
E value 4.0e-44
Match length 89
% identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142013

Seq. ID LIB3168-009-P1-K1-A6

Method BLASTX
NCBI GI g2605714
BLAST score 396
E value 2.0e-38
Match length 100
% identity 80

NCBI Description (AF026275) beta-tonoplast intrinsic protein [Arabidopsis

thaliana]

Seq. No. 142014

Seq. ID LIB3168-009-P1-K1-A7

Method BLASTN
NCBI GI g4512656
BLAST score 150
E value 1.0e-78
Match length 384
% identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic

sequence, complete sequence

Seq. No. 142015

NCBI Description



```
LIB3168-009-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112739
BLAST score
                  533
E value
                  2.0e-54
                  142
Match length
                  75
% identity
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  142016
                  LIB3168-009-P1-K1-B1
Seq. ID
Method
                  BLASTX
                  g2246456
NCBI GI
BLAST score
                  750
E value
                  6.0e-80
Match length
                  141
% identity
                  99
NCBI Description (U71400) S-adenosyl-methionine-sterol-C-methyltransferase
                  [Arabidopsis thaliana]
                  142017
Seq. No.
                  LIB3168-009-P1-K1-B12
Seq. ID
Method
                  BLASTX
                  g4204299
NCBI GI
BLAST score
                  382
                  8.0e-37
E value
Match length
                  74
                  100
% identity
NCBI Description (AC003027) lcl_prt_seq No definition line found
                  [Arabidopsis thaliana]
                  142018
Seq. No.
                  LIB3168-009-P1-K1-B2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g16473
BLAST score
                  455
                  0.0e + 00
E value
                  463
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana 25S-18S ribosomal DNA spacer
Seq. No.
                  142019
                  LIB3168-009-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112737
                  635
BLAST score
                  2.0e-66
E value
                  148
Match length
                  82
% identity
```

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -



Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

 Seq. No.
 142020

 Seq. ID
 LIB3168-009-P1-K1-B5

 Method
 BLASTX

 NCBI GI
 g112681

 PLAST grove
 811

BLAST score 811 E value 4.0e-87 Match length 153 % identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142021

Seq. ID LIB3168-009-P1-K1-B6

Method BLASTX
NCBI GI g112681
BLAST score 698
E value 7.0e-74
Match length 141
% identity 94

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142022

Seq. ID LIB3168-009-P1-K1-B7

Method BLASTX
NCBI GI g1531762
BLAST score 195
E value 7.0e-15
Match length 51
% identity 75

NCBI Description (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis

thaliana]

Seq. No. 142023

Seq. ID LIB3168-009-P1-K1-B8

Method BLASTX
NCBI GI g112682
BLAST score 570
E value 1.0e-64
Match length 152
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

Seq. ID

Method



storage protein [Arabidopsis thaliana]

```
Seq. No.
                  142024
                  LIB3168-009-P1-K1-C1
Seq. ID
Method
                  BLASTX
                  q4455297
NCBI GI
                  569
BLAST score
                  1.0e-58
E value
                  155
Match length
% identity
                  70
                  (AL035528) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  142025
                  LIB3168-009-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  625
                  3.0e-65
E value
                  120
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142026
                  LIB3168-009-P1-K1-C11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112739
BLAST score
                  516
                  2.0e-52
E value
                  139
Match length
                  75
% identity
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                   (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  142027
                  LIB3168-009-P1-K1-C12
Seq. ID
Method
                  BLASTX
                  q112682
NCBI GI
BLAST score
                   619
E value
                  1.0e-64
                   131
Match length
                   91
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605_pir_ S08510
NCBI Description
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >qi 808937 emb CAA32494 (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   142028
```

17380

LIB3168-009-P1-K1-C2

BLASTX

NCBI Description



```
NCBI GI
                  q1706749
                  615
BLAST score
                  4.0e-64
E value
                  124
Match length
                  99
% identity
                  3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR
NCBI Description
                  (BETA-KETOACYL-ACP SYNTHASE I) (KAS I) >gi_780814 (U24177)
                  3-ketoacyl-acyl carrier protein synthase I [Arabidopsis
                  thaliana]
                  142029
Seq. No.
                  LIB3168-009-P1-K1-C3
Seq. ID
Method
                  BLASTX
                  g112682
NCBI GI
                  680
BLAST score
                  9.0e-72
E value
Match length
                  153
                  84
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir_ S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  142030
                  LIB3168-009-P1-K1-C4
Seq. ID
Method
                  BLASTN
                  g4755185
NCBI GI
                  272
BLAST score
                  1.0e-151
E value
Match length
                  423
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F5G3 genomic
                   sequence, complete sequence
                   142031
Seq. No.
                  LIB3168-009-P1-K1-C5
Seq. ID
Method
                  BLASTX
                   q4678285
NCBI GI
BLAST score
                   385
                   4.0e-37
E value
                   109
Match length
% identity
                   62
                  (AL049660) putative protein [Arabidopsis thaliana]
NCBI Description
                   142032
Seq. No.
                   LIB3168-009-P1-K1-C7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q112739
BLAST score
                   537
E value
                   5.0e-55
Match length
                   143
% identity
                   76
                   2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
```

17381

PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_



(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711 emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

 Seq. No.
 142033

 Seq. ID
 LIB3168-009-P1-K1-C8

 Method
 BLASTX

NCBI GI g1628583
BLAST score 420
E value 3.0e-41
Match length 114
% identity 75

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142034

Seq. ID LIB3168-009-P1-K1-C9

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142035

Seq. ID LIB3168-009-P1-K1-D10

Method BLASTX
NCBI GI g1628583
BLAST score 256
E value 5.0e-22
Match length 89
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142036

Seq. ID LIB3168-009-P1-K1-D11

Method BLASTX
NCBI GI g1694976
BLAST score 459
E value 7.0e-46
Match length 111
% identity 84

NCBI Description (Y09482) HMG1 [Arabidopsis thaliana]

>gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis

thaliana]

Seq. No. 142037

Seq. ID LIB3168-009-P1-K1-D12

Method BLASTX
NCBI GI g1628583
BLAST score 627



E value 2.0e-65 Match length 154 % identity 81

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142038

Seq. ID LIB3168-009-P1-K1-D2

Method BLASTX
NCBI GI g2982437
BLAST score 534
E value 1.0e-54
Match length 155
% identity 66

NCBI Description (AL022224) terpene cyclase like protein [Arabidopsis

thaliana]

Seq. No. 142039

Seq. ID LIB3168-009-P1-K1-D4

Method BLASTX
NCBI GI g112682
BLAST score 669
E value 2.0e-70
Match length 152
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142040

Seq. ID LIB3168-009-P1-K1-D6

Method BLASTX
NCBI GI g1628583
BLAST score 642
E value 3.0e-67
Match length 123
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142041

Seq. ID LIB3168-009-P1-K1-D7

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142042



```
LIB3168-009-P1-K1-D8
Seq. ID
                  BLASTX
Method
                  q1628583
NCBI GI
BLAST score
                  623
E value
                  4.0e-65
                  153
Match length
% identity
                  81
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142043
Seq. No.
                  LIB3168-009-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  802
                  5.0e-86
E value
Match length
                  153
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142044
Seq. No.
                  LIB3168-009-P1-K1-E1
Seq. ID
Method
                  BLASTX
                  g4204299
NCBI GI
BLAST score
                  451
                   7.0e-45
E value
                  88
Match length
                   100
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   142045
Seq. No.
                  LIB3168-009-P1-K1-E10
Seq. ID
                   BLASTX
Method
                   g1628583
NCBI GI
BLAST score
                   625
                   3.0e-65
E value
Match length
                   120
                   100
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   142046
Seq. No.
                   LIB3168-009-P1-K1-E11
Seq. ID
Method
                   BLASTX
                   g1109699
NCBI GI
BLAST score
                   650
                   3.0e-68
E value
                   124
Match length
                   100
% identity
```

Seq. No. 142047

NCBI Description

(X83381) gibberellin 20-oxidase [Arabidopsis thaliana]



```
LIB3168-009-P1-K1-E12
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3335356
BLAST score
                   432
E value
                   0.0e + 00
Match length
                   463
                   98
% identity
                   Arabidopsis thaliana chromosome II BAC F16M14 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   142048
                   LIB3168-009-P1-K1-E2
Seq. ID
                   BLASTX
Method
                   g112739
NCBI GI
BLAST score
                   542
E value
                   1.0e-55
Match length
                   144
% identity
                   76
                   2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                   Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                   2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                   (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                   >gi 4490711 emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2
                   precursor [Arabidopsis thaliana]
Seq. No.
                   142049
                   LIB3168-009-P1-K1-E3
Seq. ID
Method
                   BLASTX
                   g419789
NCBI GI
BLAST score
                   460
                   6.0e-46
E value
                   133
Match length
                    65
% identity
NCBI Description hypothetical protein - potato
                   142050
Seq. No.
                   LIB3168-009-P1-K1-E4
Seq. ID
Method
                   BLASTX
                   g112682
NCBI GI
                    680
BLAST score
                    9.0e-72
E value
                    153
Match length
                    84
% identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                    cruciferin precursor (CRB) - Arabidopsis thaliana
                    >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                    storage protein [Arabidopsis thaliana]
                    142051
```

Seq. No. LIB3168-009-P1-K1-E6 Seq. ID BLASTX Method g1628583 NCBI GI

382 BLAST score E value 5.0e-37 80 Match length



% identity 91
NCBI Description
NCBI Description
(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142052

Seq. ID LIB3168-009-P1-K1-E7

Method BLASTX
NCBI GI g112681
BLAST score 631
E value 5.0e-66
Match length 144
% identity 85

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142053

Seq. ID LIB3168-009-P1-K1-E8

Method BLASTX
NCBI GI g3004557
BLAST score 63
E value 3.0e-42
Match length 126
% identity 72

NCBI Description (AC003673) plasma membrane proton pump H+ ATPase, PMA1

[Arabidopsis thaliana]

Seq. No. 142054

Seq. ID LIB3168-009-P1-K1-E9

Method BLASTX
NCBI GI g112681
BLAST score 534
E value 8.0e-55
Match length 101
% identity 100

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_(X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142055

Seq. ID LIB3168-009-P1-K1-F1

Method BLASTX
NCBI GI g112682
BLAST score 664
E value 7.0e-70
Match length 151
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]



```
142056
Seq. No.
                  LIB3168-009-P1-K1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1169476
                  721
BLAST score
                  1.0e-76
E value
                  138
Match length
                  100
% identity
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
                  ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632)
                  vitronectin-like adhesion protein [Nicotiana tabacum]
                  142057
Seq. No.
                  LIB3168-009-P1-K1-F11
Seq. ID
Method
                  BLASTN
                  g2924257
NCBI GI
BLAST score
                  61
                  1.0e-25
E value
                  85
Match length
                  93
% identity
NCBI Description Tobacco chloroplast genome DNA
                  142058
Seq. No.
                  LIB3168-009-P1-K1-F12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1628583
                  614
BLAST score
                   5.0e-64
E value
Match length
                   117
                   100
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   142059
Seq. No.
                   LIB3168-009-P1-K1-F2
Seq. ID
                   BLASTX
Method
                   g1628583
NCBI GI
                   318
BLAST score
                   3.0e-29
E value
                   89
Match length
                   100
 % identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   142060
Seq. No.
                   LIB3168-009-P1-K1-F3
 Seq. ID
                   BLASTX
Method
NCBI GI
                   q2129657
                   509
BLAST score
                   1.0e-51
E value
                   131
Match length
 % identity
                   81
                   oleosin isoform - Arabidopsis thaliana
 NCBI Description
```

>gi 987014 emb CAA90877_ (Z54164) oleosin [Arabidopsis



thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No. 142061

Seq. ID LIB3168-009-P1-K1-F4

Method BLASTN
NCBI GI g3869062
BLAST score 224
E value 1.0e-123
Match length 284
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K11I1, complete sequence [Arabidopsis thaliana]

Seq. No. 142062

Seq. ID LIB3168-009-P1-K1-F6

Method BLASTX
NCBI GI g3123131
BLAST score 161
E value 4.0e-22
Match length 142
% identity 43

NCBI Description HYPOTHETICAL OXIDOREDUCTASE IN CITA-SSPB INTERGENIC REGION

>gi_2226201_emb_CAA74490_ (Y14082) hypothetical protein
[Bacillus subtilis] >gi_2633280_emb_CAB12784_ (Z99109)
similar to glucose 1-dehydrogenase [Bacillus subtilis]

Seq. No. 142063

Seq. ID LIB3168-009-P1-K1-F7

Method BLASTX
NCBI GI g2129532
BLAST score 548
E value 3.0e-56
Match length 122
% identity 87

NCBI Description acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) -

Arabidopsis thaliana >gi_1107507_emb_CAA63746_ (X93461) acyl-[acyl-carrier protein] desaturase [Arabidopsis

thaliana]

Seq. No. 142064

Seq. ID LIB3168-009-P1-K1-F8

Method BLASTX
NCBI GI g2894378
BLAST score 637
E value 1.0e-66
Match length 153
% identity 75

NCBI Description (Y14573) putative ribophorin I homologue [Hordeum vulgare]

Seq. No.

Seq. ID LIB3168-009-P1-K1-G1

142065

Method BLASTX
NCBI GI g115783
BLAST score 670
E value 1.0e-70
Match length 127

Seq. ID

Method



```
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_
                                                             (X03909)
                  chlorophyll a/b binding protein (LHCP \overline{AB} 140) [Arabidopsis
                  thaliana]
                  142066
Seq. No.
                  LIB3168-009-P1-K1-G11
Seq. ID
                  BLASTX
Method
                  g1628583
NCBI GI
                   330
BLAST score
                  1.0e-30
E value
                  82
Match length
                  78
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   142067
Seq. No.
                   LIB3168-009-P1-K1-G12
Seq. ID
Method
                   BLASTX
                   g2499945
NCBI GI
                   578
BLAST score
                   7.0e-60
E value
                   116
Match length
                   100
% identity
                   URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
NCBI Description
                   PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                   DECARBOXYLASE >gi_1076363_pir__S46440 orotate
                   phosphoribosyltransferase (EC 2.4.2.10) /
                   orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -
                   Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842)
                   pyrE-F [Arabidopsis thaliana]
                   142068
Seq. No.
                   LIB3168-009-P1-K1-G2
Seq. ID
                   BLASTX
Method
                   q2464901
NCBI GI
                   170
BLAST score
                   5.0e-12
E value
                   114
Match length
 % identity
                   34
                   (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                   142069
 Seq. No.
                   LIB3168-009-P1-K1-G3
 Seq. ID
                   BLASTX
 Method
                   g2244752
 NCBI GI
 BLAST score
                   365
                   8.0e-35
 E value
 Match length
                   116
                   62
 % identity
                   (Z97335) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                   142070
 Seq. No.
```

17389

LIB3168-009-P1-K1-G4

BLASTX

```
g1628583
NCBI GI
                  625
BLAST score
                  3.0e-65
E value
                  120
Match length
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142071
Seq. No.
                  LIB3168-009-P1-K1-G5
Seq. ID
                  BLASTX
Method
                  q112682
NCBI GI
BLAST score
                  508
                   1.0e-51
E value
Match length
                   147
                   71
% identity
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
                   142072
Seq. No.
                   LIB3168-009-P1-K1-G7
Seq. ID
Method
                   BLASTX
                   g2129657
NCBI GI
BLAST score
                   236
                   8.0e-20
E value
                   87
Match length
                   63
% identity
                   oleosin isoform - Arabidopsis thaliana
NCBI Description
                   >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
                   thaliana] \overline{>}gi_\overline{9}87016_emb_CAA90878_ (Z54165) oleosin
                   [Arabidopsis thaliana]
                                                                314
                   142073
Seq. No.
                   LIB3168-009-P1-K1-G8
Seq. ID
Method
                   BLASTX
                   g3164142
NCBI GI
BLAST score
                   539
                   3.0e-55
E value
                   153
Match length
                   75
 % identity
                   (D78606) cytochrome P450 monooxygenase [Arabidopsis
NCBI Description
                   thaliana]
                    142074
 Seq. No.
                   LIB3168-009-P1-K1-G9
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                    q3738335
                    286
 BLAST score
                    1.0e-25
 E value
                    99
 Match length
 % identity
                    62
                   (AC005170) unknown protein [Arabidopsis thaliana]
 NCBI Description
```

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 Seq. No.
 142075

 Seq. ID
 LIB3168-009-P1-K1-H1

 Method
 BLASTX

 NCBI GI
 g1628583

 BLAST score
 625

E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142076

Seq. ID LIB3168-009-P1-K1-H10

Method BLASTX
NCBI GI g1628583
BLAST score 509
E value 5.0e-52
Match length 99
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142077

Seq. ID LIB3168-009-P1-K1-H11

Method BLASTN
NCBI GI g4199934
BLAST score 250
E value 1.0e-138
Match length 250
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 142078

Seq. ID LIB3168-009-P1-K1-H12

Method BLASTN
NCBI GI g2252823
BLAST score 88
E value 4.0e-42
Match length 88
% identity 100

NCBI Description Arabidopsis thaliana BAC IG005I10

Seq. No. 142079

Seq. ID LIB3168-009-P1-K1-H3

Method BLASTX
NCBI GI g541847
BLAST score 832
E value 1.0e-89
Match length 153
% identity 100

NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana

Seq. No. 142080

Seq. ID LIB3168-009-P1-K1-H4

17391



Method BLASTX NCBI GI g267069 BLAST score 231 2.0e-19 E value Match length 41 % identity 100

TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594 NCBI Description tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >qi 166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 142081

Seq. ID LIB3168-009-P1-K1-H5

Method BLASTN NCBI GI g395203 BLAST score 62 8.0e-27 E value Match length 66 52 % identity

NCBI Description A.thaliana 2S albumin gene isoforms 1 and 2, complete CDS's

142082 Seq. No.

LIB3168-009-P1-K1-H6 Seq. ID

Method BLASTX NCBI GI g2129657 BLAST score 273 E value 3.0e-24Match length 103 % identity 63

oleosin isoform - Arabidopsis thaliana NCBI Description

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 142083

Seq. ID LIB3168-009-P1-K1-H7

Method BLASTN NCBI GI g4199934 BLAST score 288 E value 1.0e-161 Match length 392 % identity 93

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 142084

LIB3168-009-P1-K1-H8 Seq. ID

Method BLASTX NCBI GI g128877 BLAST score 343 3.0e-32 E value Match length 100 % identity 73

NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4L, CHLOROPLAST NCBI Description

>gi_66167_pir_DENTNL NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L ~ common tobacco chloroplast

>gi_1223668_emb_CAA77396_ (Z00044) NADH dehydrogenase ND4L



subunit [Nicotiana tabacum] >gi_225256_prf__1211235CQ NADH
dehydrogenase 4L-like ORF 101 [Nicotiana tabacum]

 Seq. No.
 142085

 Seq. ID
 LIB3168-009-P1-K1-H9

 Method
 BLASTN

 NCBI GI
 g4678371

 BLAST score
 318

 E value
 1.0e-179

E value 1.0e
Match length 356
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15

(ESSA project)

Seq. No. 142086

Seq. ID LIB3168-010-P1-K1-A1

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142087

Seq. ID LIB3168-010-P1-K1-A10

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142088

Seq. ID LIB3168-010-P1-K1-A12

Method BLASTX
NCBI GI g112737
BLAST score 280
E value 7.0e-25
Match length 124
% identity 52

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142089

Seq. ID LIB3168-010-P1-K1-A3

Method BLASTX



NCBI GI g1169476 BLAST score 596 E value 5.0e-62 Match length 117 % identity 98

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE

ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)

vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No. 142090

Seq. ID LIB3168-010-P1-K1-A6

Method BLASTN
NCBI GI g3212846
BLAST score 276
E value 1.0e-154
Match length 459
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 142091

Seq. ID LIB3168-010-P1-K1-A8

Method BLASTN
NCBI GI g2244747
BLAST score 37
E value 2.0e-11
Match length 94
% identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 142092

Seq. ID LIB3168-010-P1-K1-A9

Method BLASTN
NCBI GI g4539353
BLAST score 102
E value 5.0e-50
Match length 142
% identity 94

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F25I24

(ESSA project)

Seq. No. 142093

Seq. ID LIB3168-010-P1-K1-B1

Method BLASTX
NCBI GI g1628583
BLAST score 644
E value 2.0e-67
Match length 156
% identity 81

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142094

Seq. ID LIB3168-010-P1-K1-B10

Method BLASTX

17394



NCBI GI g4512675 BLAST score 488 E value 3.0e-49 Match length 131 % identity 75

NCBI Description (AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No.

142095

Seq. ID

LIB3168-010-P1-K1-B11

Method BLASTX
NCBI GI g1345973
BLAST score 528
E value 6.0e-54
Match length 121
% identity 81

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No.

142096

Seq. ID

LIB3168-010-P1-K1-B12

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description

(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.

142097

Seq. ID

LIB3168-010-P1-K1-B2

Method BLASTX
NCBI GI g2129657
BLAST score 428
E value 3.0e-42
Match length 115
% identity 78

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No.

142098

Seq. ID Method LIB3168-010-P1-K1-B3

Method BLASTX
NCBI GI g2281115
BLAST score 751
E value 2.0e-80
Match length 154



% identity 96

NCBI Description (AC002330) putative cullin-like 1 protein [Arabidopsis

thaliana]

Seq. No.

142099

Seq. ID Method LIB3168-010-P1-K1-B5

Method NCBI GI BLASTX q115767

BLAST score

516

E value Match length 1.0e-52

% identity

121 86

NCBI Description

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.

142100

Seq. ID

LIB3168-010-P1-K1-B8

Method NCBI GI BLASTN

NCB1 G1 BLAST score g3327867 451

E value Match length

0.0e+00 454

% identity
NCBI Description

100 Arabidopsis thaliana CIP7 mRNA for COP1-Interacting Protein

7, complete cds

Seq. No.

142101

Seq. ID

LIB3168-010-P1-K1-B9

Method NCBI GI

BLASTX g112737 624

BLAST score E value

3.0e-65 146

Match length % identity

82

NCBI Description

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit

1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No.

142102

Seq. ID

LIB3168-010-P1-K1-C1

Method NCBI GI BLASTX g2288887

BLAST score

604 7.0e-63

E value Match length

133

% identity NCBI Description

(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi 3250736 emb CAA76803 (Y17593) mevalonate

17396



diphosphate decarboxylase [Arabidopsis thaliana]
>gi_3786002 (AC005499) mevalonate diphosphate decarboxylase
[Arabidopsis thaliana]

Seq. No. 142103

Seq. ID LIB3168-010-P1-K1-C10

Method BLASTX
NCBI GI g133960
BLAST score 213
E value 5.0e-17
Match length 49
% identity 88

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 >gi 70876 pir R3NT4

ribosomal protein S4 - common tobacco chloroplast >gi_11834_emb_CAA77354_ (Z00044) ribosomal protein S4 [Nicotiana tabacum] >gi_225202_prf__1211235AG ribosomal

protein S4 [Nicotiana tabacum]

Seq. No. 142104

Seq. ID LIB3168-010-P1-K1-C11

Method BLASTN
NCBI GI g166569
BLAST score 179
E value 2.0e-96
Match length 183
% identity 99

NCBI Description Arabidopsis thaliana glycine rich protein (RAB18) gene,

complete cds

Seq. No. 142105

Seq. ID LIB3168-010-P1-K1-C12

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142106

Seq. ID LIB3168-010-P1-K1-C2

Method BLASTX
NCBI GI g2961390
BLAST score 863
E value 3.0e-93
Match length 154
% identity 99

NCBI Description (AL022141) beta-galactosidase like protein [Arabidopsis

thaliana]

Seq. No. 142107

Seq. ID LIB3168-010-P1-K1-C3

Method BLASTX NCBI GI g4056469 BLAST score 577



E value 1.0e-59 Match length 115 % identity 97

NCBI Description (AC005990) Strong similarity to gb_M95166 ADP-ribosylation

factor from Arabidopsis thaliana. ESTs gb Z25826,

gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,

gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and

gb Z25043 come from t

Seq. No. 142108

Seq. ID LIB3168-010-P1-K1-C4

Method BLASTN
NCBI GI g4757417
BLAST score 245
E value 1.0e-135
Match length 468
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

T30G6, complete sequence

Seq. No. 142109

Seq. ID LIB3168-010-P1-K1-C5

Method BLASTX
NCBI GI g112681
BLAST score 595
E value 9.0e-62
Match length 154
% identity 79

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142110

Seq. ID LIB3168-010-P1-K1-C7

Method BLASTX
NCBI GI g4090884
BLAST score 418
E value 3.0e-41
Match length 81
% identity 99

NCBI Description (AF025333) vesicle-associated membrane protein 7B;

synaptobrevin 7B [Arabidopsis thaliana]

Seq. No. 142111

Seq. ID LIB3168-010-P1-K1-C8

Method BLASTN
NCBI GI g4760411
BLAST score 418
E value 0.0e+00
Match length 443
% identity 98

NCBI Description Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,

complete sequence

Seq. No. 142112

```
Seq. ID
                  LIB3168-010-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  q2584720
BLAST score
                  39
E value
                  1.0e-12
Match length
                  46
% identity
                  98
                  A.thaliana gene encoding sulfite reductase
NCBI Description
Seq. No.
                  142113
                  LIB3168-010-P1-K1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2842474
BLAST score
                  105
E value
                  9.0e-52
Match length
                  129
% identity
                  98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
                  (ESSAII project)
Seq. No.
                  142114
Seq. ID
                  LIB3168-010-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
E value
                  3.0e-65
Match length
                  120
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142115
Seq. ID
                  LIB3168-010-P1-K1-D12
Method
                  BLASTN
NCBI GI
                  q3789706
BLAST score
                  182
E value
                  8.0e-98
                  396
Match length
                  87
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F15K9 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  142116
                  LIB3168-010-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1705463
BLAST score
                  538
E value
                  4.0e-55
Match length
                  118
```

% identity 87

NCBI Description BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi_2129547_pir__S71201

biotin sythase - Arabidopsis thaliana >gi_1045316 (U24147) biotin sythase [Arabidopsis thaliana] >gi_1403662 (U31806) BIO2 protein [Arabidopsis thaliana] >gi_1769457 (L34413)

biotin synthase [Arabidopsis thaliana] >gi 2288983

(AC002335) biotin synthase (Bio B) [Arabidopsis thaliana]



>gi_1589016_prf__2209438A biotin synthase [Arabidopsis
thaliana]

 Seq. No.
 142117

 Seq. ID
 LIB3168-010-P1-K1-D4

 Method
 BLASTX

 NCBI GI
 g267136

 BLAST score
 538

 E value
 4.0e-55

E value 4.0 Match length 134 % identity 79

NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 2C (WATER-STRESS INDUCED

TONOPLAST INTRINSIC PROTEIN) (WSI-TIP)

>gi_217869_dbj_BAA02520_ (D13254) transmembrane channel
protein [Arabidopsis thaliana] >gi_4371283_gb_AAD18141_
(AC006260) putative plasma membrane intrinsic protein 2C

[Arabidopsis thaliana] >gi_384324_prf__1905411A transmembrane channel [Arabidopsis thaliana]

Seq. No. 142118

Seq. ID LIB3168-010-P1-K1-D5

Method BLASTX
NCBI GI g112682
BLAST score 668
E value 2.0e-70
Match length 153
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142119

Seq. ID LIB3168-010-P1-K1-D6

Method BLASTX
NCBI GI g2244799
BLAST score 640
E value 4.0e-67
Match length 143
% identity 90

NCBI Description (Z97336) carnitine racemase homolog [Arabidopsis thaliana]

Seq. No. 142120

Seq. ID LIB3168-010-P1-K1-D7

Method BLASTX
NCBI GI g2245066
BLAST score 276
E value 2.0e-24
Match length 141
% identity 39

NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 142121

Seq. ID LIB3168-010-P1-K1-D8

Method BLASTX NCBI GI g133438



BLAST score 685 E value 2.0e-72 Match length 150 % identity 85

NCBI Description DNA-DIRECTED RNA POLYMERASE BETA' CHAIN

>gi_81504_pir__B29959 DNA-directed RNA polymerase (EC
2.7.7.6) beta' chain - spinach chloroplast >gi_295120

(M55297) RNA polymerase [Spinacia oleracea]

Seq. No. 142122

Seq. ID LIB3168-010-P1-K1-D9

Method BLASTX
NCBI GI g1169476
BLAST score 747
E value 1.0e-79
Match length 145
% identity 99

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE

ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)

vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No. 142123

Seq. ID LIB3168-010-P1-K1-E1

Method BLASTX
NCBI GI g267069
BLAST score 621
E value 8.0e-65
Match length 115
% identity 100

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594

tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 142124

Seq. ID LIB3168-010-P1-K1-E11

Method BLASTX
NCBI GI g3193314
BLAST score 358
E value 5.0e-34
Match length 152
% identity 51

NCBI Description (AF069299) contains similarity to Arabidopsis scarecrow

(GB:U62798) [Arabidopsis thaliana]

Seq. No. 142125

Seq. ID LIB3168-010-P1-K1-E12

Method BLASTX
NCBI GI g112741
BLAST score 58
E value 2.0e-41
Match length 131
% identity 65

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit

3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_



(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No. 142126

Seq. ID LIB3168-010-P1-K1-E2

Method BLASTX
NCBI GI g112739
BLAST score 434
E value 4.0e-43
Match length 131
% identity 73

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 142127

Seq. ID LIB3168-010-P1-K1-E3

Method BLASTN
NCBI GI g3047074
BLAST score 60
E value 5.0e-25
Match length 162
% identity 91

NCBI Description Arabidopsis thaliana BAC F21E10

Seq. No. 142128

Seq. ID LIB3168-010-P1-K1-E4

Method BLASTN
NCBI GI g397397
BLAST score 301
E value 1.0e-169
Match length 345
% identity 97

NCBI Description A.thaliana chloroplast trnL gene, intron

Seq. No. 142129

Seq. ID LIB3168-010-P1-K1-E5

Method BLASTX
NCBI GI g2118307
BLAST score 561
E value 9.0e-61
Match length 129
% identity 99

NCBI Description cysteine synthase (EC 4.2.99.8) 3A - Arabidopsis thaliana

>gi_804950_emb_CAA58893_ (X84097) cysteine synthase

[Arabidopsis thaliana] >gi 1096196 prf 2111276A Ser(Ac)

thiol lyase [Arabidopsis thaliana]

Seq. No. 142130

Seq. ID LIB3168-010-P1-K1-E6

Method BLASTX NCBI GI g112682



BLAST score 614 E value 5.0e-64 Match length 143 % identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142131

Seq. ID LIB3168-010-P1-K1-E7

Method BLASTX
NCBI GI g1169515
BLAST score 545
E value 6.0e-56
Match length 103
% identity 61

NCBI Description EM-LIKE PROTEIN GEA1 >gi 2119768 pir S34819 embryonic

abundant protein Em1 - Arabidopsis thaliana

>gi_298070_emb_CAA77509_ (Z11158) Em protein [Arabidopsis
thaliana] >gi_298072_emb_CAA77979_ (Z11921) Em protein
homologue [Arabidopsis thaliana] >gi_3068708 (AF049236) Em1

protein [Arabidopsis thaliana]

Seq. No. 142132

Seq. ID LIB3168-010-P1-K1-E8

Method BLASTX
NCBI GI g136636
BLAST score 380
E value 7.0e-37
Match length 77
% identity 94

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -

Arabidopsis thaliana >gi 442594 pdb 1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi 2981894 pdb 2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi 431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 142133

Seq. ID LIB3168-010-P1-K1-E9

Method BLASTX
NCBI GI g1616785
BLAST score 659
E value 3.0e-69
Match length 125
% identity 100

NCBI Description (U71121) pyruvate decarboxylase [Arabidopsis thaliana]

Seq. No. 142134

Seq. ID LIB3168-010-P1-K1-F1

Method BLASTX NCBI GI q4038039



```
BLAST score
E value
                  5.0e-12
Match length
                  44
                  68
% identity
NCBI Description
                  (AC005936) putative proteinase inhibitor II [Arabidopsis
Seq. No.
                  142135
Seq. ID
                  LIB3168-010-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q2493696
BLAST score
                  602
E value
                  1.0e-62
Match length
                  124
% identity
                  95
                  HYPOTHETICAL 21.5 KD PROTEIN (ORF 185) >gi 1480440 (U34204)
NCBI Description
                  ORF185; hypothetical 21.4 kD protein [Brassica oleracea]
Seq. No.
                  142136
Seq. ID
                  LIB3168-010-P1-K1-F11
Method
                  BLASTN
NCBI GI
                  g2828185
BLAST score
                  198
E value
                  1.0e-107
Match length
                  294
                  94
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUD21, complete sequence [Arabidopsis thaliana]
Seq. No.
                  142137
Seq. ID
                  LIB3168-010-P1-K1-F12
Method
                  BLASTN
NCBI GI
                  g4630745
BLAST score
                  440
E value
                  0.0e + 00
Match length
                  461
% identity
                  98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T3D7 genomic
                  sequence, complete sequence
                  142138
Seq. No.
Seq. ID
                  LIB3168-010-P1-K1-F3
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  625
E value
                  3.0e-65
Match length
                  120
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
```

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142139

Seq. ID LIB3168-010-P1-K1-F4

Method BLASTX NCBI GI q1518540 BLAST score 357



E value 4.0e-34
Match length 73
% identity 93

NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 142140

Seq. ID LIB3168-010-P1-K1-F5

Method BLASTX
NCBI GI g112737
BLAST score 743
E value 4.0e-79
Match length 154
% identity 91

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir_ NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142141

Seq. ID LIB3168-010-P1-K1-F6

Method BLASTN
NCBI GI g3789706
BLAST score 175
E value 1.0e-93
Match length 360
% identity 88

NCBI Description Arabidopsis thaliana chromosome 1 BAC F15K9 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 142142

Seq. ID LIB3168-010-P1-K1-F7

Method BLASTX
NCBI GI g584892
BLAST score 626
E value 2.0e-65
Match length 152
% identity 75

NCBI Description SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)

>gi_629805_pir__S43516 serine carboxypeptidase I - rice
>gi_409580_dbj_BAA04510_ (D17586) serine carboxypeptidase I

[Oryza sativa]

Seq. No. 142143

Seq. ID LIB3168-010-P1-K1-F8

Method BLASTX
NCBI GI g3152576
BLAST score 331
E value 8.0e-31
Match length 147
% identity 46

NCBI Description (AC002986) Similar to liver-specific transport protein

gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No. 142144



LIB3168-010-P1-K1-G1 Seq. ID Method BLASTX NCBI GI a112737 BLAST score 580 5.0e-60 E value Match length 139 % identity 81 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710_emb CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142145

LIB3168-010-P1-K1-G10 Seq. ID

Method BLASTN g3650026 NCBI GI BLAST score 158 E value 2.0e-83 Match length 359 % identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC T26I20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 142146

Seq. ID LIB3168-010-P1-K1-G12

Method BLASTX NCBI GI g1336648 BLAST score 148 E value 9.0e-10 Match length 49 % identity 55

NCBI Description (U57824) endopeptidase-like protein [Nicotiana tabacum]

Seq. No. 142147

Seq. ID LIB3168-010-P1-K1-G3

Method BLASTX NCBI GI g112682 BLAST score 631 5.0e-66 E value Match length 148 % identity 82

12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB (Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142148

Seq. ID LIB3168-010-P1-K1-G4

Method BLASTN NCBI GI g2264309 BLAST score 357 0.0e+00E value Match length 440



% identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No. 142149

Seq. ID LIB3168-010-P1-K1-G5

Method BLASTX NCBI GI q2648800 BLAST score 195 E value 7.0e-15 Match length 154 % identity 34

(AE000982) phosphonopyruvate decarboxylase (bcpC-2) NCBI Description

[Archaeoglobus fulgidus]

142150 Seq. No.

Seq. ID LIB3168-010-P1-K1-G6

Method BLASTX NCBI GI q119143 BLAST score 735 E value 3.0e-78 Match length 141 % identity 100

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

> >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453 (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_(X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi 1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana] 1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]

>gi 1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No. 142151

Seq. ID LIB3168-010-P1-K1-G7

Method BLASTX NCBI GI q112737 BLAST score 624 E value 3.0e-65 146 Match length 82 % identity

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142152

Seq. ID LIB3168-010-P1-K1-G8

Method BLASTN NCBI GI g3702734 BLAST score 178 E value 2.0e-95 Match length 455

17407



% identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana] Seq. No. 142153 Seq. ID LIB3168-010-P1-K1-G9 Method BLASTX NCBI GI q4038043 BLAST score 333 4.0e-31 E value Match length 98 % identity 70 NCBI Description (AC005936) putative DNA-binding protein [Arabidopsis thaliana] 142154 Seq. No. Seq. ID LIB3168-010-P1-K1-H10 Method BLASTN NCBI GI g4544381 BLAST score 424 0.0e + 00E value 444 Match length % identity 99 NCBI Description Arabidopsis thaliana chromosome II BAC F16F14 genomic sequence, complete sequence Seq. No. Seq. ID 142155 LIB3168-010-P1-K1-H12 Method BLASTN NCBI GI q2252639 BLAST score 201 E value 1.0e-109 Match length 234 % identity 96 NCBI Description Genomic sequence of Arabidopsis BAC F8A5, complete sequence [Arabidopsis thaliana] Seq. No. 142156 Seq. ID LIB3168-010-P1-K1-H2 Method BLASTX NCBI GI q4558547 BLAST score 423 1.0e-41 E value Match length 153

% identity 64

NCBI Description (AC007138) hypothetical protein [Arabidopsis thaliana]

Seq. No. 142157

Seq. ID LIB3168-010-P1-K1-H3

Method BLASTN NCBI GI q3860242 BLAST score 441 E value 0.0e+00Match length 460 99 % identity

Arabidopsis thaliana chromosome I BAC T13M11 genomic NCBI Description

sequence, complete sequence



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Seq. No.
                   142158
Seq. ID
                   LIB3168-010-P1-K1-H4
Method
                   BLASTX
                   g1169476
NCBI GI
                   759
BLAST score
E value
                   5.0e-81
Match length
                   146
% identity
                   100
NCBI Description
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
                   ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)
                   vitronectin-like adhesion protein [Nicotiana tabacum]
Seq. No.
                   142159
Seq. ID
                   LIB3168-010-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   q2894378
BLAST score
                   349
                   6.0e-33
E value
Match length
                   99
% identity
                   67
NCBI Description
                  (Y14573) putative ribophorin I homologue [Hordeum vulgare]
Seq. No.
                   142160
Seq. ID
                   LIB3168-010-P1-K1-H6
Method
                   BLASTX
                   g1628583
NCBI GI
BLAST score
                   62
E value
                   3.0e-46
Match length
                   146
% identity
                   71
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No. Seq. ID
                   142161
                   LIB3168-010-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g112737
BLAST score
                   624
                   3.0e-65
E value
Match length
                   146
% identity
                   82
NCBI Description
                   2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                   PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                   Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                   >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                   precursor [Arabidopsis thaliana]
```

Seq. No. 142162

Seq. ID LIB3168-010-P1-K1-H8

Method BLASTX
NCBI GI g112681
BLAST score 725
E value 5.0e-77



Match length 145 % identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142163

Seq. ID LIB3168-011-P1-K1-A1

Method BLASTX
NCBI GI g112681
BLAST score 490
E value 1.0e-49
Match length 103
% identity 91

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142164

Seq. ID LIB3168-011-P1-K1-A10

Method BLASTX
NCBI GI g112681
BLAST score 436
E value 3.0e-43
Match length 126
% identity 75

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142165

Seq. ID LIB3168-011-P1-K1-A12

Method BLASTX
NCBI GI 94586021
BLAST score 650
E value 2.0e-68
Match length 126
% identity 100

NCBI Description (AC007170) putative cytoplasmic aconitate hydratase

[Arabidopsis thaliana]

Seq. No. 142166

Seq. ID LIB3168-011-P1-K1-A2

Method BLASTX
NCBI GI g112737
BLAST score 313
E value 7.0e-29
Match length 101
% identity 66

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -



Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No. 142167

Seq. ID LIB3168-011-P1-K1-A3

Method BLASTX
NCBI GI g1628583
BLAST score 218
E value 1.0e-17
Match length 66
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142168

Seq. ID LIB3168-011-P1-K1-A4

Method BLASTX
NCBI GI g112739
BLAST score 425
E value 6.0e-42
Match length 121
% identity 71

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 142169

Seq. ID LIB3168-011-P1-K1-A5

Method BLASTX
NCBI GI g112737
BLAST score 506
E value 2.0e-51
Match length 125
% identity 79

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142170

Seq. ID LIB3168-011-P1-K1-A6

Method BLASTN
NCBI GI g4097693
BLAST score 78
E value 3.0e-36
Match length 154



% identity 90

NCBI Description Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete

cds

Seq. No. 142171

Seq. ID LIB3168-011-P1-K1-A7

Method BLASTX
NCBI GI g1628583
BLAST score 610
E value 1.0e-63
Match length 117
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142172

Seq. ID LIB3168-011-P1-K1-A8

Method BLASTX
NCBI GI g1628583
BLAST score 484
E value 4.0e-49
Match length 96
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142173

Seq. ID LIB3168-011-P1-K1-B1

Method BLASTX
NCBI GI g1628583
BLAST score 668
E value 2.0e-70
Match length 128
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142174

Seq. ID LIB3168-011-P1-K1-B10

Method BLASTX
NCBI GI g112681
BLAST score 515
E value 2.0e-52
Match length 124
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142175

Seq. ID LIB3168-011-P1-K1-B11

Method BLASTN



NCBI GI g3046852 BLAST score 244 E value 1.0e-135 Match length 395 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQJ16, complete sequence [Arabidopsis thaliana]

Seq. No. 142176

Seq. ID LIB3168-011-P1-K1-B2

Method BLASTX
NCBI GI g112681
BLAST score 484
E value 5.0e-49
Match length 100
% identity 92

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142177

Seq. ID LIB3168-011-P1-K1-B3

Method BLASTX
NCBI GI g1628583
BLAST score 687
E value 1.0e-72
Match length 131
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142178

Seq. ID LIB3168-011-P1-K1-B4

Method BLASTX
NCBI GI g112682
BLAST score 639
E value 5.0e-67
Match length 130
% identity 92

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidops $\overline{\mathbf{i}}$ s thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142179

Seq. ID LIB3168-011-P1-K1-B5

Method BLASTX
NCBI GI g112737
BLAST score 394
E value 2.0e-38
Match length 104
% identity 75

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE



PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

 Seq. No.
 142180

 Seq. ID
 LIB3168-011-P1-K1-B6

 Method
 BLASTX

 NCBI GI
 g1628583

 BLAST score
 642

 E value
 2.0e-67

 Match length
 123

% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142181

Seq. ID LIB3168-011-P1-K1-B7

Method BLASTX
NCBI GI g1628583
BLAST score 575
E value 1.0e-59
Match length 111
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142182

Seq. ID LIB3168-011-P1-K1-B9

Method BLASTX
NCBI GI g112741
BLAST score 659
E value 2.0e-69
Match length 123
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201 emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 142183

Seq. ID LIB3168-011-P1-K1-C1

Method BLASTX
NCBI GI g3808062
BLAST score 159
E value 1.0e-10
Match length 66
% identity 45

NCBI Description (AB019195) PV100 [Cucurbita maxima]



Seq. No. 142184

Seq. ID LIB3168-011-P1-K1-C11

Method BLASTX
NCBI GI g112682
BLAST score 540
E value 2.0e-55
Match length 128
% identity 80

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142185

Seq. ID LIB3168-011-P1-K1-C12

Method BLASTX
NCBI GI g112682
BLAST score 597
E-value 4.0e-62
Match length 126
% identity 89

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142186

Seq. ID LIB3168-011-P1-K1-C2

Method BLASTX
NCBI GI g112681
BLAST score 700
E value 3.0e-74
Match length 131
% identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142187

Seq. ID LIB3168-011-P1-K1-C3

Method BLASTN
NCBI GI g3228389
BLAST score 376
E value 0.0e+00
Match length 376
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17L21,

complete sequence [Arabidopsis thaliana]

Seq. No. 142188

Seq. ID LIB3168-011-P1-K1-C4

Method BLASTN NCBI GI g2656031



BLAST score 314 E value 1.0e-176 Match length 362 % identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXC20

Seq. No. 142189

Seq. ID LIB3168-011-P1-K1-C6

Method BLASTX
NCBI GI g1628583
BLAST score 108
E value 3.0e-20
Match length 113
% identity 51

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142190

Seq. ID LIB3168-011-P1-K1-C7

Method BLASTX
NCBI GI g112737
BLAST score 519
E value 6.0e-53
Match length 127
% identity 80

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__ NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142191

Seq. ID LIB3168-011-P1-K1-C8

Method BLASTX
NCBI GI g1628583
BLAST score 593
E value 1.0e-61
Match length 114
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142192

Seq. ID LIB3168-011-P1-K1-C9

Method BLASTX
NCBI GI g3367529
BLAST score 617
E value 2.0e-64
Match length 130
% identity 95

NCBI Description (AC004392) Strong similarity to gi_2160138 F19K23.6 gene

product from A. thaliana BAC gb AC000375. [Arabidopsis

3.5



thaliana]

142193 Seq. No. Seq. ID LIB3168-011-P1-K1-D1 Method BLASTX NCBI GI g2088654 BLAST score 517 E value 1.0e-52 Match length 114 % identity 90 (AF002109) 60S acidic ribosomal protein PO isolog NCBI Description [Arabidopsis thaliana]

Seq. No. 142194 Seq. ID LIB3168-011-P1-K1-D11

Method BLASTX
NCBI GI g1628583
BLAST score 674
E value 4.0e-71
Match length 129
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142195

Seq. ID LIB3168-011-P1-K1-D12

Method BLASTX
NCBI GI g1705677
BLAST score 457
E value 1.0e-45
Match length 106
% identity 88

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG

>gi_2118115_pir__S60112 cell division control protein CDC48
homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell

division cycle protein [Arabidopsis thaliana]

Seq. No. 142196

Seq. ID LIB3168-011-P1-K1-D3

Method BLASTX
NCBI GI g1628583
BLAST score 658
E value 3.0e-69
Match length 126
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142197

Seq. ID LIB3168-011-P1-K1-D4

Method BLASTX
NCBI GI g3808062
BLAST score 167
E value 1.0e-11
Match length 71

Seq. ID

BLAST score

Method NCBI GI



```
% identity
NCBI Description
                  (AB019195) PV100 [Cucurbita maxima]
                  142198
Seq. No.
                  LIB3168-011-P1-K1-D5
Seq. ID
Method
                  BLASTX
                  g3915961
NCBI GI
                  604
BLAST score
                  6.0e-63
E value
Match length
                  127
% identity
                  91
NCBI Description
                  HYPOTHETICAL 267 KD PROTEIN (ORF 2280)
                  >gi_2924274_emb_CAA77427 (Z00044) Ycf2 protein [Nicotiana
                  tabacum] >gi 2924285 emb CAA77438 (Z00044) hypothetical
                  protein [Nicotiana tabacum]
Seq. No.
                  142199
Seq. ID
                  LIB3168-011-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  544
                  6.0e-56
E value
Match length
                  116
% identity
                  88
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  142200
Seq. ID
                  LIB3168-011-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  q3046855
BLAST score
                  385
E value
                  0.0e + 00
Match length
                  389
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSL1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  142201
Seq. ID
                  LIB3168-011-P1-K1-D8
Method
                  BLASTX
                  q3819164
NCBI GI
BLAST score
                  520
                  4.0e-53
E value
Match length
                  119
                  87
% identity
NCBI Description
                  (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
                  max]
Seq. No.
                  142202
```

17418

LIB3168-011-P1-K1-D9

BLASTX

667

g2245076



E value 2.0e-70 Match length 128 % identity 99

NCBI Description (Z97343) GTP-binding RAB2A protein [Arabidopsis thaliana]

Seq. No. 142203

Seq. ID LIB3168-011-P1-K1-E1

Method BLASTN
NCBI GI g2341023
BLAST score 243
E value 1.0e-134
Match length 390
% identity 100

NCBI Description Sequence of BAC F19P19 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 142204

Seq. ID LIB3168-011-P1-K1-E10

Method BLASTX
NCBI GI g4262250
BLAST score 673
E value 5.0e-71
Match length 129
% identity 100

NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No. 142205

Seq. ID LIB3168-011-P1-K1-E12

Method BLASTX
NCBI GI g112681
BLAST score 540
E value 2.0e-55
Match length 126
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142206

Seq. ID LIB3168-011-P1-K1-E2

Method BLASTX
NCBI GI g3396079
BLAST score 376
E value 3.0e-36
Match length 72
% identity 100

NCBI Description (AF080173) inositol 1,3,4-trisphosphate 5/6-kinase

[Arabidopsis thaliana]

Seq. No. 142207

Seq. ID LIB3168-011-P1-K1-E3

Method BLASTX
NCBI GI g1628583
BLAST score 412
E value 2.0e-40



Match length 112 % identity 74

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142208

Seq. ID LIB3168-011-P1-K1-E4

Method BLASTX
NCBI GI g112737
BLAST score 506
E value 2.0e-51
Match length 125
% identity 79

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

44. 1

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142209

Seq. ID LIB3168-011-P1-K1-E6

Method BLASTX
NCBI GI g1628583
BLAST score 699
E value 4.0e-74
Match length 132
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142210

Seq. ID LIB3168-011-P1-K1-E8

Method BLASTX
NCBI GI g82051
BLAST score 313
E value 7.0e-29
Match length 119
% identity 54

NCBI Description lipid body-associated membrane protein - carrot

>gi 259453 bbs 117620 (S47635) lipid body membrane

protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide,

180 aa] [Daucus carota]

Seq. No. 142211

Seq. ID LIB3168-011-P1-K1-E9

Method BLASTX
NCBI GI g1628583
BLAST score 322
E value 7.0e-30
Match length 60
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

BLAST score

E value

663

7.0e-70



cruciferin seed storage protein [Arabidopsis thaliana]

```
142212
Seq. No.
                  LIB3168-011-P1-K1-F1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112681
BLAST score
                  527
E value
                  6.0e-54
                  125
Match length
% identity
                  82
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  142213
Seq. No.
                  LIB3168-011-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4490732
BLAST score
                  340
                  5.0e-32
E value
Match length
                  72
                  90
% identity
NCBI Description
                  (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
                  protein [Arabidopsis thaliana]
Seq. No.
                  142214
Seq. ID
                  LIB3168-011-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  432
                  9.0e-43
E value
Match length
                  105
% identity
                  82
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142215
Seq. ID
                  LIB3168-011-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  412
E value
                  2.0e-40
Match length
                  112
% identity
                  74
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142216
Seq. No.
Seq. ID
                  LIB3168-011-P1-K1-F3
                  BLASTX
Method
NCBI GI
                  g1628583
```

17421



Match length 127 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142217

Seq. ID LIB3168-011-P1-K1-F4

Method BLASTX
NCBI GI g2058456
BLAST score 376
E value 3.0e-36
Match length 74
% identity 100

NCBI Description (U66408) GTP-binding protein [Arabidopsis thaliana]

>gi_2345150_gb_AAB67830_ (AF014822) developmentally regulated GTP binding protein [Arabidopsis thaliana]

Seq. No. 142218

Seq. ID LIB3168-011-P1-K1-F5

Method BLASTX
NCBI GI g1628583
BLAST score 658
E value 3.0e-69
Match length 126
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142219

Seq. ID LIB3168-011-P1-K1-F6

Method BLASTN
NCBI GI g3063438
BLAST score 224
E value 1.0e-123
Match length 368
% identity 100

NCBI Description Complete sequence of Arabidopsis F22013, complete sequence

[Arabidopsis thaliana]

Seq. No. 142220

Seq. ID LIB3168-011-P1-K1-F8

Method BLASTX
NCBI GI g3201627
BLAST score 204
E value 2.0e-30
Match length 103
% identity 65

NCBI Description (AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No. 142221

Seq. ID LIB3168-011-P1-K1-G1

Method BLASTN
NCBI GI g3047074
BLAST score 376
E value 0.0e+00



Match length 388 % identity 99

NCBI Description Arabidopsis thaliana BAC F21E10

Seq. No. 142222

Seq. ID LIB3168-011-P1-K1-G10

Method BLASTX
NCBI GI g112682
BLAST score 563
E value 4.0e-58
Match length 116
% identity 91

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142223

Seq. ID LIB3168-011-P1-K1-G11

Method BLASTX
NCBI GI g112682
BLAST score 544
E value 6.0e-56
Match length 116
% identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142224

Seq. ID LIB3168-011-P1-K1-G2

Method BLASTX
NCBI GI g112682
BLAST score 545
E value 5.0e-56
Match length 129
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142225

Seq. ID LIB3168-011-P1-K1-G3

Method BLASTN
NCBI GI 94220510
BLAST score 280
E value 1.0e-156
Match length 304
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18

(ESSAII project)



```
Seq. No.
                  142226
Seq. ID
                  LIB3168-011-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q112740
BLAST score
                  271
E value
                  7.0e-24
Match length
                  119
% identity
                  52
                  NAPIN 2 PRECURSOR (1.7S SEED STORAGE PROTEIN)
NCBI Description
                  >gi_81691 pir_A25997 napin precursor (napA) - rape
                  >gi 167153 (J02586) prepronapin [Brassica napus] >gi 167155
                  (J02798) napin [Brassica napus]
Seq. No.
                  142227
                  LIB3168-011-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  519
E value
                  6.0e-53
Match length
                  127
                  80
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  142228
Seq. ID
                  LIB3168-011-P1-K1-H10
Method
                  BLASTN
                  g395203
NCBI GI
BLAST score
                  72
                  9.0e-33
E value
Match length
                  80
% identity
                  49
NCBI Description A.thaliana 2S albumin gene isoforms 1 and 2, complete CDS's
Seq. No.
                  142229
                  LIB3168-011-P1-K1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2564045
BLAST score
                  121
E value
                  2.0e-61
Match length
                  384
                  93
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K8K14, complete sequence [Arabidopsis thaliana]
```

Seq. No. 142230 Seq. ID LIB3168-011-P1-K1-H2 Method BLASTX

NCBI GI g112681 BLAST score 562 E value 5.0e-58 Match length 111



% identity

12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142231

Seq. ID LIB3168-011-P1-K1-H3

Method BLASTN NCBI GI g2351065 BLAST score 222 E value 1.0e-121 Match length 395 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MHF15, complete sequence [Arabidopsis thaliana]

Seq. No. 142232

LIB3168-011-P1-K1-H4 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 279 E value 2.0e-25 Match length 55 % identity 96

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142233

Seq. ID LIB3168-011-P1-K1-H5

Method BLASTX NCBI GI q1628583 BLAST score 362 E value 6.0e-35 Match length 69 99 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142234

Seq. ID LIB3168-011-P1-K1-H6

Method BLASTX NCBI GI q135858 BLAST score 286 E value 1.0e-25 Match length 58 % identity 97

TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP) NCBI Description

> >gi 99760 pir S22201 tonoplast intrinsic protein alpha -Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein

[Arabidopsis thaliana] >gi 445128 prf 1908432A tonoplast

intrinsic protein alpha [Arabidopsis thaliana]



```
Seq. No.
                  142235
Seq. ID
                  LIB3168-011-P1-K1-H7
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  663
E value
                  7.0e-70
Match length
                  127
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142236
                  LIB3168-011-P1-K1-H8
Seq. ID
Method
                  BLASTX
                  g4204299
NCBI GI
BLAST score
                  681
E value
                  5.0e-72
Match length
                  130
                  99
% identity
NCBI Description
                  (AC003027) lcl_prt_seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  142237
Seq. ID
                  LIB3168-011-P1-K1-H9
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  614
                  4.0e-64
E value
                  130
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142238
Seq. ID
                  LIB3168-012-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  664
                  6.0e-70
E value
Match length
                  136
% identity
                  92
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  142239
```

Seq. ID LIB3168-012-P1-K1-A10

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120



% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142240

Seq. ID LIB3168-012-P1-K1-A11

Method BLASTX
NCBI GI g4468994
BLAST score 695
E value 1.0e-73
Match length 127
% identity 100

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 142241

Seq. ID LIB3168-012-P1-K1-A12

Method BLASTX
NCBI GI g117822
BLAST score 517
E value 8.0e-53
Match length 120
% identity 82

NCBI Description CYTOCHROME B6 >gi_65635_pir__CBNT6

plastoquinol--plastocyanin reductase (EC 1.10.99.1)

cytochrome b6 - common tobacco chloroplast

>gi_11858_emb_CAA77375_ (Z00044) cytochrome b6 [Nicotiana tabacum] >gi_225226_prf__1211235BH cytochrome b6 [Nicotiana

tabacum]

Seq. No. 142242

Seq. ID LIB3168-012-P1-K1-A2

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142243

Seq. ID LIB3168-012-P1-K1-A3

Method BLASTX
NCBI GI g1628583
BLAST score 544
E value 7.0e-56
Match length 137
% identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142244

Seq. ID LIB3168-012-P1-K1-A4

Method BLASTN



```
NCBI GI
                  q1628582
BLAST score
E value
                  4.0e-20
Match length
                  159
% identity
                  43
                  Arabidopsis thaliana 12S cruciferin seed storage protein
NCBI Description
                  (ATCRU3) gene, complete cds
Seq. No.
                  142245
Seq. ID
                  LIB3168-012-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g226120
BLAST score
                  224
E value
                  2.0e-18
                  134
Match length
% identity
NCBI Description vicilin gene B [Saguinus oedipus]
Seq. No.
                  142246
                  LIB3168-012-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  508
E value
                  1.0e-51
Match length
                  126
% identity
                  78
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142247
Seq. ID
                  LIB3168-012-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  619
E value
                  1.0e-64
Match length
                  120
                  99
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142248
Seq. ID
                  LIB3168-012-P1-K1-A8
```

Method BLASTN NCBI GI g4538990 BLAST score 168 E value 2.0e-89 Match length 410 99 % identity

Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 NCBI Description

(ESSA project)

Seq. No. 142249

Seq. ID LIB3168-012-P1-K1-A9

Method BLASTX NCBI GI q1628583



```
BLAST score
E value
                  2.0e-65
Match length
                  120
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142250
Seq. ID
                  LIB3168-012-P1-K1-B10
Method
                  BLASTN
NCBI GI
                  q16231
BLAST score
                  68
E value
                  2.0e-30
                  80
Match length
                  97
% identity
                  Arabidopsis CRA1 gene for 12S seed storage protein
NCBI Description
                  >gi 166675 gb M37247 ATHCRA1AA A.thaliana 12S storage
                  protein CRA1 gene, exons 1-4
                  142251
```

Seq. No. Seq. ID LIB3168-012-P1-K1-B11 Method BLASTN NCBI GI q414549 BLAST score 38 E value 6.0e-13 Match length 45

98

NCBI Description Arabidopsis thaliana Columbia cytosolic triose phosphate isomerase (Atctimc) mRNA, complete cds

142252 Seq. No.

% identity

Seq. ID LIB3168-012-P1-K1-B12

Method BLASTX NCBI GI q112737 BLAST score 441 4.0e-44 E value 86 Match length % identity 99

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142253

LIB3168-012-P1-K1-B2 Seq. ID

BLASTX Method NCBI GI g2129659 BLAST score 416 E value 7.0e-41Match length 129 70 % identity

NCBI Description oleosin, isoform 21K - Arabidopsis thaliana >gi_725260

(L40954) oleosin [Arabidopsis thaliana]

NCBI GI

E value

BLAST score

g1628583

7.0e-05

109



```
Seq. No.
                  142254
Seq. ID
                  LIB3168-012-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  606
E value
                  4.0e-63
                  131
Match length
% identity
                  89
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  142255
Seq. ID
                  LIB3168-012-P1-K1-B4
Method
                  BLASTN
NCBI GI
                  g3399678
BLAST score
                  45
E value
                  1.0e-16
Match length
                  91
% identity
                  93
                  Arabidopsis thaliana chromosome 1 BAC F13M7 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  142256
Seq. ID
                  LIB3168-012-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  277
E value
                  9.0e-25
Match length
                  103
% identity
                  62
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142257
Seq. ID
                  LIB3168-012-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g3702739
BLAST score
                  140
E value
                  8.0e-73
Match length
                  223
% identity
                  90
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MXE2, complete sequence [Arabidopsis thaliana]
Seq. No.
                  142258
                  LIB3168-012-P1-K1-B7
Seq. ID
Method
                  BLASTX
```

17430



Match length 64 % identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142259

Seq. ID LIB3168-012-P1-K1-B8

Method BLASTX
NCBI GI g133959
BLAST score 438
E value 2.0e-43
Match length 94
% identity 93

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 >gi_81526_pir__A30833

ribosomal protein S4 - spinach chloroplast >gi_343377 (M16878) ribosomal protein S4 [Spinacia oleracea] >gi_225464_prf__1303355A ribosomal protein S4 [Spinacia

oleracea]

Seq. No. 142260

Seq. ID LIB3168-012-P1-K1-C1

Method BLASTX
NCBI GI g1628583
BLAST score 616
E value 2.0e-64
Match length 120
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142261

Seq. ID LIB3168-012-P1-K1-C10

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142262

Seq. ID LIB3168-012-P1-K1-C11

Method BLASTN
NCBI GI g3449329
BLAST score 123
E value 1.0e-62
Match length 411
% identity 56

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDH9, complete sequence [Arabidopsis thaliana]

Seq. No. 142263

Seq. ID LIB3168-012-P1-K1-C12

17431

NCBI Description



```
BLASTX
Method
                  g1655424
NCBI GI
                  461
BLAST score
                  4.0e-46
E value
                  89
Match length
                  99
% identity
                  (D83531) GDP dissociation inhibitor [Arabidopsis thaliana]
NCBI Description
                  >gi_3212878 (AC004005) GDP dissociation inhibitor
                  [Arabidopsis thaliana]
Seq. No.
                  142264
                  LIB3168-012-P1-K1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112681
BLAST score
                  605
                  5.0e-63
E value
Match length
                  122
                  93
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  142265
                  LIB3168-012-P1-K1-C4
Seq. ID
Method
                  BLASTX
                  g3169171
NCBI GI
                  191
BLAST score
E value
                  2.0e-14
                  93
Match length
                   44
% identity
                   (AC004401) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                   thaliana] >gi 3445213 (AC004786) putative serine
                   carboxypeptidase I [Arabidopsis thaliana]
                   142266
Seq. No.
                  LIB3168-012-P1-K1-C5
Seq. ID
Method
                   BLASTN
                   g16472
NCBI GI
                   399
BLAST score
                   0.0e+00
E value
                   415
Match length
% identity
NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type
                   142267
Seq. No.
Seq. ID
                   LIB3168-012-P1-K1-C6
Method
                  BLASTX
NCBI GI
                   q2129659
BLAST score
                   366
                   5.0e-35
E value
                   127
Match length
% identity
                   65
```

(L40954) oleosin [Arabidopsis thaliana]

oleosin, isoform 21K - Arabidopsis thaliana >gi_725260



Seq. No. 142268 Seq. ID LIB3168-012-P1-K1-C7 Method BLASTX NCBI GI q1628583 BLAST score 642 2.0e-67 E value Match length 123 % identity 100 (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S craciferin seed storage protein [Arabidopsis thaliana] Seq. No. 142269 LIB3168-012-P1-K1-C8

Seq. ID Method BLASTX g1628583 NCBI GI BLAST score 533 : E value 1.0e-54 Match length 135

% identity 79 NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142270

LIB3168-012-P1-K1-C9 Seq. ID

Method BLASTX NCBI GI q112681 BLAST score 581 3.0e-60 E value 134 Match length % identity 84

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142271

Seq. ID LIB3168-012-P1-K1-D1

Method BLASTX NCBI GI g1628583 BLAST score 484 E value 6.0e-49113 Match length % identity 84

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

142272 Seq. No.

Seq. ID LIB3168-012-P1-K1-D10

BLASTX Method NCBI GI g112743 BLAST score 593 1.0e-61 E value Match length 126



% identity NCBI Description

2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_

(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4

precursor [Arabidopsis thaliana]

Seq. No. 142273

Seq. ID LIB3168-012-P1-K1-D11

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142274

Seq. ID LIB3168-012-P1-K1-D12

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142275

Seq. ID LIB3168-012-P1-K1-D2

Method BLASTN

NCBI GI g2828183

BLAST score 210

E value 1.0e-114

Match length 395

% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MPL12, complete sequence [Arabidopsis thaliana]

Seq. No. 142276

Seq. ID LIB3168-012-P1-K1-D3

Method BLASTX
NCBI GI g112682
BLAST score 574
E value 2.0e-59
Match length 134
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937 emb_CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

NCBI GI

E value

BLAST score

g112737

526 9.0e-54



```
Seq. No.
                  142277
                  LIB3168-012-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  548
E value
                  2.0e-56
Match length
                  138
                  79
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142278
Seq. ID
                  LIB3168-012-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  700
E value
                  4.0e-74
                  130
Match length
% identity
                  100
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  142279
Seq. ID
                  LIB3168-012-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g3128180
BLAST score
                  576
E value
                  1.0e-59
                  119
Match length
                  99
% identity
NCBI Description (AC004521) citrate synthetase [Arabidopsis thaliana]
                  142280
Seq. No.
Seq. ID
                  LIB3168-012-P1-K1-D7
                  BLASTX
Method
NCBI GI
                  q1628583
BLAST score
                  362
                  2.0e-34
E value
Match length
                  90
                  79
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142281
Seq. No.
Seq. ID
                  LIB3168-012-P1-K1-D8
Method
                  BLASTX
```



Match length 128 % identity 80

NCBI Description

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__ NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No. 142282

Seq. ID LIB3168-012-P1-K1-D9

Method BLASTN
NCBI GI g2351069
BLAST score 314
E value 1.0e-176
Match length 322
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSH12, complete sequence [Arabidopsis thaliana]

Seq. No. 142283

Seq. ID LIB3168-012-P1-K1-E12

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142284

Seq. ID LIB3168-012-P1-K1-E4

Method BLASTN
NCBI GI g3873174
BLAST score 412
E value 0.0e+00
Match length 412
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14N23,

complete sequence [Arabidopsis thaliana]

Seq. No. 142285

Seq. ID LIB3168-012-P1-K1-E5

Method BLASTX
NCBI GI g112682
BLAST score 574
E value 2.0e-59
Match length 134
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir __S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

```
Seq. No.
                  142286
Seq. ID
                  LIB3168-012-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  q1628583
                  504
BLAST score
E value
                  3.0e-51
Match length
                  139
% identity
                  73
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142287
                  LIB3168-012-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  611
                  9.0e-64
E value
Match length
                  117
                  100
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142288
Seq. ID
                  LIB3168-012-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  625
E value
                  2.0e-65
Match length
                  120
% identity
                  100
NCBI Description
                  cruciferin seed storage protein [Arabidopsis thaliana]
```

(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

Seq. No. 142289 Seq. ID LIB3168-012-P1-K1-F1

Method BLASTX NCBI GI g1628583 BLAST score 625 E value 2.0e-65 120 Match length 100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. Seq. ID LIB3168-012-P1-K1-F10

142290

Method BLASTX NCBI GI g2129767 BLAST score 613 E value 6.0e-64 Match length 123 % identity 93



NCBI Description vacuolar processing enzyme (EC 3.4.22.-) isozyme beta precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_ (D61394) beta-VPE [Arabidopsis thaliana]

Seq. No. 142291

Seq. ID LIB3168-012-P1-K1-F11

Method BLASTX
NCBI GI g1495251
BLAST score 692
E value 3.0e-73
Match length 137
% identity 100

NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No. 142292

Seq. ID LIB3168-012-P1-K1-F12

Method BLASTN
NCBI GI g2924729
BLAST score 177
E value 6.0e-95
Match length 309
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNA5, complete sequence [Arabidopsis thaliana]

Seq. No. 142293

Seq. ID LIB3168-012-P1-K1-F2

Method BLASTX
NCBI GI g112682
BLAST score 567
E value 1.0e-58
Match length 134
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >qi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142294

Seq. ID LIB3168-012-P1-K1-F3

Method BLASTX
NCBI GI g112682
BLAST score 578
E value 7.0e-60
Match length 135
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142295

Seq. ID LIB3168-012-P1-K1-F4

Method BLASTX NCBI GI g112682



BLAST score 630 E value 6.0e-66 Match length 138 % identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142296

Seq. ID LIB3168-012-P1-K1-F5

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142297

Seq. ID LIB3168-012-P1-K1-F6

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142298

Seq. ID LIB3168-012-P1-K1-F7

Method BLASTX
NCBI GI g112682
BLAST score 544
E value 7.0e-56
Match length 116
% identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142299

Seq. ID LIB3168-012-P1-K1-F8

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis





thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142300

Seg. ID LIB3168-012-P1-K1-F9

Method BLASTN
NCBI GI g2262155
BLAST score 89
E value 6.0e-43

E value 6.0e-Match length 93 % identity 99

NCBI Description DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No. 142301

Seq. ID LIB3168-012-P1-K1-G1

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142302

Seq. ID LIB3168-012-P1-K1-G12

Method BLASTX
NCBI GI g112739
BLAST score 338
E value 8.0e-32
Match length 105
% identity 67

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 142303

Seq. ID LIB3168-012-P1-K1-G2

Method BLASTX
NCBI GI g633890
BLAST score 371
E value 1.0e-35
Match length 88
% identity 78

NCBI Description (S72926) glucose and ribitol dehydrogenase homolog [Hordeum

vulgare]

Seq. No. 142304

Seq. ID LIB3168-012-P1-K1-G3

Method BLASTX NCBI GI g112681



BLAST score E value 3.0e-45 Match length 115 77 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir \$08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142305

Seq. ID LIB3168-012-P1-K1-G4

Method BLASTX NCBI GI q1628583 BLAST score 575 1.0e-59 E value 117 Match length % identity 95

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

> thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142306

Seq. ID LIB3168-012-P1-K1-G5

Method BLASTX NCBI GI q1628583 BLAST score 625 2.0e-65 E value Match length 120 100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142307

Seq. ID LIB3168-012-P1-K1-G6

Method BLASTX NCBI GI q1628583 BLAST score 625 2.0e-65 E value 120 Match length 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

142308 Seq. No.

LIB3168-012-P1-K1-G8 Seq. ID

Method BLASTX NCBI GI g137580 BLAST score 217 2.0e-17 E value Match length 130 % identity 35

NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72)

> >gi 72286 pir FWCNAB alpha-globulin B precursor (clone C72) - upland cotton >gi 167375 (M16891) vicilin precursor



[Gossypium hirsutum]

 Seq. No.
 142309

 Seq. ID
 LIB3168-012-P1-K1-G9

 Method
 BLASTX

 NCBI GI
 g1628583

 BLAST score
 451

E value 1.0e-60
Match length 121
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142310

Seq. ID LIB3168-012-P1-K1-H1

Method BLASTX
NCBI GI g3334123
BLAST score 422
E value 1.0e-41
Match length 109
% identity 83

NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR

>gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of

mitochondrial FI-ATPase [Arabidopsis thaliana] >gi_2924787

(AC002334) mitochondrial F1-ATPase, gamma subunit

[Arabidopsis thaliana]

Seq. No. 142311

Seq. ID LIB3168-012-P1-K1-H10

Method BLASTN
NCBI GI g2565435
BLAST score 323
E value 0.0e+00
Match length 355
% identity 100

NCBI Description Arabidopsis thaliana DegP protease mRNA, nuclear gene

encoding chloroplast protein, complete cds

Seq. No. 142312

Seq. ID LIB3168-012-P1-K1-H12

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142313

Seq. ID LIB3168-012-P1-K1-H2

Method BLASTX
NCBI GI g2129657
BLAST score 287
E value 9.0e-26



Match length 88 % identity 70

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 142314

Seq. ID LIB3168-012-P1-K1-H3

Method BLASTX
NCBI GI g2459432
BLAST score 522
E value 3.0e-53
Match length 98
% identity 97

NCBI Description (AC002332) CONSTANS-like protein [Arabidopsis thaliana]

g Seq. No. 142315

Seq. ID LIB3168-012-P1-K1-H4

Method BLASTX
NCBI GI g2961390
BLAST score 776
E value 4.0e-83
Match length 138
% identity 100

NCBI Description (AL022141) beta-galactosidase like protein [Arabidopsis

thaliana]

Seq. No. 142316

Seq. ID LIB3168-012-P1-K1-H5

Method BLASTX
NCBI GI g1628583
BLAST score 616
E value 3.0e-64
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142317

Seq. ID LIB3168-012-P1-K1-H6

Method BLASTN
NCBI GI g2264311
BLAST score 65
E value 6.0e-28
Match length 141
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MLN1, complete sequence [Arabidopsis thaliana]

Seq. No. 142318

Seq. ID LIB3168-012-P1-K1-H7

Method BLASTX
NCBI GI g1628583
BLAST score 640
E value 4.0e-67



Match length 135 % identity 93

NCBI Description

(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142319

Seq. ID LIB3168-012-P1-K1-H8

Method BLASTX
NCBI GI g2832698
BLAST score 351
E value 1.0e-33
Match length 65
% identity 97

NCBI Description (AL021713) starch synthase-like protein [Arabidopsis

thaliana]

Seq. No. 142320

Seq. ID LIB3168-013-P1-K1-A1

Method BLASTN
NCBI GI g4753195
BLAST score 261
E value 1.0e-145
Match length 261
% identity 100

NCBI Description Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5

cM, complete sequence

Seq. No. 142321

Seq. ID LIB3168-013-P1-K1-A10

Method BLASTX
NCBI GI g112682
BLAST score 229
E value 2.0e-19
Match length 59
% identity 75

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142322

Seq. ID LIB3168-013-P1-K1-A12

Method BLASTX
NCBI GI g1628583
BLAST score 659
E value 2.0e-69
Match length 141
% identity 91

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142323

Seq. ID LIB3168-013-P1-K1-A2

Method BLASTX



NCBI GI g112682 BLAST score 553 E value 6.0e-57 Match length 126 % identity 85

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142324

Seq. ID LIB3168-013-P1-K1-A3

Method BLASTX
NCBI GI g112737
BLAST score 588
E value 5.0e-61
Match length 140
% identity 81

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142325

Seq. ID LIB3168-013-P1-K1-A4

Method BLASTX
NCBI GI g1628583
BLAST score 635
E value 1.0e-66
Match length 137
% identity 91

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142326

Seq. ID LIB3168-013-P1-K1-A5

Method BLASTX
NCBI GI g112682
BLAST score 579
E value 6.0e-60
Match length 136
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142327

Seq. ID LIB3168-013-P1-K1-A6

Method BLASTX NCBI GI g112681



```
BLAST score
                  162
E value
                  4.0e-11
Match length
                  85
% identity
                  49
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  142328
Seq. No.
                  LIB3168-013-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  563
E value
                  3.0e-58
                  119
Match length
                  91
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142329
                  LIB3168-013-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  600
E value
                  2.0e-62
                  120
Match length
                  97
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142330
                  LIB3168-013-P1-K1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4097693
BLAST score
                  47
                  2.0e-17
E value
Match length
                  59
                  95
% identity
                  Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete
NCBI Description
                  142331
Seq. No.
                  LIB3168-013-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  595
E value
                  7.0e-62
Match length
                  138
% identity
                  82
```

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed



storage protein [Arabidopsis thaliana]

```
Seq. No.
                  142332
                  LIB3168-013-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
E value
                  2.0e-65
                  120
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142333
                  LIB3168-013-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
                  625
BLAST score
                  2.0e-65
E value
                  120
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142334
Seq. ID
                  LIB3168-013-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
E value
                  2.0e-65
Match length
                  120
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142335
Seq. ID
                  LIB3168-013-P1-K1-B3
                  BLASTX
Method
NCBI GI
                  g112737
BLAST score
                   651
                  2.0e-68
E value
                  132
Match length
                   91
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204_emb_CAA80870_
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
```

17447

142336

BLASTX

LIB3168-013-P1-K1-B4

Seq. No.

Seq. ID Method

170



NCBI GI a1628583 BLAST score 747 E value 1.0e-79 Match length 141 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

142337 Seq. No.

Seq. ID LIB3168-013-P1-K1-B6

Method BLASTX g1628583 NCBI GI BLAST score 93 5.0e-03 E value Match length 72 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

142338 Seq. No.

LIB3168-013-P1-K1-B7 Seq. ID

Method BLASTX NCBI GI q1628583 BLAST score 625 2.0e-65 E value Match length 120 100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142339

LIB3168-013-P1-K1-B8 Seq. ID

Method BLASTX NCBI GI q112682 628 BLAST score 1.0e-65 E value Match length 128 % identity

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142340

Seq. ID LIB3168-013-P1-K1-B9

Method BLASTX NCBI GI g1628583 BLAST score 625 E value 2.0e-65 Match length 120 % identity 100

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S



cruciferin seed storage protein [Arabidopsis thaliana]

```
142341
Seq. No.
                  LIB3168-013-P1-K1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q112682
BLAST score
                  648
E value
                  5.0e-68
                  143
Match length
                  87
% identity
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir___S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  142342
Seq. No.
                  LIB3168-013-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  497
                  2.0e-50
E value
                  118
Match length
% identity
                  82
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  142343
Seq. No.
                  LIB3168-013-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3522956
BLAST score
                  389
E value
                  1.0e-37
Match length
                  130
% identity
                  54
                  (AC004411) putative pectinacetylesterase precursor
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  142344
Seq. ID
                  LIB3168-013-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1351837
BLAST score
                  672
E value
                  7.0e-71
Match length
                  140
% identity
                  94
                  ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT
NCBI Description
                  BETA >gi 2144155 pir S66564 acetyl CoA carboxylase type II
                  beta-carboxyltransferase chain - rape chloroplast
                  >gi 1069998 emb CAA90747 (Z50868) acetyl CoA carboxylase
                  carboxyltransferase (beta subunit) [Brassica napus]
```

[Brassica napus]

>gi 1589046 prf 2210244G Ac-CoA carboxylase:SUBUNIT=beta



```
Seq. No.
Seq. ID
                  LIB3168-013-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
                  2.0e-65
E value
Match length
                  120
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142346
                  LIB3168-013-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  a1628583
                  625
BLAST score
E value
                  2.0e-65
                  120
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142347
                  LIB3168-013-P1-K1-C4
Seq. ID
Method
                  BLASTX
                  g3850914
NCBI GI
BLAST score
                  558
E value
                  2.0e-57
                  118
Match length
                  95
% identity
NCBI Description
                  (AF060397) ATP synthase beta subunit [Stirlingia latifolia]
Seq. No.
                  142348
                  LIB3168-013-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  595
                  7.0e-62
E value
Match length
                  138
% identity
                  82
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  142349
                  LIB3168-013-P1-K1-C6
Seq. ID
                  BLASTX
Method
                  g112682
NCBI GI
BLAST score
                   612
                  7.0e-64
E value
                  130
Match length
                  88
% identity
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
```



142350

cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. Seq. ID LIB3168-013-P1-K1-C7 Method BLASTX g1628583 NCBI GI BLAST score 619 E value 1.0e-64 Match length 120

% identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

-, 5

Seq. No. 142351

Seq. ID LIB3168-013-P1-K1-C8

Method BLASTX NCBI GI g2129657 BLAST score 415 E value 9.0e-41 Match length 113 % identity

oleosin isoform - Arabidopsis thaliana NCBI Description

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 142352

LIB3168-013-P1-K1-C9 Seq. ID

BLASTX Method NCBI GI q1628583 625 BLAST score E value 2.0e-65 Match length 120 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142353

Seq. ID LIB3168-013-P1-K1-D10

Method BLASTX q112681 NCBI GI BLAST score 592 E value 2.0e-61 Match length 121 % identity 93

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142354



```
LIB3168-013-P1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q112741
                   709
BLAST score
                   3.0e-75
E value
Match length
                   132
% identity
                   100
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68855_pir_ NWMU3 2S albumin 3 precursor -
Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                   3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >gi 4490712 emb_CAB38846.1 (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
Seq. No.
                   142355
Seq. ID
                   LIB3168-013-P1-K1-D12
Method
                   BLASTX
                   q1628583
NCBI GI
                   625
BLAST score
                   2.0e-65
E value
Match length
                   120
% identity
                   100
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   142356
Seq. ID
                   LIB3168-013-P1-K1-D2
Method
                   BLASTN
NCBI GI
                   g395203
BLAST score
                   60
                   4.0e-25
E value
Match length
                   202
% identity
NCBI Description A.thaliana 2S albumin gene isoforms 1 and 2, complete CDS's
                   142357
Seq. No.
                   LIB3168-013-P1-K1-D3
Seq. ID
                   BLASTX
Method
                   g112737
NCBI GI
BLAST score
                   636
                   1.0e-66
E value
                   137
Match length
                   90
% identity
                   2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
```

Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

142358 Seq. No.

Seq. ID LIB3168-013-P1-K1-D4

Method BLASTX NCBI GI g860891



```
BLAST score 425
E value 6.0e-42
Match length 92
% identity 89
```

NCBI Description (X87636) PSII cytochome b559 alpha chain [Beta vulgaris] >gi 860897 emb CAA60972 (X87637) PSII cytochrome b599

alpha chain [Beta vulgaris]

Seq. No. 142359

Seq. ID LIB3168-013-P1-K1-D5

Method BLASTX
NCBI GI g3335169
BLAST score 707
E value 5.0e-75
Match length 134
% identity 98

NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No. 142360

Seq. ID LIB3168-013-P1-K1-D6

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142361

Seq. ID LIB3168-013-P1-K1-D7

Method BLASTX
NCBI GI g3157931
BLAST score 247
E value 5.0e-41
Match length 92
% identity 96

NCBI Description (AC002131) Similar to pyrophosphate-dependent

phosphofuctokinase beta subunit gb_Z32850 from Ricinus communis. ESTs gb_N65773, gb_N64925 and gb_F15232 come

from this gene. [Arabidopsis thaliana]

Seq. No. 142362

Seq. ID LIB3168-013-P1-K1-D8

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]



```
Seq. No.
                  142363
Seq. ID
                  LIB3168-013-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q112737
                  566
BLAST score
                  2.0e-58
E value
Match length
                  136
% identity
                  81
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
```

1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_(AL035680) NWMU1-2S albumin 1

¥:6

precursor [Arabidopsis thaliana]

 Seq. No.
 142364

 Seq. ID
 LIB3168-013-P1-K1-E1

 Method
 BLASTN

 NCBI GI
 g1628582

 BLAST score
 57

E value 3.0e-23
Match length 166
% identity 87
NCRI Description Archide

NCBI Description Arabidopsis thaliana 12S cruciferin seed storage protein

(ATCRU3) gene, complete cds

Seq. No. 142365

Seq. ID LIB3168-013-P1-K1-E10

Method BLASTX
NCBI GI g1628583
BLAST score 354
E value 1.0e-33
Match length 88
% identity 78

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142366

Seq. ID LIB3168-013-P1-K1-E11

Method BLASTX
NCBI GI g112681
BLAST score 538
E value 4.0e-55
Match length 141
% identity 79

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142367

Seq. ID LIB3168-013-P1-K1-E12

Method BLASTX NCBI GI g2129659



BLAST score 336 E value 2.0e-31 Match length 64 % identity 100

NCBI Description oleosin, isoform 21K - Arabidopsis thaliana >gi_725260

(L40954) oleosin [Arabidopsis thaliana]

Seq. No. 142368

Seq. ID LIB3168-013-P1-K1-E2

Method BLASTX
NCBI GI g1628583
BLAST score 551
E value 1.0e-56
Match length 140
% identity 78

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142369

Seq. ID LIB3168-013-P1-K1-E3

Method BLASTX
NCBI GI g112682
BLAST score 564
E value 3.0e-58
Match length 132
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142370

Seq. ID LIB3168-013-P1-K1-E4

Method BLASTX
NCBI GI g112681
BLAST score 547
E value 3.0e-56
Match length 140
% identity 79

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142371

Seq. ID LIB3168-013-P1-K1-E5

Method BLASTX
NCBI GI g1628583
BLAST score 172
E value 2.0e-12
Match length 71
% identity 58

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S

Method

NCBI GI BLAST score BLASTX q1072480

135



cruciferin seed storage protein [Arabidopsis thaliana]

```
142372
Seq. No.
Seq. ID
                  LIB3168-013-P1-K1-E6
Method
                  BLASTX
                  q1628583
NCBI GI
BLAST score
                  112
                  3.0e-05
E value
Match length
                  67
                  97
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142373
                  LIB3168-013-P1-K1-E7
Seq. ID
Method
                  BLASTX
                  q1628583
NCBI GI
BLAST score
                  620
                  9.0e-65
E value
                  119
Match length
% identity
                  100
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495 emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142374
                  LIB3168-013-P1-K1-E8
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                   668
                   2.0e-70
E value
                   128
Match length
                   100
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   142375
                   LIB3168-013-P1-K1-E9
Seq. ID
Method
                   BLASTX
                   q112681
NCBI GI
                   527
BLAST score
                   6.0e-54
E value
Match length
                   125
% identity
                   82
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81604_pir__S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] > gi_808936_emb_CAA32493_ (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
                   142376
Seq. No.
                   LIB3168-013-P1-K1-F1
Seq. ID
```

17456



```
E value 2.0e-20
Match length 72
% identity 60
NCBI Description cruciferin 1 precursor - rape
```

Seq. No. 142377 Seq. ID LIB3168-013-P1-K1-F10

Seq. ID LIB3168Method BLASTX
NCBI GI g112681
BLAST score 506
E value 2.0e-51
Match length 120
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142378

Seq. ID LIB3168-013-P1-K1-F11

Method BLASTX
NCBI GI g1628583
BLAST score 413
E value 2.0e-40
Match length 110
% identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142379

Seq. ID LIB3168-013-P1-K1-F12

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142380

Seq. ID LIB3168-013-P1-K1-F2

Method BLASTX
NCBI GI g112681
BLAST score 614
E value 4.0e-64
Match length 141
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936 emb_CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]



LIB3168-013-P1-K1-F3

Method BLASTX
NCBI GI g112681
BLAST score 596
E value 6.0e-62
Match length 138
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142382

Seq. ID LIB3168-013-P1-K1-F4

Method BLASTX
NCBI GI g112737
BLAST score 559
E value 1.0e-57
Match length 137
% identity 80

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142383

Seq. ID LIB3168-013-P1-K1-F6

Method BLASTN
NCBI GI 94757392
BLAST score 329
E value 0.0e+00
Match length 350
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K14A17, complete sequence

Seq. No. 142384

Seq. ID LIB3168-013-P1-K1-F7

Method BLASTX
NCBI GI g112681
BLAST score 504
E value 3.0e-51
Match length 121
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142385

Seq. ID LIB3168-013-P1-K1-F9

```
Method
NCBI GI
                   q2760171
BLAST score
                   149
                   4.0e-78
E value
                   357
Match length
                   97
% identity
```

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MPA24, complete sequence [Arabidopsis thaliana]

142386 Seq. No.

LIB3168-013-P1-K1-G10 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 648 4.0e-68 E value Match length 128 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142387

Seq. ID LIB3168-013-P1-K1-G11

Method BLASTX g1628583 NCBI GI BLAST score 382 2.0e-37 E value Match length 73 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142388

Seq. ID LIB3168-013-P1-K1-G12

Method BLASTX NCBI GI g112743 565 BLAST score E value 2.0e-58 123 Match length 86 % identity

2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor -Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi 395202_emb_CAA80869_

(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]

>qi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4

precursor [Arabidopsis thaliana]

142389 Seq. No.

Seq. ID LIB3168-013-P1-K1-G3

Method BLASTN NCBI GI g3241926 BLAST score 35 3.0e-10 E value Match length 188 % identity 85



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No. 142390

Seq. ID LIB3168-013-P1-K1-G4

Method BLASTN
NCBI GI g4455321
BLAST score 94
E value 2.0e-45
Match length 329

Match length 329 % identity 93

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10

(ESSAII project)

Seq. No. 142391

Seq. ID LIB3168-013-P1-K1-G6

Method BLASTX
NCBI GI g112682
BLAST score 279
E value 3.0e-25
Match length 72
% identity 72

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142392

Seq. ID LIB3168-013-P1-K1-G7

Method BLASTX
NCBI GI g112741
BLAST score 721
E value 1.0e-76
Match length 134
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 142393

Seq. ID LIB3168-013-P1-K1-G9

Method BLASTX
NCBI GI g112741
BLAST score 632
E value 3.0e-66
Match length 119
% identity 99

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]



>qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

142394 Seq. No.

LIB3168-013-P1-K1-H1 Seq. ID

Method BLASTX NCBI GI q112737 560 BLAST score 1.0e-57 E value Match length 136 % identity

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

142395 Seq. No.

LIB3168-013-P1-K1-H10 Seq. ID

Method BLASTX NCBI GI q1628583 BLAST score 625 E value 2.0e-65 Match length 120 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

142396 Seq. No.

Seq. ID LIB3168-013-P1-K1-H12

Method BLASTX NCBI GI g1628583 BLAST score 617 E value 2.0e-64 Match length 120 % identity 99

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142397

Seq. ID LIB3168-013-P1-K1-H4

BLASTX Method g1628583 NCBI GI 667 BLAST score 3.0e-70 E value 132 Match length 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

142398 Seq. No.

LIB3168-013-P1-K1-H7 Seq. ID



```
BLASTX
Method
NCBI GI
                  q1628583
                  195
BLAST score
                  6.0e-15
E value
                  75
Match length
                  97
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495 emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142399
Seq. No.
                  LIB3168-013-P1-K1-H8
Seq. ID
Method
                  BLASTN
                  q4185128
NCBI GI
BLAST score
                  215
                  1.0e-117
E value
Match length
                  357
% identity
                  99
                  Arabidopsis thaliana chromosome II P1 MSF3 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  142400
Seq. ID
                  LIB3168-014-P1-K1-A1
Method
                  BLASTX
                  g112740
NCBI GI
BLAST score
                  271
                  7.0e-24
E value
Match length
                  119
% identity
                  52
                  NAPIN 2 PRECURSOR (1.7S SEED STORAGE PROTEIN)
NCBI Description
                  >gi 81691 pir A25997 napin precursor (napA) - rape
                  >gi 167153 (J02586) prepronapin [Brassica napus] >gi_167155
                   (J02798) napin [Brassica napus]
Seq. No.
                  142401
Seq. ID
                  LIB3168-014-P1-K1-A10
Method
                  BLASTX
NCBI GI
                   q112737
BLAST score
                   546
E value
                   4.0e-56
Match length
                   133
                   80
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                   1 precursor [Arabidopsis thaliana] >gi_395204 emb_CAA80870_
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                   >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                   142402
Seq. No.
Seq. ID
                   LIB3168-014-P1-K1-A11
```

BLASTX Method NCBI GI g3123264

BLAST score 528 5.0e-54 E value 123 Match length



```
% identity
                  60S RIBOSOMAL PROTEIN L27 >qi 2244857 emb CAB10279
NCBI Description
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
                  142403
Seq. No.
                  LIB3168-014-P1-K1-A12
Seq. ID
Method
                  BLASTX
                  q2252844
NCBI GI
                  625
BLAST score
                  2.0e-65
E value
Match length
                  112
                  100
% identity
                 (AF013293) belongs to the cytochrome p450 family
NCBI Description
                  [Arabidopsis thaliana]
                  142404
Seq. No.
                  LIB3168-014-P1-K1-A2
Seq. ID
Method
                  BLASTX
                  g112737
NCBI GI
BLAST score
                  527
E value
                  7.0e-54
                  131
Match length
                  79
% identity
NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  142405
Seq. No.
                  LIB3168-014-P1-K1-A3
Seq. ID
Method
                  BLASTX
                  q1628583
NCBI GI
BLAST score
                  590
E value
                  3.0e-61
Match length
                  147
                  80
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142406
                  LIB3168-014-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2605714
```

Method BLASTX
NCBI GI g2605714
BLAST score 622
E value 5.0e-65
Match length 142
% identity 87

NCBI Description (AF026275) beta-tonoplast intrinsic protein [Arabidopsis

thaliana]

Seq. No. 142407

Seq. ID LIB3168-014-P1-K1-A5

Method BLASTX



```
q3600031
NCBI GI
BLAST score
                  555
                  4.0e-57
E value
                  133
Match length
                  85
% identity
                  (AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic
NCBI Description
                  acid aldolases [Arabidopsis thaliana]
                  142408
Seq. No.
                  LIB3168-014-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
                  2.0e-65
E value
                  120
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142409
Seq. No.
                  LIB3168-014-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1628583
BLAST score
                   532
                   2.0e-54
E value
Match length
                   136
                   78
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495 emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   142410
Seq. No.
Seq. ID
                   LIB3168-014-P1-K1-A8
Method
                   BLASTX
                   g1628583
NCBI GI
BLAST score
                   660
E value
                   2.0e-69
Match length
                   128
% identity
                   99
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   142411
Seq. ID
                   LIB3168-014-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   g633890
                   277
BLAST score
                   7.0e-25
E value
                   93
Match length
                   61
% identity
                   (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
NCBI Description
                   vulgare]
```

142412

LIB3168-014-P1-K1-B1

Seq. No. Seq. ID

17464



Method BLASTX
NCBI GI g112682
BLAST score 569
E value 8.0e-59
Match length 133
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142413

Seq. ID LIB3168-014-P1-K1-B10

Method BLASTX
NCBI GI g112681
BLAST score 539
E value 3.0e-55
Match length 142
% identity 79

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142414

Seq. ID LIB3168-014-P1-K1-B11

Method BLASTX
NCBI GI g112682
BLAST score 582
E value 2.0e-60
Match length 124
% identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142415

Seq. ID LIB3168-014-P1-K1-B2

Method BLASTN
NCBI GI g553039
BLAST score 217
E value 1.0e-119
Match length 298
% identity 99

NCBI Description Arabidopsis thaliana GF14 mRNA, complete cds

Seq. No. 142416

Seq. ID LIB3168-014-P1-K1-B3

Method BLASTN
NCBI GI g4376087
BLAST score 262
E value 1.0e-145
Match length 394

% identity NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No 142417 Seq. No. LIB3168-014-P1-K1-B4 Seq. ID Method BLASTN NCBI GI g2244788 BLAST score 389 E value 0.0e+00422 Match length 98 % identity Arabidopsis thaliana DNA chromosome 4, ESSA I contig NCBI Description fragment No 142418 Seq. No. LIB3168-014-P1-K1-B6 Seq. ID Method BLASTX NCBI GI q1628583 BLAST score 518 9.0e-53 E value 132 Match length 78 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142419

Seq. ID LIB3168-014-P1-K1-B7

Method BLASTX NCBI GI g112737 BLAST score 588 5.0e-61 E value Match length 140 % identity 81

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142420

Seq. ID LIB3168-014-P1-K1-B9

Method BLASTN NCBI GI g4512690 BLAST score 296 E value 1.0e-166 Match length 311 % identity 99

Arabidopsis thaliana chromosome II BAC F11A3 genomic NCBI Description

sequence, complete sequence

Seq. No. 142421

Seq. ID LIB3168-014-P1-K1-C1

Method BLASTX



```
NCBI GI
                  q4455223
BLAST score
                  327
E value
                  2.0e-30
                  113
Match length
% identity
                  (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  142422
Seq. No.
                  LIB3168-014-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  609
E value
                  2.0e-63
                  140
Match length
                  82
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  142423
Seq. No.
                  LIB3168-014-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  632
                  3.0e-66
E value
Match length
                  123
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142424
                  LIB3168-014-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q399013
BLAST score
                  520
E value
                  5.0e-53
Match length
                  102
                  100
% identity
                  ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                  >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                  thaliana (fragment) >gi 16175 emb_CAA46518_ (X65549)
                  adenylate translocator [Arabidopsis thaliana]
                  >gi 445607 prf 1909354A adenylate translocator
```

[Arabidopsis thaliana]

142425 Seq. No.

LIB3168-014-P1-K1-C2 Seq. ID

BLASTX Method NCBI GI g1628583 BLAST score 625 2.0e-65 E value Match length 120



% identity 100
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142426

Seq. ID LIB3168-014-P1-K1-C3

Method BLASTX
NCBI GI g2129657
BLAST score 377
E variue 3.0e-36
Match length 105
% identity 76

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 142427

Seq. ID LIB3168-014-P1-K1-C5

Method BLASTX
NCBI GI g112681
BLAST score 71
E value 2.0e-66
Match length 133
% identity 98

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142428

Seq. ID LIB3168-014-P1-K1-C6

Method BLASTX
NCBI GI g112681
BLAST score 439
E value 1.0e-43
Match length 100
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142429

Seq. ID LIB3168-014-P1-K1-C8

Method BLASTX
NCBI GI g1628583
BLAST score 301
E value 4.0e-47
Match length 118
% identity 86

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]



```
Seq. No.
                    142430
Seq. ID
                    LIB3168-014-P1-K1-D1
Method
                    BLASTX
NCBI GI
                     g4056469
                    242
BLAST score
E value
                     1.0e-20
                     50
Match length
                     100
% identity
                    (AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,
NCBI Description
                     gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and
                     gb_Z25043 come \overline{f}rom t
                     142431
Seq. No.
                    LIB3168-014-P1-K1-D10
Seq. ID
Method
                    BLASTX
                     g1628583
NCBI GI
                     279
BLAST score
                     5.0e-25
E value
                     86
Match length
% identity
NCBI Description
                     (U66916) 12S cruciferin seed storage protein [Arabidopsis
                     thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                     cruciferin seed storage protein [Arabidopsis thaliana]
                     142432
Seq. No.
Seq. ID
                     LIB3168-014-P1-K1-D11
Method
                     BLASTX
NCBI GI
                     g112741
BLAST score
                     718
                     3.0e-76
E value
Match length
                     135
                     99
% identity
                     2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                     PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                     3 precursor [Arabidopsis thaliana] >gi 395201_emb_CAA80868_
                     (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                     >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                     precursor [Arabidopsis thaliana]
                     142433
Seq. No.
Seq. ID
                     LIB3168-014-P1-K1-D12
                     {\tt BLASTX}
Method
NCBI GI
                     g4204298
BLAST score
                     568
E value
                     1.0e-58
                     138
Match length
                     80
% identity
                     (AC003027) 1cl prt seq No definition line found
NCBI Description
```

Seq. No. 142434

Seq. ID LIB3168-014-P1-K1-D2

[Arabidopsis thaliana]

Method BLASTX



NCBI GI g112681 BLAST score 591 E value 2.0e-61 Match length 137 % identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142435

Seq. ID LIB3168-014-P1-K1-D3

Method BLASTN
NCBI GI g2842474
BLAST score 222
E value 1.0e-122
Match length 222
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009

(ESSAII project)

Seq. No. 142436

Seq. ID LIB3168-014-P1-K1-D5

Method BLASTX
NCBI GI g112739
BLAST score 454
E value 3.0e-45
Match length 131
% identity 70

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205 emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 142437

Seq. ID LIB3168-014-P1-K1-D6

Method BLASTX
NCBI GI g2129659
BLAST score 187
E value 5.0e-19
Match length 82
% identity 71

NCBI Description oleosin, isoform 21K - Arabidopsis thaliana >gi_725260

(L40954) oleosin [Arabidopsis thaliana]

Seq. No. 142438

Seq. ID LIB3168-014-P1-K1-D7

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

- 17470



```
(U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142439
Seq. ID
                  LIB3168-014-P1-K1-D8
Method
                  BLASTX
                  q112681
NCBI GI
BLAST score
                  562
E value
                  5.0e-58
                  133
Match length
% identity
                  83
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  142440
                  LIB3168-014-P1-K1-D9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3985931
BLAST score
                  420
E value
                  0.0e + 00
Match length
                  420
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21H1, complete sequence [Arabidopsis thaliana]
                  142441
Seq. No.
                  LIB3168-014-P1-K1-E1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  667
                  3.0e-70
E value
                  132
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142442
Seq. No.
Seq. ID
                  LIB3168-014-P1-K1-E10
                  BLASTX
Method
NCBI GI
                  q4544399
BLAST score
                  305
                  7.0e-28
E value
Match length
                  112
                  47
% identity
                  (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
```

thaliana]

142443 Seq. No.

LIB3168-014-P1-K1-E11 Seq. ID

Method BLASTX NCBI GI q3108347 BLAST score 413



2.0e-40 E value Match length 83 100 % identity (AF061517) putative copper/zinc superoxide dismutase copper NCBI Description chaperone [Arabidopsis thaliana] Seq. No. 142444 LIB3168-014-P1-K1-E12 Seq. ID Method BLASTX NCBI GI q4006897

NCBI GI g400689°
BLAST score 462
E value 3.0e-46
Match length 142
% identity 69

NCBI Description (Z99708) globulin-like protein [Arabidopsis thaliana]

Seq. No. 142445

Seq. ID LIB3168-014-P1-K1-E4

Method BLASTX
NCBI GI g112682
BLAST score 595
E value 7.0e-62
Match length 138
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142446

Seq. ID LIB3168-014-P1-K1-E5

Method BLASTX
NCBI GI g112682
BLAST score 609
E value 2.0e-63
Match length 140
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142447

Seq. ID LIB3168-014-P1-K1-E8

Method BLASTX
NCBI GI g2149640
BLAST score 184
E value 5.0e-14
Match length 76
% identity 59

NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No. 142448

Seq. ID LIB3168-014-P1-K1-F10

Method BLASTX



```
NCBI GI
                     q112682
BLAST score
                     562
                     6.0e-58
E value
                     131
Match length
% identity
                     12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir_ S08510
NCBI Description
                     cruciferin precursor (CRB) - Arabidopsis thaliana
                     >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed
                     storage protein [Arabidopsis thaliana]
Seq. No.
                     142449
                     LIB3168-014-P1-K1-F11
```

Seq. ID LIB3168-014-P1-K1-F11
Method BLASTN
NCBI GI g3449331
BLAST score 433
E value 0.0e+00
Match length 433
% identity 26

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNC17, complete sequence [Arabidopsis thaliana]

 Seq. No.
 142450

 Seq. ID
 LIB3168-014-P1-K1-F12

 Method
 BLASTN

NCBI GI g2828185
BLAST score 401
E value 0.0e+00
Match length 405
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUD21, complete sequence [Arabidopsis thaliana]

Seq. No. 142451

Seq. ID LIB3168-014-P1-K1-F2

Method BLASTX
NCBI GI g112681
BLAST score 353
E value 1.0e-33
Match length 91
% identity 76

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142452

Seq. ID LIB3168-014-P1-K1-F4

Method BLASTX
NCBI GI g112682
BLAST score 769
E value 3.0e-82
Match length 146
% identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana



>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
storage protein [Arabidopsis thaliana]

Seq. No. 142453

Seq. ID LIB3168-014-P1-K1-F5

Method BLASTX
NCBI GI g112681
BLAST score 541
E value 2.0e-55
Match length 145
% identity 79

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142454

Seq. ID LIB3168-014-P1-K1-F6

Method BLASTX
NCBI GI g4567265
BLAST score 177
E value 8.0e-13
Match length 57
% identity 58

NCBI Description (AC006841) putative kinesin protein [Arabidopsis thaliana]

Seq. No. 142455

Seq. ID LIB3168-014-P1-K1-F7

Method BLASTN
NCBI GI 94589436
BLAST score 391
E value 0.0e+00
Match length 399
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MPA22, complete sequence

Seq. No. 142456

Seq. ID LIB3168-014-P1-K1-F8

Method BLASTX
NCBI GI g2738248
BLAST score 595
E value 7.0e-62
Match length 128
% identity 91

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No. 142457

Seq. ID LIB3168-014-P1-K1-F9

Method BLASTN
NCBI GI g4206762
BLAST score 251
E value 1.0e-139
Match length 334

17474

E value

Match length

1.0e-21 78



```
% identity
                  Arabidopsis thaliana cell wall-plasma membrane linker
NCBI Description
                  protein homolog (CWLP) mRNA, complete cds
                  142458
Seq. No.
                  LIB3168-014-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1709006
BLAST score
                  318
E value
                  2.0e-29
Match length
                  69
% identity
                  87
                  S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi 726032
                   (U17241) S-adenosylmethionine synthetase [Actinidia
                  chinensis]
                  142459
Seq. No.
                  LIB3168-014-P1-K1-G10
Seq. ID
Method
                  BLASTN
                  q2924257
NCBI GI
                  43
BLAST score
E value
                  7.0e-15
Match length
                  167
% identity
                  Tobacco chloroplast genome DNA
NCBI Description
                  142460
Seq. No.
                  LIB3168-014-P1-K1-G11
Seq. ID
Method
                  BLASTX
                   g2129579
NCBI GI
BLAST score
                   671
E value
                   9.0e-71
                   129
Match length
% identity
                   98
                  Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400)
NCBI Description
                  Dwarf1 [Arabidopsis thaliana]
Seq. No.
                   142461
Seq. ID
                  LIB3168-014-P1-K1-G2
                  BLASTX
Method
NCBI GI
                   g1628583
BLAST score
                   625
                   2.0e-65
E value
Match length
                   120
                   100
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   142462
Seq. ID
                   LIB3168-014-P1-K1-G3
                   BLASTX
Method
                   g1628583
NCBI GI
BLAST score
                   44
```

17475



% identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

142463 Seq. No.

Seq. ID LIB3168-014-P1-K1-G4

Method BLASTX g1628583 NCBI GI BLAST score 606 E value 4.0e-63 Match length 147 % identity 80

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

142464 Seq. No.

LIB3168-014-P1-K1-G5 Seq. ID

Method BLASTN g2842474 NCBI GI 51 BLAST score E value 1.0e-19 Match length 87

% identity

Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 NCBI Description

(ESSAII project)

Seq. No. 142465

Seq. ID LIB3168-014-P1-K1-G7

Method BLASTX NCBI GI g112681 BLAST score 552 E value 7.0e-57 Match length 118 % identity 92

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

tha $\overline{1}$ iana] >gi_808936 emb_CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

142466 Seq. No.

Seq. ID LIB3168-014-P1-K1-G8

BLASTX Method NCBI GI g1628583 BLAST score 747 1.0e-79 E value Match length 142 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

> thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

142467 Seq. No.

Seq. ID LIB3168-014-P1-K1-G9

Method BLASTX



a1628583 NCBI GI BLAST score 625 2.0e 5 E value Match length 120 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

142468 Seq. No.

LIB3168-014-P1-K1-H1 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 625 2.0e-65 E value 120 Match length 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

142469 Seq. No.

LIB3168-014-P1-K1-H10 Seq. ID

Method BLASTX NCBI GI q112741 BLAST score 741 6.0e-79 E value Match length 138 100 % identity

2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 142470

Seq. ID LIB3168-014-P1-K1-H11

Method BLASTX NCBI GI g1628583 BLAST score 618 1.0e-64 E value Match length 120 % identity 99

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142471

Seq. ID LIB3168-014-P1-K1-H12

BLASTX Method g2494896 NCBI GI 342 BLAST score 2.0e-32 E value 62 Match length 97 % identity



NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 3 DELTA SUBUNIT (EIF-3 DELTA) (EIF3 P36) (TGF-BETA RECEPTOR INTERACTING PROTEIN 1) (TRIP-1) >gi 2129749 pir S60256 TGF-beta receptor interacting protein 1 homolog - Arabidopsis thaliana >gi_1036803 (U36765) TGF-beta receptor interacting protein 1 homolog [Arabidopsis thaliana] 142472 Seq. No. LIB3168-014-P1-K1-H2 Seq. ID Method BLASTX g1628583 NCBI GI 123 BLAST score 2.0e-06 E value Match length 78 100 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 142473 LIB3168-014-P1-K1-H3 Seq. ID BLASTX Method g2129767 NCBI GI 720 BLAST score E value 2.0e-76 Match length 138 99 % identity NCBI Description vacuolar processing enzyme (EC 3.4.22.-) isozyme beta precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_ (D61394) beta-VPE [Arabidopsis thaliana] 142474 Seq. No. LIB3168-014-P1-K1-H4 Seq. ID Method BLASTN NCBI GI g4582411 BLAST score 344 E value 0.0e + 00440 Match length % identity Arabidopsis thaliana chromosome 1 BAC T23K8 sequence, NCBI Description complete sequence 142475 Seq. No. LIB3168-014-P1-K1-H5 Seq. ID Method BLASTN NCBI GI q3269280 BLAST score 418 0.0e + 00E value Match length 429 99 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22 (ESSAII project)

142476 Seq. No.

LIB3168-014-P1-K1-H7 Seq. ID

BLASTX Method g1903034 NCBI GI

17478



```
BLAST score
                  9.0e-17
E value
                  87
Match length
% identity
                  48
                  (X94625) amp-binding protein [Brassica napus]
NCBI Description
                  142477
Seq. No.
                  LIB3168-014-P1-K1-H8
Seq. ID
                  BLASTX
Method
                  g1628583
NCBI GI
BLAST score
                  613
                  6.0e-64
E value
                  123
Match length
                  96
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142478
Seq. No.
                  LIB3168-014-P1-K1-H9
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  625
                  2.0e-65
E value
                  120
Match length
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142479
Seq. No.
                  LIB3168-015-P1-K1-A1
Seq. ID
                  BLASTX
Method
                  g112741
NCBI GI
BLAST score
                  248
                  9.0e-22
E value
                  50
Match length
                   94
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                   3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >gi 4490712_emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                   142480
Seq. No.
                  LIB3168-015-P1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q21112
```

Method BLASTX
NCBI GI g21112
BLAST score 52
E value 5.0e-31
Match length 126
% identity 60

NCBI Description (X59805) cruciferin [Raphanus sativus]

Seq. No. 142481

17479



```
LIB3168-015-P1-K1-A11
Seq. ID
                  BLASTX
Method
                  g2832644
NCBI GI
                  375
BLAST score
                  5.0e-36
E value
                  73
Match length
                  100
% identity
                  (AL021710) teosinte branched1 - like protein [Arabidopsis
NCBI Description
                  thaliana]
                  142482
Seq. No.
                  LIB3168-015-P1-K1-A12
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3063690
                  231
BLAST score
                  1.0e-127
E value
                  365
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11
                   (ESSAII project)
                  142483
Seq. No.
                  LIB3168-015-P1-K1-A3
Seq. ID
                  BLASTN
Method
NCBI GI
                   g2947056
                   90
BLAST score
                   5.0e-43
E value
                   98
Match length
                   98
% identity
                  Arabidopsis thaliana chromosome II BAC T20F6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   142484
Seq. No.
                   LIB3168-015-P1-K1-A4
Seq. ID
Method
                   BLASTN
                   g2281648
NCBI GI
BLAST score
                   174
                   4.0e-93
E value
                   178
Match length
% identity
                   99
                  Arabidopsis thaliana AP2 domain containing protein RAP2.12
NCBI Description
                   mRNA, partial cds
                   142485
Seq. No.
Seq. ID
                   LIB3168-015-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   167
E value
                   1.0e-57
Match length
                   126
% identity
                   93
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
```

Seq. No. 142486

Seq. ID LIB3168-015-P1-K1-A6



```
BLASTX
Method
                  g1628583
NCBI GI
BLAST score
                  512
                  3.0e-52
E value
                  107
Match length
                  93
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142487
Seq. No.
                  LIB3168-015-P1-K1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1628583
BLAST score
                  550
                  1.0e-56
E value
Match length
                  115
                  93
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142488
Seq. No.
                  LIB3168-015-P1-K1-A8
Seq. ID
                  BLASTX
Method
                   g1628583
NCBI GI
                   407
BLAST score
                   8.0e-40
E value
                   109
Match length
                   74
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   142489
                   LIB3168-015-P1-K1-A9
Seq. ID
Method
                   BLASTN
                   q1628582
NCBI GI
                   76
BLAST score
E value
                   9.0e-35
                   187
Match length
                   43
% identity
                   Arabidopsis thaliana 12S cruciferin seed storage protein
NCBI Description
                   (ATCRU3) gene, complete cds
                   142490
Seq. No.
                   LIB3168-015-P1-K1-B10
Seq. ID
Method
                   BLASTX
```

q1628583 NCBI GI BLAST score 605 5.0e-63 E value 128 Match length % identity 91

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]



```
Seq. No.
                  142491
Seq. ID
                  LIB3168-015-P1-K1-B11
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  55
E value
                  1.0e-57
                  115
Match length
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142492
Seq. No.
                  LIB3168-015-P1-K1-B12
Seq. ID
Method
                  BLASTX
                  g112682
NCBI GI
BLAST score
                  355
E value
                  6.0e-34
Match length
                  83
                  86
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  142493
Seq. No.
                  LIB3168-015-P1-K1-B4
Seq. ID
Method
                  BLASTX
                  g112681
NCBI GI
                  565
BLAST score
                  2.0e-58
E value
                  114
Match length
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
                  142494
Seq. No.
                  LIB3168-015-P1-K1-B5
Seq. ID
                  BLASTX
Method
                  g112681
NCBI GI
                   519
BLAST score
                   4.0e-53
E value
                   108
Match length
                   92
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
```

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936 emb_CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142495

Seq. ID LIB3168-015-P1-K1-B6

Method BLASTX



```
g2623962
NCBI GI
BLAST score
                  426
                  5.0e-42
E value
                  89
Match length
                  92
% identity
                  (Y12540) isocitrate dehydrogenase (NADP+) [Apium
NCBI Description
                  graveolens]
                  142496
Seq. No.
                  LIB3168-015-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  257
                  8.0e-23
E value
                  47
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142497
                  LIB3168-015-P1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  8.0e-11
                  36
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   142498
Seq. No.
Seq. ID
                   LIB3168-015-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g112739
BLAST score
                   224
                   7.0e-19
E value
Match length
                   42
                   100
% identity
                   2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                   Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                   2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                   (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                   >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                   precursor [Arabidopsis thaliana]
Seq. No.
                   142499
Seq. ID
                   LIB3168-015-P1-K1-C1
                   BLASTX
Method
                   g1628583
NCBI GI
                   496
BLAST score
                   2.0e-50
E value
```

108 Match length 94 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

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142500
Seq. No.
                  LIB3168-015-P1-K1-C10
Seq. ID
                  BLASTX
Method
                  g2443876
NCBI GI
                  216
BLAST score
                  2.0e-17
E value
                  132
Match length
% identity
                   (AC002294) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  142501
Seq. No.
                  LIB3168-015-P1-K1-C11
Seq. ID
                  BLASTN
Method
NCBI GI
                   q4006885
                   149
BLAST score
E value
                   4.0e-78
                   378
Match length
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                   fragment No
                   142502
Seq. No.
                   LIB3168-015-P1-K1-C2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g16231
BLAST score
                   38
                   3.0e-12
E value
Match length
                   154
                   84
% identity
                   Arabidopsis CRA1 gene for 12S seed storage protein
NCBI Description
                   >qi 166675 gb M37247 ATHCRA1AA A.thaliana 12S storage
                   protein CRA1 gene, exons 1-4
                   142503
Seq. No.
                   LIB3168-015-P1-K1-C3
Seq. ID
                   BLASTX
Method
                   g1628583
NCBI GI
                   185
BLAST score
                   5.0e-29
E value
                   84
Match length
                   85
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749)_ 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   142504
Seq. No.
                   LIB3168-015-P1-K1-C5
Seq. ID
                   BLASTX
Method
                   g1628583
NCBI GI
BLAST score
                   135
                   5.0e-26
E value
                   108
Match length
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
```

17484

cruciferin seed storage protein [Arabidopsis thaliana]



```
142505
Seq. No.
                  LIB3168-015-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
                  518
BLAST score
                  8.0e-54
E value
Match length
                  112
% identity
                  95
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495_emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142506
Seq. No.
Seq. ID
                  LIB3168-015-P1-K1-C7
Method
                  BLASTX
                  q1628583
NCBI GI
BLAST score
                  170
                  1.0e-12
E value
Match length
                  60
                  57
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142507
                  LIB3168-015-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112682
                   464
BLAST score
                   1.0e-46
E value
                   100
Match length
                   87
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
                   142508
Seq. No.
                   LIB3168-015-P1-K1-C9
Seq. ID
                   BLASTN
Method
                   q3548797
NCBI GI
BLAST score
                   204
                   1.0e-111
E value
Match length
                   359
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC T18E12 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   142509
                   LIB3168-015-P1-K1-D1
Seq. ID
```

Method BLASTX NCBI GI g1628583 BLAST score 297 2.0e-27 E value Match length 65



```
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142510
Seq. No.
                  LIB3168-015-P1-K1-D10
Seq. ID
Method
                  BLASTN
                  g4159701
NCBI GI
                  325
BLAST score
                  0.0e + 00
E value
                  366
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K22G18, complete sequence
                  142511
Seq. No.
                  LIB3168-015-P1-K1-D11
Seq. ID
                  BLASTX
Method
                  g1169476
NCBI GI
                   611
BLAST score
                   1.0e-63
E value
                   117
Match length
                   100
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
NCBI Description
                   ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)
                   vitronectin-like adhesion protein [Nicotiana tabacum]
                   142512
Seq. No.
                   LIB3168-015-P1-K1-D3
Seq. ID
                   BLASTX
Method
                   g1628583
NCBI GI
                   309
BLAST score
                   2.0e-28
E value
Match length
                   70
                   86
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   142513
                   LIB3168-015-P1-K1-D4
Seq. ID
                   BLASTX
Method
                   q1628583
NCBI GI
BLAST score
                   77
E value
                   3.0e-42
                   125
Match length
                   74
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
```

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142514

LIB3168-015-P1-K1-D5 Seq. ID

Method BLASTX q1061040 NCBI GI 544 BLAST score

Seq. ID

Method



```
7.0e-56
E value
                  113
Match length
% identity
                  (X89867) sterol-C-methyltransferase [Arabidopsis thaliana]
NCBI Description
                  >qi 1587694 prf 2207220A sterol C-methyltransferase
                  [Arabidopsis thaliana]
                  142515
Seq. No.
                  LIB3168-015-P1-K1-D6
Seq. ID
Method
                  BLASTX
                  g2129659
NCBI GI
                  223
BLAST score
                  2.0e-18
E value
Match length
                  99
% identity
                  54
                  oleosin, isoform 21K - Arabidopsis thaliana >gi 725260
NCBI Description
                  (L40954) oleosin [Arabidopsis thaliana]
                  142516
Seq. No.
                  LIB3168-015-P1-K1-D7
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  234
                  7.0e-20
E value
Match length
                  70
                  66
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142517
                  LIB3168-015-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2961390
BLAST score
                   413
E value
                   9.0e-41
Match length
                   79
                   99
% identity
                  (AL022141) beta-galactosidase like protein [Arabidopsis
NCBI Description
                   thalianal
                   142518
Seq. No.
                   LIB3168-015-P1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129657
BLAST score
                   216
E value
                   1.0e-17
Match length
                   61
% identity
                   75
                   oleosin isoform - Arabidopsis thaliana
NCBI Description
                   >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
                   thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin
                   [Arabidopsis thaliana]
                   142519
Seq. No.
```

17487

LIB3168-015-P1-K1-E1

BLASTX



NCBI GI q3335169 BLAST score 502 E value 6.0e-51 Match length 111 % identity 79

NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No. 142520

Seq. ID LIB3168-015-P1-K1-E10

Method BLASTX NCBI GI q112741 BLAST score 637 E value 9.0e-67 Match length 118 % identity 99

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 142521

Seq. ID LIB3168-015-P1-K1-E11

Method BLASTX NCBI GI g112682 BLAST score 665 E value 4.0e-70 Match length 137 % identity 92

12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142522

Seq. ID LIB3168-015-P1-K1-E12

Method BLASTX NCBI GI g135858 BLAST score 349 E value 5.0e-33 Match length 68 % identity 100

NCBI Description TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)

>gi_99760_pir__S22201 tonoplast intrinsic protein alpha -Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi 445128 prf 1908432A tonoplast

intrinsic protein alpha [Arabidopsis thaliana]

Seq. No. 142523

Seq. ID LIB3168-015-P1-K1-E2



```
Method BLASTX
NCBI GI g1628583
BLAST score 283
E value 2.0e-36
Match length 101
% identity 84
```

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142524

Seq. ID LIB3168-015-P1-K1-E3

Method BLASTX
NCBI GI g1628583
BLAST score 566
E value 2.0e-58
Match length 119
% identity 92

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142525

Seq. ID LIB3168-015-P1-K1-E4

Method BLASTX
NCBI GI g1628583
BLAST score 76
E value 3.0e-38
Match length 98
% identity 86

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142526

Seq. ID LIB3168-015-P1-K1-E7

Method BLASTX
NCBI GI g1628583
BLAST score 444
E value 2.0e-44
Match length 100
% identity 87

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142527

Seq. ID LIB3168-015-P1-K1-E8

Method BLASTX
NCBI GI g1628583
BLAST score 49
E value 7.0e-58
Match length 128
% identity 91

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]



```
Seq. No.
                  142528
                  LIB3168-015-P1-K1-E9
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  44
E value
                  2.0e-54
Match length
                  112
                  98
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142529
                  LIB3168-015-P1-K1-F1
Seq. ID
Method
                  BLASTX
                  g21112
NCBI GI
BLAST score
                  225
E value
                  2.0e-18
Match length
                  48
                  85
% identity
NCBI Description
                  (X59805) cruciferin [Raphanus sativus]
Seq. No.
                  142530
                  LIB3168-015-P1-K1-F11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q166909
BLAST score
                  244
E value
                  1.0e-135
                  286
Match length
% identity
                  100
                  Arabidopsis thaliana beta-9 tubulin (TUB9) gene, complete
NCBI Description
                  cds
Seq. No.
                  142531
Seq. ID
                  LIB3168-015-P1-K1-F12
Method
                  BLASTN
NCBI GI
                  g2262155
BLAST score
                  331
E value
                  0.0e + 00
Match length
                  402
                  98
% identity
NCBI Description
                  DNA sequence of Arabidopsis thaliana BAC F5J6 from
                  chromosome IV, complete sequence [Arabidopsis thaliana]
Seq. No.
                  142532
Seq. ID
                  LIB3168-015-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g118926
BLAST score
                  283
E value
                  3.0e-25
Match length
                  111
% identity
                  52
                  DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
NCBI Description
                  >gi_320600_pir__E45509 desiccation-related protein (clone
```

PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991) dessication-related protein [Craterostigma plantagineum]



>gi_227781_prf__1710351E abscisic acid responsive protein E
[Craterostigma plantagineum]

 Seq. No.
 142533

 Seq. ID
 LIB3168-015-P1-K1-F3

 Method
 BLASTX

 NCBI GI
 g112741

 BLAST score
 414

 E value
 7.0e-41

E value 7.0 Match length 94 % identity 84

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 142534

Seq. ID LIB3168-015-P1-K1-F4

Method BLASTN
NCBI GI g16472
BLAST score 317
E value 1.0e-178
Match length 379
% identity 98

NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No. 142535

Seq. ID LIB3168-015-P1-K1-F5

Method BLASTN
NCBI GI g4220640
BLAST score 286
E value 1.0e-160
Match length 384
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MPE11, complete sequence [Arabidopsis thaliana]

Seq. No. 142536

Seq. ID LIB3168-015-P1-K1-F6

Method BLASTX
NCBI GI g112682
BLAST score 638
E value 7.0e-67
Match length 140
% identity 87

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142537

Seq. ID LIB3168-015-P1-K1-F8

Method BLASTX



```
g112681
NCBI GI
BLAST score
                  55
                  5.0e-46
E value
Match length
                  99
% identity
                  98
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  142538
Seq. No.
                  LIB3168-015-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
                  555
BLAST score
                  3.0e-57
E value
                  131
Match length
% identity
                  82
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  142539
Seq. No.
                  LIB3168-015-P1-K1-G10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3869069
BLAST score
                  181
                  3.0e-97
E value
Match length
                  397
                  100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  142540
                  LIB3168-015-P1-K1-G11
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  586
                  8.0e-61
E value
                  120
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142541
Seq. ID
                  LIB3168-015-P1-K1-G12
```

Method BLASTX
NCBI GI g1531762
BLAST score 195
E value 6.0e-15
Match length 51
% identity 75

NCBI Description (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis



thaliana]

142542 Seq. No. LIB3168-015-P1-K1-G3 Seq. ID Method BLASTX NCBI GI g1628583 BLAST score 671 9.0e-71 E value Match length 138 % identity 94 (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 142543 LIB3168-015-P1-K1-G4 Seq. ID BLASTX Method q112682 NCBI GI BLAST score 631 5.0e-66 E value Match length 141 % identity 86 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 NCBI Description cruciferin precursor (CRB) - Arabidopsis thaliana >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana] 142544 Seq. No. LIB3168-015-P1-K1-G5 Seq. ID BLASTX Method g1628583 NCBI GI BLAST score 548 E value 2.0e-56 Match length 103 100 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 142545 LIB3168-015-P1-K1-G6 Seq. ID Method BLASTX NCBI GI q464775 BLAST score 429 2.0e-42E value Match length 112 72 % identity SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi 542013 pir S39492 NCBI Description superoxide dismutase - Para rubber tree >gi_348137 (L11707) superoxide dismutase (manganese) [Hevea brasiliensis]

Seq. No. 142546

Seq. ID LIB3168-015-P1-K1-G7

Method BLASTX NCBI GI g112681 BLAST score 59



```
E value
                  5.0e-54
Match length
                  114
% identity
                  99
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  142547
Seq. No.
                  LIB3168-015-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112739
BLAST score
                  386
                  2.0e-37
E value
Match length
                  114
                  68
% identity
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  142548
                  LIB3168-015-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  371
                  1.0e-35
E value
Match length
                  92
% identity
                  79
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142549
Seq. ID
                  LIB3168-015-P1-K1-H10
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1628583
BLAST score 584
E value 1.0e-60
Match length 120
% identity 94

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142550

Seq. ID LIB3168-015-P1-K1-H12

Method BLASTX
NCBI GI g112681
BLAST score 618
E value 2.0e-64
Match length 131
% identity 94



NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142551

Seq. ID LIB3168-015-P1-K1-H4

Method BLASTX
NCBI GI g112682
BLAST score 615
E value 3.0e-64
Match length 143
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142552

Seq. ID LIB3168-015-P1-K1-H5

Method BLASTX
NCBI GI g1628583
BLAST score 593
E value 1.0e-61
Match length 141
% identity 82

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142553

Seq. ID LIB3168-015-P1-K1-H6

Method BLASTX
NCBI GI g418908
BLAST score 182
E value 2.0e-13
Match length 75
% identity 44

NCBI Description vicilin precursor - cacao

Seq. No. 142554

Seq. ID LIB3168-015-P1-K1-H7

Method BLASTX
NCBI GI g112682
BLAST score 690
E value 5.0e-73
Match length 138
% identity 95

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142555

NCBI Description



```
LIB3168-015-P1-K1-H8
Seq. ID
Method
                  BLASTN
NCBI GI
                  a3046849
                  148
BLAST score
                  1.0e-77
E value
                  381
Match length
                  50
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K18L3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  142556
Seq. ID
                  LIB3168-015-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g2347192
BLAST score
                  534
E value
                  1.0e-54
Match length
                  103
% identity
                  55
NCBI Description
                  (AC002338) spliceosomal protein U2B isolog [Arabidopsis
                  thaliana]
                  142557
Seq. No.
                  LIB3168-016-P1-K1-A1
Seq. ID
Method
                  BLASTX
                  g112681
NCBI GI
BLAST score
                  256
E value
                  1.0e-22
Match length
                  55
% identity
                  91
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  142558
                  LIB3168-016-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2160142
BLAST score
                  360
E value
                  3.0e - 34
Match length
                  112
% identity
                  68
NCBI Description
                  (AC000375) Strong similarity to Arabidopsis APR2
                   (gb_U56921). [Arabidopsis thaliana] >gi_2738758 (AF016283)
                  5'-adenylylsulfate reductase [Arabidopsis thaliana]
Seq. No.
                  142559
Seq. ID
                  LIB3168-016-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  585
E value
                  1.0e-60
Match length
                  145
% identity
                  80
```

17496

(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S



cruciferin seed storage protein [Arabidopsis thaliana]

```
Seq. No.
                  142560
                  LIB3168-016-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129657
BLAST score
                  238
E value
                  5.0e-20
Match length
                  120
                  49
% identity
                  oleosin isoform - Arabidopsis thaliana
NCBI Description
                  >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
                  thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin
                  [Arabidopsis thaliana]
Seq. No.
                  142561
                  LIB3168-016-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131289
BLAST score
                  716
                  5.0e-76
E value
Match length
                  141
                  97
% identity
NCBI Description
                  PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN)
                  (CP43) >gi_72709_pir__F2NT44 photosystem II chlorophyll
                  a-binding protein psbC - common tobacco chloroplast
                  >gi_225285_prf__1211235W photosystem II 44kD protein
                  [Nicotiana tabacum]
Seq. No.
                  142562
Seq. ID
                  LIB3168-016-P1-K1-A6
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  203
                  1.0e-55
E value
Match length
                  140
% identity
                  79
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142563
                  LIB3168-016-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  637
E value
                  9.0e-67
Match length
                  126
% identity
                  98
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
```

Seq. No. 142564

Seq. ID LIB3168-016-P1-K1-A8



```
BLASTN
Method
NCBI GI
                  q3241917
BLAST score
                  339
                  0.0e + 00
E value
Match length
                  382
% identity
                  97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19B1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  142565
Seq. ID
                  LIB3168-016-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  q4468103
                  197
BLAST score
                  1.0e-107
E value
Match length
                  382
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9
                  (ESSA project)
Seq. No.
                  142566
Seq. ID
                  LIB3168-016-P1-K1-B12
Method
                  BLASTX
                  g4753882
NCBI GI
                  350
BLAST score
                  4.0e-33
E value
Match length
                  130
% identity
                  54
NCBI Description
                  (AL049754) putative aspartate aminotransferase
                   [Streptomyces coelicolor]
Seq. No.
                  142567
Seq. ID
                  LIB3168-016-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  g4581043
BLAST score
                  53
                  7.0e-21
E value
Match length
                  69
% identity
                  94
                  Populus deltoides Qa-binding protein PsbD (psbD) and
NCBI Description
                  chlorophyll a-binding protein PsbC (psbC) genes,
                  chloroplast genes encoding chloroplast proteins, complete
                  cds
                  142568
Seq. No.
                  LIB3168-016-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  695
```

E value 1.0e-73 Match length 131 100 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir__S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]





```
142569
Seq. No.
Seq. ID
                  LIB3168-016-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  g4519193
BLAST score
                  133
E value
                  1.0e-68
Match length
                  426
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDC11, complete sequence
Seq. No.
                  142570
                  LIB3168-016-P1-K1-B8
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  625
                  2.0e-65
E value
Match length
                  120
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142571
                  LIB3168-016-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  578
E value
                  8.0e-60
Match length
                  143
                  80
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142572
                  LIB3168-016-P1-K1-C10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q112682
BLAST score
                  578
                  7.0e-60
E value
                  135
Match length
% identity
                  81
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  142573
                  LIB3168-016-P1-K1-C11
Seq. ID
```

Seq. ID LIB3168-016-P1-K1-Method BLASTN
NCBI GI g3298532
BLAST score 391
E value 0.0e+00
Match length 415





```
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T26B15 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  142574
Seq. No.
                  LIB3168-016-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2916772
BLAST score
                  656
                  5.0e-69
E value
Match length
                  132
                  99
% identity
NCBI Description (AJ224119) AT-hook protein 2 [Arabidopsis thaliana]
Seq. No.
                  142575
                  LIB3168-016-P1-K1-C5
Seq. ID
                  BLASTX
Method
```

NCBI GI g112682 BLAST score 564 3.0e-58 E value

Match length 132 81 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

142576 Seq. No.

Seq. ID LIB3168-016-P1-K1-C7

Method BLASTX NCBI GI g112682 BLAST score 647 6.0e-68 E value Match length 142 88 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142577

LIB3168-016-P1-K1-C8 Seq. ID

Method BLASTX q1628583 NCBI GI BLAST score 462 3.0e-46 E value Match length 122 76 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142578

LIB3168-016-P1-K1-D10 Seq. ID

Method BLASTX



```
NCBI GI
                  q1628583
BLAST score
                  656
E value
                  5.0e-69
Match length
                  128
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142579
                  LIB3168-016-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q103313
                  470
BLAST score
                  3.0e-47
E value
Match length
                  131
                  12
% identity
NCBI Description
                  probable cell cycle control protein crn - fruit fly
                  (Drosophila melanogaster) >gi 2827496 emb CAA15705.1
                  (AL009195) EG:30B8.1 [Drosophila melanogaster]
Seq. No.
                  142580
Seq. ID
                  LIB3168-016-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  260
                  7.0e-23
E value
Match length
                  86
% identity
                  67
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  142581
Seq. ID
                  LIB3168-016-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  q2114077
BLAST score
                  136
                  2.0e-70
E value
Match length
                  286
% identity
                  90
NCBI Description
                  Arabidopsis thaliana DNA for larger subunit of Rubisco,
                  beta subunit of coupling factor one, partial cds
Seq. No.
                  142582
Seq. ID
                  LIB3168-016-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q112739
BLAST score
                  446
```

2.0e-44 E value Match length 126 % identity 72

NCBI Description

2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir_NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit



2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
>gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2
precursor [Arabidopsis thaliana]

Seq. No. 142583

Seq. ID LIB3168-016-P1-K1-D5

Method BLASTX
NCBI GI g1628583
BLAST score 701
E value 3.0e-74
Match length 139
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142584

Seq. ID LIB3168-016-P1-K1-D6

Method BLASTX
NCBI GI g3152605
BLAST score 608
E value 2.0e-63
Match length 124
% identity 100

NCBI Description (AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 142585

Seq. ID LIB3168-016-P1-K1-D7

Method BLASTX
NCBI GI g112682
BLAST score 564
E value 3.0e-58
Match length 132
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142586

Seq. ID LIB3168-016-P1-K1-D8

Method BLASTX
NCBI GI g1628583
BLAST score 663
E value 7.0e-70
Match length 131
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142587

Seq. ID LIB3168-016-P1-K1-D9

Method BLASTX NCBI GI g112682

17502



BLAST score 564
E value 3.0e-58
Match length 132
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__\$08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142588

Seq. ID LIB3168-016-P1-K1-E1

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 126
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142589

Seq. ID LIB3168-016-P1-K1-E10

Method BLASTX
NCBI GI g1628583
BLAST score 200
E value 8.0e-16
Match length 75
% identity 57

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142590

Seq. ID LIB3168-016-P1-K1-E12

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142591

Seq. ID LIB3168-016-P1-K1-E3

Method BLASTN
NCBI GI g3510347
BLAST score 62
E value 6.0e-27
Match length 93
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MSJ11, complete sequence [Arabidopsis thaliana]



Seq. No. 142592

Seq. ID LIB3168-016-P1-K1-E4

Method BLASTX NCBI GI q112737 BLAST score 182 E value 1.0e-26 Match length 108 % identity 64

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142593

Seq. ID LIB3168-016-P1-K1-E7

Method BLASTX NCBI GI g1628583 BLAST score 625 E value 2.0e-65 Match length 120 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142594

Seq. ID LIB3168-016-P1-K1-E8

Method BLASTN NCBI GI q2828186 BLAST score 138 E value 1.0e-71 Match length 374 % identity 96

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K18I23, complete sequence [Arabidopsis thaliana]

Seq. No. 142595

Seq. ID LIB3168-016-P1-K1-E9

Method BLASTX NCBI GI g1628583 BLAST score 625 E value 2.0e-65 Match length 120 % identity 100

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142596

Seq. ID LIB3168-016-P1-K1-F1

Method BLASTX NCBI GI g461841 BLAST score 208 E value 5.0e-17



Match length 53 % identity 72

NCBI Description CRUCIFERIN CRU4 PRECURSOR (11S GLOBULIN) (12S STORAGE

PROTEIN)

Seq. No. 142597

Seq. ID LIB3168-016-P1-K1-F10

Method BLASTN
NCBI GI g3540210
BLAST score 381
E value 0.0e+00
Match length 413
% identity 98

NCBI Description Arabidopsis thaliana chromosome I BAC F5A8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 142598

Seq. ID LIB3168-016-P1-K1-F11

Method BLASTN
NCBI GI g4199934
BLAST score 277
E value 1.0e-154
Match length 371
% identity 93

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 142599

Seq. ID LIB3168-016-P1-K1-F12

Method BLASTX
NCBI GI g112682
BLAST score 583
E value 2.0e-60
Match length 136
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142600

Seq. ID LIB3168-016-P1-K1-F6

Method BLASTX
NCBI GI 94539293
BLAST score 560
E value 8.0e-58
Match length 115
% identity 100

NCBI Description (AL049480) putative membrane transporter [Arabidopsis

thaliana]

Seq. No. 142601

Seq. ID LIB3168-016-P1-K1-F7

Method BLASTX NCBI GI g112737 BLAST score 554

17505



E value 5.0e-57 Match length 134 % identity 81

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >qi 68853 pir NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204 emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142602

Seq. ID LIB3168-016-P1-K1-G1

Method BLASTX
NCBI GI g112681
BLAST score 265
E value 3.0e-23
Match length 118
% identity 52

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142603

Seq. ID LIB3168-016-P1-K1-G10

Method BLASTX
NCBI GI g1628583
BLAST score 658
E value 3.0e-69
Match length 138
% identity 93

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142604

Seq. ID LIB3168-016-P1-K1-G11

Method BLASTX
NCBI GI g1628583
BLAST score 620
E value 9.0e-65
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142605

Seq. ID LIB3168-016-P1-K1-G12

Method BLASTX
NCBI GI g1628583
BLAST score 573
E value 3.0e-59
Match length 121
% identity 92



NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142606

Seq. ID LIB3168-016-P1-K1-G2

Method BLASTX
NCBI GI g112737
BLAST score 208
E value 1.0e-17
Match length 75
% identity 69

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142607

Seq. ID LIB3168-016-P1-K1-G3

Method BLASTX
NCBI GI g1628583
BLAST score 562
E value 5.0e-58
Match length 140
% identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142608

Seq. ID LIB3168-016-P1-K1-G4

Method BLASTX
NCBI GI g4204299
BLAST score 688
E value 9.0e-73
Match length 134
% identity 100

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 142609

Seq. ID LIB3168-016-P1-K1-G5

Method BLASTX
NCBI GI g4586263
BLAST score 231
E value 9.0e-29
Match length 124
% identity 57

NCBI Description (AL049640) putative protein [Arabidopsis thaliana]

Seq. No. 142610

Seq. ID LIB3168-016-P1-K1-G6

Method BLASTN NCBI GI g3128139



BLAST score 181 E value 3.0e-97 Match length 411 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MIK19, complete sequence [Arabidopsis thaliana]

Seq. No. 142611

Seq. ID LIB3168-016-P1-K1-G7

Method BLASTN
NCBI GI g12307
BLAST score 37
E value 3.0e-11
Match length 94
% identity 97

NCBI Description Spinach plastid genes rps3, rps19, rpl14, rpl16 and rpl22

for ribosomal proteins S3, S19, L14, L16 and L22

Seq. No. 142612

Seq. ID LIB3168-016-P1-K1-G8

Method BLASTX
NCBI GI g1628583
BLAST score 243
E value 1.0e-20
Match length 74
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142613

Seq. ID LIB3168-016-P1-K1-G9

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142614

Seq. ID LIB3168-016-P1-K1-H1

Method BLASTX
NCBI GI g112682
BLAST score 644
E value 1.0e-67
Match length 141
% identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142615



Seq. ID LIB3168-016-P1-K1-H10

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142616

Seq. ID LIB3168-016-P1-K1-H11

Method BLASTX
NCBI GI g112741
BLAST score 725
E value 4.0e-77
Match length 135
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 142617

Seq. ID LIB3168-016-P1-K1-H3

Method BLASTX
NCBI GI g1628583
BLAST score 299
E value 1.0e-27
Match length 71
% identity 85

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142618

Seq. ID LIB3168-016-P1-K1-H4

Method BLASTX
NCBI GI g112682
BLAST score 568
E value 1.0e-58
Match length 118
% identity 90

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142619

Seq. ID LIB3168-016-P1-K1-H5

Method BLASTX NCBI GI g1628583



BLAST score 627 E value 1.0e-65 Match length 128 % identity 95

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142620

Seq. ID LIB3168-016-P1-K1-H6

Method BLASTN
NCBI GI g16236
BLAST score 110
E value 3.0e-55
Match length 154
% identity 95

NCBI Description Arabidopsis CRB gene for 12S seed storage protein

>qi 166677 qb M37248 ATHCRBAA A.thaliana 12S storage

protein CRA1 gene, exons 1-4

Seq. No. 142621

Seq. ID LIB3168-016-P1-K1-H7

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142622

Seq. ID LIB3168-016-P1-K1-H8

Method BLASTX
NCBI GI g112682
BLAST score 595
E value 7.0e-62
Match length 138
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142623

Seq. ID LIB3168-016-P1-K1-H9

Method BLASTX
NCBI GI g112681
BLAST score 590
E value 3.0e-61
Match length 138
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis





thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

 Seq. No.
 142624

 Seq. ID
 LIB3168-017-P1-K1-A1

 Method
 BLASTX

 NCBI GI
 g112741

 BLAST score
 209

E value 4.0e-17 Match length 69 % identity 62

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir_ NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 142625

Seq. ID LIB3168-017-P1-K1-A10

Method BLASTX
NCBI GI g112681
BLAST score 633
E value 2.0e-66
Match length 118
% identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142626

Seq. ID LIB3168-017-P1-K1-A11

Method BLASTX
NCBI GI g3335169
BLAST score 699
E value 5.0e-74
Match length 130
% identity 100

NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi_4455197 emb CAB36520.1 (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No. 142627

Seq. ID LIB3168-017-P1-K1-A12

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]



Seq. No. 142628

Seq. ID LIB3168-017-P1-K1-A2

Method BLASTX
NCBI GI g112681
BLAST score 416
E value 5.0e-41
Match length 103
% identity 79

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142629

Seq. ID LIB3168-017-P1-K1-A3

Method BLASTX
NCBI GI g112739
BLAST score 467
E value 8.0e-47
Match length 131
% identity 73

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 142630

Seq. ID LIB3168-017-P1-K1-A4

Method BLASTX
NCBI GI g1628583
BLAST score 478
E value 4.0e-48
Match length 119
% identity 81

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_(AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142631

Seq. ID LIB3168-017-P1-K1-A5

Method BLASTX
NCBI GI g112741
BLAST score 705
E value 9.0e-75
Match length 131
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868 (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]



Seq. No. 142632

Seq. ID LIB3168-017-P1-K1-A6

Method BLASTX
NCBI GI g1628583
BLAST score 424
E value 8.0e-42
Match length 80
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142633

Seq. ID LIB3168-017-P1-K1-A8

Method BLASTX
NCBI GI g112681
BLAST score 235
E value 7.0e-28
Match length 85
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142634

Seq. ID LIB3168-017-P1-K1-A9

Method BLASTX
NCBI GI g112741
BLAST score 536
E value 3.0e-55
Match length 100
% identity 97

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 142635

Seq. ID LIB3168-017-P1-K1-B1

Method BLASTX
NCBI GI g112741
BLAST score 253
E value 7.0e-22
Match length 104
% identity 36

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3



precursor [Arabidopsis thaliana]

Seq. No. 142636 Seq. ID LIB3168-017-P1-K1-B10 Method BLASTX NCBI GI q1628583 BLAST score 516 E value 1.0e-52 Match length 130 % identity 78

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142637

Seq. ID LIB3168-017-P1-K1-B11

Method BLASTX
NCBI GI g112739
BLAST score 487
E value 3.0e-49
Match length 133
% identity 74

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68854_pir__ NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 142638

Seq. ID LIB3168-017-P1-K1-B12

Method BLASTX
NCBI GI g1628583
BLAST score 432
E value 9.0e-43
Match length 105
% identity 82

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142639

Seq. ID LIB3168-017-P1-K1-B2

Method BLASTX
NCBI GI g132863
BLAST score 285
E value 3.0e-32
Match length 94
% identity 81

NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L2

>gi_12214_emb_CAA46568 (X65615) ribosomal protein L2

[Sinapis alba]

Seq. No. 142640

Seq. ID LIB3168-017-P1-K1-B3

Method BLASTX



NCBI GI g1628583 BLAST score 602 E value 1.0e-62 120 Match length 97 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142641

Seq. ID LIB3168-017-P1-K1-B4

Method BLASTX NCBI GI g2129659 BLAST score 579 E value 5.0e-60 Match length 132 % identity 87

NCBI Description oleosin, isoform 21K - Arabidopsis thaliana >gi 725260

(L40954) oleosin [Arabidopsis thaliana]

Seq. No. 142642

LIB3168-017-P1-K1-B5 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 609 E value 2.0e-63 Match length 120 % identity 98

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142643

Seq. ID LIB3168-017-P1-K1-B6

Method BLASTX NCBI GI q112681 BLAST score 335 3.0e-31 E value Match length 69 % identity 97

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142644

Seq. ID LIB3168-017-P1-K1-B7

Method BLASTX NCBI GI q1628583 BLAST score 522 E value 2.0e-53 Match length 102 % identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]



Seq. No. 142645

Seq. ID LIB3168-017-P1-K1-B8

Method BLASTX
NCBI GI g4678322
BLAST score 384
E value 2.0e-37
Match length 86
% identity 91

NCBI Description (AL049658) putative protein [Arabidopsis thaliana]

Seq. No. 142646

Seq. ID LIB3168-017-P1-K1-B9

Method BLASTX
NCBI GI g1628583
BLAST score 494
E value 3.0e-50
Match length 97
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142647

Seq. ID LIB3168-017-P1-K1-C1

Method BLASTX NCBI GI g112681 BLAST score 473 E value 1.0e-47 Match length 117 % identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142648

Seq. ID LIB3168-017-P1-K1-C10

Method BLASTX
NCBI GI g112741
BLAST score 686
E value 2.0e-72
Match length 127
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 142649

Seq. ID LIB3168-017-P1-K1-C11

Method BLASTX NCBI GI g112682



BLAST score 676 E value 2.0e-71 Match length 140 % identity 92

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142650

Seq. ID LIB3168-017-P1-K1-C12

Method BLASTX
NCBI GI g1628583
BLAST score 500
E value 1.0e-58
Match length 119
% identity 96

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142651

Seq. ID LIB3168-017-P1-K1-C3

Method BLASTX
NCBI GI g1628583
BLAST score 562
E value 5.0e-58
Match length 113
% identity 96

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142652

Seq. ID LIB3168-017-P1-K1-C5

Method BLASTX
NCBI GI g1628583
BLAST score 627
E value 1.0e-65
Match length 123
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142653

Seq. ID LIB3168-017-P1-K1-C6

Method BLASTX
NCBI GI g4585873
BLAST score 159
E value 1.0e-10
Match length 91
% identity 42

NCBI Description (AC005850) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 142654



Seq. ID LIB3168-017-P1-K1-C7

Method BLASTX
NCBI GI g1628583
BLAST score 661
E value 1.0e-69
Match length 138
% identity 93

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

142655

Seq. ID LIB3168-017-P1-K1-C8

Method BLASTX
NCBI GI g112739
BLAST score 450
E value 7.0e-45
Match length 127
% identity 72

Seq. No.

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 142656

Seq. ID LIB3168-017-P1-K1-C9

Method BLASTX
NCBI GI g1628583
BLAST score 612
E value 7.0e-64
Match length 120
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142657

Seq. ID LIB3168-017-P1-K1-D1

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142658

Seq. ID LIB3168-017-P1-K1-D11

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65



Match length % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142659

LIB3168-017-P1-K1-D12 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 131 E value 2.0e-07 Match length 71 % identity 100

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142660

LIB3168-017-P1-K1-D2 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 562 E value 4.0e-58 Match length 113 % identity 95

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142661

LIB3168-017-P1-K1-D3 Seq. ID

Method BLASTX NCBI GI g4204299 BLAST score 76 E value 5.3e-01Match length 136 % identity 26

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 142662

Seq. ID LIB3168-017-P1-K1-D4

Method BLASTX NCBI GI g1628583 BLAST score 642 E value 2.0e-67 Match length 127 % identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142663

Seq. ID LIB3168-017-P1-K1-D5

Method BLASTX NCBI GI g1628583



BLAST score 438 E value 9.0e-44 Match length 87 % identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142664

Seq. ID LIB3168-017-P1-K1-D6

Method BLASTN
NCBI GI g2244870
BLAST score 243
E value 1.0e-134
Match length 296
% identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 142665

Seq. ID LIB3168-017-P1-K1-D7

Method BLASTN
NCBI GI g1279569
BLAST score 86
E value 1.0e-40
Match length 234

% identity 89

NCBI Description Nicotiana acuminata chloroplast JLA region, 1-1028bp

Seq. No. 142666

Seq. ID LIB3168-017-P1-K1-D8

Method BLASTX
NCBI GI g112681
BLAST score 585
E value 1.0e-60
Match length 136
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142667

Seq. ID LIB3168-017-P1-K1-D9

Method BLASTX
NCBI GI g3080403
BLAST score 418
E value 4.0e-41
Match length 94
% identity 86

NCBI Description (AL022603) hypothetical protein [Arabidopsis thaliana]

>gi_4455267_emb_CAB36803.1_ (AL035527) putative bifunctional nuclease [Arabidopsis thaliana]

Seq. No. 142668

Seq. ID LIB3168-017-P1-K1-E1



Method BLASTX
NCBI GI g1628583
BLAST score 337
E value 1.0e-31
Match length 67
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142669

Seq. ID LIB3168-017-P1-K1-E10

Method BLASTX
NCBI GI g1628583
BLAST score 687
E value 1.0e-72
Match length 130
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142670

Seq. ID LIB3168-017-P1-K1-E11

Method BLASTX
NCBI GI g1628583
BLAST score 669
E value 2.0e-70
Match length 140
% identity 93

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142671

Seq. ID LIB3168-017-P1-K1-E12

Method BLASTN
NCBI GI g4199934
BLAST score 291
E value 1.0e-163
Match length 295
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 142672

Seq. ID LIB3168-017-P1-K1-E2

Method BLASTN
NCBI GI g2660661
BLAST score 280
E value 1.0e-156
Match length 352
% identity 94

NCBI Description Arabidopsis thaliana chromosome V BAC T19K24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 142673



LIB3168-017-P1-K1-E3 Seq. ID

Method BLASTX NCBI GI q112682 BLAST score 630 5.0e-66 E value 129 Match length % identity 91

12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142674

LIB3168-017-P1-K1-E6 Seq. ID

Method BLASTX NCBI GI q1628583 BLAST score 625 E value 2.0e-65 Match length 120 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142675

LIB3168-017-P1-K1-E7 Seq. ID

Method BLASTX NCBI GI q1628583 BLAST score 634 2.0e-66 E value 135 Match length 91 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142676

Seq. ID LIB3168-017-P1-K1-E8

Method BLASTX NCBI GI q1628583 BLAST score 547 3.0e-56 E value Match length 137 % identity 79

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142677

Seq. ID LIB3168-017-P1-K1-E9

99

BLASTN Method g4678266 NCBI GI 97 BLAST score 4.0e-47 E value Match length 281

% identity



NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8 (ESSA project)

Seq. No. 142678

Seq. ID LIB3168-017-P1-K1-F1

Method BLASTN
NCBI GI g3135250
BLAST score 54
E value 1.0e-21

Match length 58 % identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F27F23 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 142679

Seq. ID LIB3168-017-P1-K1-F10

Method BLASTX
NCBI GI g4510397
BLAST score 461
E value 3.0e-46
Match length 109
% identity 86

NCBI Description (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]

Seq. No. 142680

Seq. ID LIB3168-017-P1-K1-F11

Method BLASTX
NCBI GI g1628583
BLAST score 162
E value 4.0e-11
Match length 73
% identity 96

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142681

Seq. ID LIB3168-017-P1-K1-F12

Method BLASTX
NCBI GI 94510373
BLAST score 276
E value 2.0e-24
Match length 112
% identity 56

NCBI Description (AC007017) putative harpin-induced protein [Arabidopsis

thaliana]

Seq. No. 142682

Seq. ID LIB3168-017-P1-K1-F2

Method BLASTX
NCBI GI g1628583
BLAST score 336
E value 2.0e-31
Match length 134
% identity 54

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S



cruciferin seed storage protein [Arabidopsis thaliana]

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Seq. No.
                  142683
                  LIB3168-017-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g114654
BLAST score
                  289
                  5.0e-26
E value
Match length
                  81
                  79
% identity
NCBI Description
                  ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III)
                  >gi_67898_pir__LWNTA H+-transporting ATP synthase (EC
                  3.6.1.34) lipid-binding protein - common tobacco
                  chloroplast >gi 11812 emb CAA77343 (Z00044) ATPase III
                  subunit [Nicotiana tabacum] >gi_343484 (M10124) ATPase
                  subunit III [Nicotiana tabacum] >gi 224347 prf 1102209A
                  ATPase III, H translocating [Nicotiana sp.]
                  >gi 225272 prf 1211235G ATPase III [Nicotiana tabacum]
Seq. No.
                  142684
                  LIB3168-017-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  653
                  1.0e-68
E value
Match length
                  125
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142685
Seq. ID
                  LIB3168-017-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  g2842474
BLAST score
                  39
E value
                  3.0e-13
                  79
Match length
% identity
                  87
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
NCBI Description
                  (ESSAII project)
Seq. No.
                  142686
Seq. ID
                  LIB3168-017-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g3482918
BLAST score
                  213
                  3.0e-17
E value
Match length
                  58
% identity
                  69
                  (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  142687
Seq. ID
                  LIB3168-017-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g1628583
```

17524



BLAST score 468
E value 2.0e-48
Match length 103
% identity 87

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142688

Seq. ID LIB3168-017-P1-K1-G1

Method BLASTX
NCBI GI g112681
BLAST score 276
E value 1.0e-24
Match length 65
% identity 80

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142689

Seq. ID LIB3168-017-P1-K1-G11

Method BLASTX
NCBI GI 94204298
BLAST score 521
E value 3.0e-53
Match length 121
% identity 84

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 142690

Seq. ID LIB3168-017-P1-K1-G2

Method BLASTX
NCBI GI g1628583
BLAST score 620
E value 8.0e-65
Match length 119
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142691

Seq. ID LIB3168-017-P1-K1-G3

Method BLASTX
NCBI GI g112743
BLAST score 632
E value 3.0e-66
Match length 133
% identity 89

NCBI Description 2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit

4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_



(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

 Seq. No.
 142692

 Seq. ID
 LIB3168-017-P1-K1-G4

 Method
 BLASTX

 NCBI GI
 g112682

 BLAST score
 647 ***

E value 6.0e-68
Match length 134
% identity 92

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142693

Seq. ID LIB3168-017-P1-K1-G5

Method BLASTX
NCBI GI g1628583
BLAST score 363
E value 5.0e-35
Match length 76
% identity 93

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142694

Seq. ID LIB3168-017-P1-K1-G7

Method BLASTX
NCBI GI g728880
BLAST score 446
E value 2.0e-44
Match length 128
% identity 67

NCBI Description N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG

transferase related protein [Homo sapiens]

Seq. No. 142695

Seq. ID LIB3168-017-P1-K1-G8

Method BLASTX
NCBI GI g112681
BLAST score 570
E value 6.0e-59
Match length 133
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thalianal >gi_808936 cmb_CAN32493 (V14312) 13S good

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]



```
Seq. No.
                  142696
Seq. ID
                  LIB3168-017-P1-K1-G9
Method
                  BLASTN
NCBI GI
                  q4691223
BLAST score
                  315
E value
                  1.0e-177
Match length
                  335
% identity
                  99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
                  (ESSA project)
Seq. No.
                  142697
Seq. ID
                  LIB3168-017-P1-K1-H1
Method
                  BLASTN
NCBI GI
                  q4585890
BLAST score
                  401
E value
                  0.0e + 00
Match length
                  421
                  99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T3G21 genomic
                  sequence, complete sequence
Seq. No.
                  142698
Seq. ID
                  LIB3168-017-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  253
                  7.0e-22
E value
Match length
                  50
% identity
                  100
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  142699
Seq. ID
                  LIB3168-017-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  582
E value
                  2.0e-60
Match length
                  116
% identity
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
```

(U66916) 12S cruciferin seed storage protein [Arabidopsis

Seq. No. 142700

Seq. ID LIB3168-017-P1-K1-H12

Method BLASTX NCBI GI g4539316 BLAST score 559 E value 1.0e-57 Match length 115 % identity 100

(AL035679) putative fructose-bisphosphate aldolase NCBI Description



[Arabidopsis thaliana]

```
142701
Seq. No.
Seq. ID
                  LIB3168-017-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g1107501
BLAST score
                  397
                  1.0e-38
E value
                  99
Match length
% identity
NCBI Description
                  (X91954) orf [Arabidopsis thaliana] >gi 3367530 (AC004392)
                  Match to gb X91954 orf gene product from A. thaliana. ESTs
                  gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from
                  this gene. [Arabidopsis thaliana]
                  142702
Seq. No.
Seq. ID
                  LIB3168-017-P1-K1-H3
Method
                  BLASTN
NCBI GI
                  g511598
                  372
BLAST score
                  0.0e + 00
E value
Match length
                  380
% identity
                  30
                  Arabidopsis thaliana cell wall protein (APTR-1) gene,
NCBI Description
                  complete cds
Seq. No.
                  142703
Seq. ID
                  LIB3168-017-P1-K1-H4
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  625
                  2.0e-65
E value
Match length
                  120
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142704
                  LIB3168-017-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  648
                  5.0e-68
E value
                  142
Match length
                  88
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  142705
Seq. No.
```

Seq. ID LIB3168-017-P1-K1-H6

Method BLASTX NCBI GI g2842424 BLAST score 511



```
E value 5.0e-52
Match length 141
% identity 64
NCBI Description (AJ223948) RNA helicase [Homo sapiens]
```

Seq. No. 142706 Seg. ID LIB3168

Seq. ID LIB3168-017-P1-K1-H7 Method BLASTX

Method BLASTX
NCBI GI g1628583
BLAST score 621
E value 6.0e-65
Match length 126
% identity 95

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142707

Seq. ID LIB3168-017-P1-K1-H8

Method BLASTX
NCBI GI g1628583
BLAST score 345
E value 1.0e-32
Match length 86
% identity 78

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142708

Seq. ID LIB3168-017-P1-K1-H9

Method BLASTN
NCBI GI g3063690
BLAST score 287
E value 1.0e-160
Match length 412
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11

(ESSAII project)

Seq. No. 142709

Seq. ID LIB3168-018-P1-K1-A1

Method BLASTN
NCBI GI g1628582
BLAST score 50
E value 9.0e-20
Match length 74
% identity 92

NCBI Description Arabidopsis thaliana 12S cruciferin seed storage protein

(ATCRU3) gene, complete cds

Seq. No. 142710

Seq. ID LIB3168-018-P1-K1-A10

Method BLASTN
NCBI GI g4199934
BLAST score 216
E value 1.0e-118

17529



Match length 276 % identity 95

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 142711

Seq. ID LIB3168-018-P1-K1-A11

Method BLASTX
NCBI GI g2252472
BLAST score 449
E value 9.0e-45
Match length 115
% identity 77

NCBI Description (Z97558) argininosuccinate lyase [Arabidopsis thaliana]

Seq. No. 142712

Seq. ID LIB3168-018-P1-K1-A12

Method BLASTN
NCBI GI g2252471
BLAST score 164
E value 4.0e-87
Match length 216
% identity 94

NCBI Description Arabidopsis thaliana mRNA for argininosuccinate lyase

Seq. No. 142713

Seq. ID LIB3168-018-P1-K1-A2

Method BLASTX
NCBI GI g112681
BLAST score 444
E value 3.0e-44
Match length 112
% identity 78

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142714

Seq. ID LIB3168-018-P1-K1-A4

Method BLASTN
NCBI GI g2827513
BLAST score 223
E value 1.0e-122
Match length 402
% identity 94

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16

(ESSAII project)

Seq. No. 142715

Seq. ID LIB3168-018-P1-K1-A5

Method BLASTN
NCBI GI g4206762
BLAST score 212
E value 1.0e-115
Match length 322



% identity 94
NCBI Description Arabidopsis thaliana cell wall-plasma membrane linker protein homolog (CWLP) mRNA, complete cds

Seq. No. 142716

Seq. ID LIB3168-018-P1-K1-A6

Method BLASTX
NCBI GI g1628583
BLAST score 599
E value 2.0e-62
Match length 119
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142717

Seq. ID LIB3168-018-P1-K1-A7

Method BLASTX
NCBI GI g1628583
BLAST score 220
E value 2.0e-18
Match length 70
% identity 71

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142718

Seq. ID LIB3168-018-P1-K1-A8

Method BLASTX
NCBI GI g1628583
BLAST score 511
E value 3.0e-52
Match length 98
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142719

Seq. ID LIB3168-018-P1-K1-A9

Method BLASTX
NCBI GI g4204298
BLAST score 449
E value 7.0e-45
Match length 107
% identity 82

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 142720

Seq. ID LIB3168-018-P1-K1-B1

Method BLASTX
NCBI GI g1628583
BLAST score 458
E value 8.0e-46

17531



```
Match length 125 % identity 74
```

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142721

Seq. ID LIB3168-018-P1-K1-B10

Method BLASTX
NCBI GI g1628583
BLAST score 619
E value 1.0e-64
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142722

Seq. ID LIB3168-018-P1-K1-B11

Method BLASTX
NCBI GI g1402914
BLAST score 93
E value 5.0e-34
Match length 105
% identity 77

NCBI Description (X98318) peroxidase [Arabidopsis thaliana]

Seq. No. 142723

Seq. ID LIB3168-018-P1-K1-B12

Method BLASTX
NCBI GI g112743
BLAST score 610
E value 1.0e-63
Match length 137
% identity 84

NCBI Description 2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_

(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >qi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4

precursor [Arabidopsis thaliana]

Seq. No. 142724

Seq. ID LIB3168-018-P1-K1-B2

Method BLASTX
NCBI GI g112737
BLAST score 374
E value 4.0e-36
Match length 104
% identity 71
NCBI Description 2S SEED

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]



>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No. 142725

LIB3168-018-P1-K1-B3 Seq. ID

Method BLASTX q112741 NCBI GI BLAST score 619 1.0e-64 E value Match length 117 % identity 98

2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

> PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 142726

Seq. ID LIB3168-018-P1-K1-B4

Method BLASTX NCBI GI g112681 BLAST score 707 5.0e-75 E value Match length 137 % identity 96

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

142727 Seq. No.

Seq. ID LIB3168-018-P1-K1-B5

Method BLASTN NCBI GI g1448916 323 BLAST score E value 0.0e + 00Match length 367 % identity 97

NCBI Description Arabidopsis thaliana threonine synthase mRNA, 3' end of cds

142728 Seq. No.

Seq. ID LIB3168-018-P1-K1-B6

Method BLASTX g112682 NCBI GI 550 BLAST score E value 1.0e-56 Match length 116 % identity 91

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]



Seq. No. 142729

Seq. ID LIB3168-018-P1-K1-B7

Method BLASTX
NCBI GI g4510345
BLAST score 451
E value 5.0e-45
Match length 82
% identity 100

NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 142730

Seq. ID LIB3168-018-P1-K1-B9

Method BLASTX
NCBI GI g1628583
BLAST score 461
E value 3.0e-46
Match length 122
% identity 75

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142731

Seq. ID LIB3168-018-P1-K1-C1

Method BLASTX
NCBI GI g112682
BLAST score 735
E value 3.0e-78
Match length 142
% identity 98

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir \$08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142732

Seq. ID LIB3168-018-P1-K1-C10

Method BLASTX
NCBI GI g1628583
BLAST score 369
E value 3.0e-41
Match length 122
% identity 74

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142733

Seq. ID LIB3168-018-P1-K1-C11

Method BLASTX
NCBI GI g1628583
BLAST score 189
E value 1.0e-14
Match length 49
% identity 78

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis



thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

142734 Seq. No. Seq. ID LIB3168-018-P1-K1-C2 Method BLASTX NCBI GI g1628583 BLAST score 706 7.0e-75 E value 137 Match length

98

% identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142735

LIB3168-018-P1-K1-C3 Seq. ID

BLASTX Method NCBI GI g112741 BLAST score 51 7.0e-67 E value Match length 132 95 % identity

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

> PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 142736

Seq. ID LIB3168-018-P1-K1-C5

Method BLASTX NCBI GI q112741 BLAST score 665 E value 5.0e-70 Match length 128 % identity 96

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

> PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 142737

Seq. ID LIB3168-018-P1-K1-C8

Method BLASTX NCBI GI g119350 BLAST score 638 E value 6.0e-67 Match length 130 % identity 96

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 81608 pir JQ1187



phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase

[Arabidopsis thaliana]

>gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase
(2-phospho-D-glycerate hydroylase);identical to P25696
[Arabidopsis thaliana]

Seq. No. 142738

Seq. ID LIB3168-018-P1-K1-C9

Method BLASTX
NCBI GI g4191791
BLAST score 570
E value 6.0e-59
Match length 126
% identity 80

NCBI Description (AC005917) putative sf21 {Helianthus annuus} protein

[Arabidopsis thaliana]

Seq. No. 142739

Seq. ID LIB3168-018-P1-K1-D1

Method BLASTX
NCBI GI g112682
BLAST score 583
E value 2.0e-60
Match length 136
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142740

Seq. ID LIB3168-018-P1-K1-D10

Method BLASTX
NCBI GI g1628583
BLAST score 581
E value 2.0e-60
Match length 115
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142741

Seq. ID LIB3168-018-P1-K1-D11

Method BLASTX
NCBI GI g1628583
BLAST score 546
E value 4.0e-56
Match length 136
% identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142742



LIB3168-018-P1-K1-D2 Seq. ID Method BLASTX NCBI GI a112681 739 BLAST score 1.0e-78 E value 140 Match length % identity 99 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 142743 LIB3168-018-P1-K1-D3 Seq. ID Method BLASTX NCBI GI q112682 BLAST score 692 E value 3.0e-73 Match length 139 96 % identity 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__\$08510 NCBI Description cruciferin precursor (CRB) - Arabidopsis thaliana >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 142744 LIB3168-018-P1-K1-D4 Seq. ID Method BLASTX NCBI GI g2851455 220 BLAST score 6.0e-18 E value Match length 52 % identity 88 NCBI Description DYNAMIN-LIKE PROTEIN >gi 2267213 (L36939) dynamin-like GTP binding protein [Arabidopsis thaliana] Seq. No. 142745 Seq. ID LIB3168-018-P1-K1-D6 Method BLASTX NCBI GI g1628583 BLAST score 638

E value 6.0e-67 Match length 133 92 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142746

Seq. ID LIB3168-018-P1-K1-D8

Method BLASTX NCBI GI g4204299 BLAST score 598 3.0e-62 E value Match length 135



% identity 87

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 142747

Seq. ID LIB3168-018-P1-K1-D9

Method BLASTX
NCBI GI g1628583
BLAST score 639
E value 4.0e-67
Match length 123
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142748

Seq. ID LIB3168-018-P1-K1-E1

Method BLASTX
NCBI GI g1628583
BLAST score 230
E value 7.0e-38
Match length 106
% identity 81

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142749

Seq. ID LIB3168-018-P1-K1-E10

Method BLASTX
NCBI GI g112681
BLAST score 601
E value 1.0e-62
Match length 120
% identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142750

Seq. ID LIB3168-018-P1-K1-E11

Method BLASTX
NCBI GI g115783
BLAST score 571
E value 5.0e-59
Match length 107
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 142751

Seq. ID LIB3168-018-P1-K1-E12



Method BLASTX
NCBI GI g115767
BLAST score 232
E value 2.0e-19
Match length 87
% identity 59

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 142752

Seq. ID LIB3168-018-P1-K1-E2

Method BLASTX
NCBI GI g112741
BLAST score 711
E value 2.0e-75
Match length 133
% identity 99

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir_ NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit

3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 142753

Seq. ID LIB3168-018-P1-K1-E3

Method BLASTN
NCBI GI g2351071
BLAST score 390
E value 0.0e+00
Match length 417
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MVA3, complete sequence [Arabidopsis thaliana]

Seq. No. 142754

Seq. ID LIB3168-018-P1-K1-E4

Method BLASTX
NCBI GI g112682
BLAST score 574
E value 2.0e-59
Match length 125
% identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142755

Seq. ID LIB3168-018-P1-K1-E5



Method BLASTX
NCBI GI g1628583
BLAST score 620
E value 8.0e-65
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142756

Seq. ID LIB3168-018-P1-K1-E6

Method BLASTX
NCBI GI g1628583
BLAST score 706
E value 8.0e-75
Match length 138
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142757

Seq. ID LIB3168-018-P1-K1-E7

Method BLASTX
NCBI GI g112682
BLAST score 652
E value 1.0e-68
Match length 136
% identity 90

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142758

Seq. ID LIB3168-018-P1-K1-E8

Method BLASTX
NCBI GI g112682
BLAST score 526
E value 7.0e-54
Match length 113
% identity 90

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142759

Seq. ID LIB3168-018-P1-K1-E9

Method BLASTX
NCBI GI g112681
BLAST score 628
E value 8.0e-66
Match length 123



% identity 96

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142760

Seq. ID LIB3168-018-P1-K1-F1

Method BLASTX
NCBI GI g1255951
BLAST score 376
E value 3.0e-36
Match length 89
% identity 78

NCBI Description (X96932) PS60 [Nicotiana tabacum]

Seq. No. 142761

Seq. ID LIB3168-018-P1-K1-F10

Method BLASTN
NCBI GI 94757392
BLAST score 331
E value 0.0e+00
Match length 377
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K14A17, complete sequence

Seq. No. 142762

Seq. ID LIB3168-018-P1-K1-F11

Method BLASTX
NCBI GI g112737
BLAST score 524
E value 1.0e-53
Match length 129
% identity 79

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142763

Seq. ID LIB3168-018-P1-K1-F2

Method BLASTX
NCBI GI g3249096
BLAST score 516
E value 1.0e-52
Match length 120
% identity 88

NCBI Description (AC003114) Match to mRNA for importin alpha-like protein 4

(impa4) gb_Y14616 from A. thaliana. ESTs gb_N96440, gb N37503, gb N37498 and gb_T42198 come from this gene.

[Arabidopsis thaliana]



Seq. No. 142764

Seq. ID LIB3168-018-P1-K1-F4

Method BLASTX
NCBI GI g112682
BLAST score 602
E value 1.0e-62
Match length 135
% identity 86

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142765

Seq. ID LIB3168-018-P1-K1-F5

Method BLASTX
NCBI GI g112682
BLAST score 436
E value 2.0e-43
Match length 110
% identity 75

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir __S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142766

Seq. ID LIB3168-018-P1-K1-F6

Method BLASTX
NCBI GI g418908
BLAST score 218
E value 1.0e-17
Match length 131
% identity 37

NCBI Description vicilin precursor - cacao

Seq. No. 142767

Seq. ID LIB3168-018-P1-K1-F7

Method BLASTX
NCBI GI g2501064
BLAST score 562
E value 5.0e-58
Match length 136
% identity 81

NCBI Description PROBABLE THREONYL-TRNA SYNTHETASE, CYTOPLASMIC

(THREONINE--TRNA LIGASE) (THRRS) >gi_2191162 (AF007270) Similar to threonyl-tRNA synthetase; coded for by A.

thaliana cDNA R65376 [Arabidopsis thaliana]

Seq. No. 142768

Seq. ID LIB3168-018-P1-K1-F8

Method BLASTX
NCBI GI g112682
BLAST score 578
E value 6.0e-60



Match length 124 % identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidops $\overline{ ext{is}}$ s thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142769

Seq. ID LIB3168-018-P1-K1-F9

Method BLASTX
NCBI GI g112682
BLAST score 576
E value 1.0e-59
Match length 120
% identity 90

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142770

Seq. ID LIB3168-018-P1-K1-G10

Method BLASTN
NCBI GI g4510392
BLAST score 122
E value 3.0e-62
Match length 282
% identity 92

NCBI Description Arabidopsis thaliana chromosome II BAC T17D12 genomic

sequence, complete sequence

Seq. No. 142771

Seq. ID LIB3168-018-P1-K1-G11

Method BLASTN
NCBI GI g2618677
BLAST score 152
E value 4.0e-80
Match length 228
% identity 92

NCBI Description Arabidopsis thaliana BAC F21B7 chromosome 1, complete

sequence [Arabidopsis thaliana]

Seq. No. 142772

Seq. ID LIB3168-018-P1-K1-G2

Method BLASTX
NCBI GI 94204298
BLAST score 556
E value 3.0e-57
Match length 126
% identity 86

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 142773

Seq. ID LIB3168-018-P1-K1-G3



Method BLASTX
NCBI GI g1628583
BLAST score 617
E value 2.0e-64
Match length 127
% identity 94

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142774

Seq. ID LIB3168-018-P1-K1-G4

Method BLASTX
NCBI GI g112743
BLAST score 628
E value 1.0e-65
Match length 132
% identity 89

NCBI Description 2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_

(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4

precursor [Arabidopsis thaliana]

Seq. No. 142775

Seq. ID LIB3168-018-P1-K1-G5

Method BLASTX
NCBI GI g4204298
BLAST score 324
E value 3.0e-30
Match length 86
% identity 74

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 142776

Seq. ID LIB3168-018-P1-K1-G6

Method BLASTX
NCBI GI g112681
BLAST score 569
E value 8.0e-59
Match length 133
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142777

Seq. ID LIB3168-018-P1-K1-G7

Method BLASTN
NCBI GI g3985955
BLAST score 307
E value 1.0e-172



Match length 360 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTH16, complete sequence [Arabidopsis thaliana]

Seq. No. 142778

Seq. ID LIB3168-018-P1-K1-G8

Method BLASTN
NCBI GI g3985955
BLAST score 207
E value 1.0e-113
Match length 306
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTH16, complete sequence [Arabidopsis thaliana]

Seq. No. 142779

Seq. ID LIB3168-018-P1-K1-G9

Method BLASTX
NCBI GI g112737
BLAST score 524
E value 2.0e-53
Match length 134
% identity 77

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142780

Seq. ID LIB3168-018-P1-K1-H1

Method BLASTX
NCBI GI g1628583
BLAST score 717
E value 4.0e-76
Match length 140
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142781

Seq. ID LIB3168-018-P1-K1-H12

Method BLASTX
NCBI GI g112681
BLAST score 482
E value 1.0e-48
Match length 115
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]



Seq. No. 142782

Seq. ID LIB3168-018-P1-K1-H2

Method BLASTX
NCBI GI g1628583
BLAST score 619
E value 1.0e-64
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142783

Seq. ID LIB3168-018-P1-K1-H4

Method BLASTX
NCBI GI g1628583
BLAST score 593
E value 1.0e-61
Match length 120
% identity 95

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142784

Seq. ID LIB3168-018-P1-K1-H6

Method BLASTX
NCBI GI g1628583
BLAST score 631
E value 4.0e-66
Match length 124
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142785

Seq. ID LIB3168-018-P1-K1-H7

Method BLASTX
NCBI GI g112739
BLAST score 310
E value 1.0e-28
Match length 103
% identity 63

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

progurgor [Arabidopaia thaliana]

precursor [Arabidopsis thaliana]

Seq. No. 142786

Seq. ID LIB3168-018-P1-K1-H8

Method BLASTX NCBI GI g112739



BLAST score 3.0e-26 E value Match length 109 % identity 63 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No. 142787 Seq. ID LIB3168-018-P1-K1-H9 Method BLASTX NCBI GI g2832620 BLAST score 483 1.0e-48 E value

125 Match length % identity 71

(AL021711) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 142788

LIB3168-019-P1-K1-A1 Seq. ID

BLASTX Method NCBI GI g1628583 BLAST score 619 E value 1.0e-64 120 Match length 99 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142789

Seq. ID LIB3168-019-P1-K1-A10

Method BLASTX NCBI GI q1628583 BLAST score 695 1.0e-73 E value Match length 137 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

142790 Seq. No.

Seq. ID LIB3168-019-P1-K1-A11

Method BLASTX NCBI GI q114532 BLAST score 550 E value 1.0e-56 Match length 119 % identity 95

NCBI Description

ATP SYNTHASE ALPHA CHAIN >gi_67824_pir_PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain common tobacco chloroplast >gi_11769_emb_CAA23471_ (V00162)



alpha subunit of ATPase [Nicotiana tabacum]
>gi_11811_emb_CAA77341_ (Z00044) ATPase alpha subunit
[Nicotiana tabacum] >gi_225270_prf__1211235E ATPase alpha
[Nicotiana tabacum]

Seq. No. 142791

Seq. ID LIB3168-019-P1-K1-A12

Method BLASTX
NCBI GI g112737
BLAST score 540
E value 2.0e-55
Match length 131
% identity 80

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142792

Seq. ID LIB3168-019-P1-K1-A2

Method BLASTX
NCBI GI g112737
BLAST score 490
E value 2.0e-49
Match length 119
% identity 81

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142793

Seq. ID LIB3168-019-P1-K1-A4

Method BLASTX
NCBI GI g1628583
BLAST score 560
E value 9.0e-58
Match length 139
% identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142794

Seq. ID LIB3168-019-P1-K1-A6

Method BLASTN
NCBI GI 94079614
BLAST score 48
E value 1.0e-18
Match length 52
% identity 98

17548



NCBI Description Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 142795

Seq. ID LIB3168-019-P1-K1-A9

Method BLASTN
NCBI GI g2864607
BLAST score 241
E value 1.0e-133
Match length 383
% identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6

(ESSAII project)

Seq. No. 142796

Seq. ID LIB3168-019-P1-K1-B1

Method BLASTX
NCBI GI g1628583
BLAST score 620
E value 9.0e-65
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142797

Seq. ID LIB3168-019-P1-K1-B12

Method BLASTN
NCBI GI g3335170
BLAST score 110
E value 3.0e-55
Match length 190
% identity 99

NCBI Description Arabidopsis thaliana embryo-specific protein 3 (ATS3) gene,

complete cds

Seq. No. 142798

Seq. ID LIB3168-019-P1-K1-B2

Method BLASTX
NCBI GI g1628583
BLAST score 294
E value 8.0e-27
Match length 64
% identity 92

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142799

Seq. ID LIB3168-019-P1-K1-B4

Method BLASTN
NCBI GI g16236
BLAST score 109
E value 1.0e-54
Match length 145
% identity 94

17549



NCBI Description Arabidopsis CRB gene for 12S seed storage protein >qi 166677 qb M37248 ATHCRBAA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No. 142800

LIB3168-019-P1-K1-C1 Seq. ID

Method BLASTX NCBI GI q4204299 BLAST score 629 E value 8.0e-66 Match length 142 % identity 88

(AC003027) lcl prt seq No definition line found NCBI Description

[Arabidopsis thaliana]

Seq. No. 142801

Seq. ID LIB3168-019-P1-K1-C10

Method BLASTX NCBI GI q2244897 BLAST score 307 E value 4.0e-28 Match length 134 % identity 52

NCBI Description (Z97338) hypothetical protein [Arabidopsis thaliana]

Seq. No. 142802

LIB3168-019-P1-K1-C12 Seq. ID

Method BLASTX g112682 NCBI GI BLAST score 310 E value 7.0e-50 Match length 131 73 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605_pir__S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142803

Seq. ID LIB3168-019-P1-K1-C2

Method BLASTX NCBI GI q464621 BLAST score 542 E value 1.0e-55 Match length 136 % identity 78

60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 NCBI Description

ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16

[Mesembryanthemum crystallinum]

Seq. No. 142804

Seq. ID LIB3168-019-P1-K1-C9

Method BLASTX NCBI GI q1628583 BLAST score 625



E value 2.0e-65 Match length 120 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142805

LIB3168-019-P1-K1-D1 Seq. ID

Method BLASTN NCBI GI g1628582 BLAST score 55 E value 3.0e-22 Match length 210 % identity 42

Arabidopsis thaliana 12S cruciferin seed storage protein NCBI Description

(ATCRU3) gene, complete cds

142806 Seq. No.

LIB3168-019-P1-K1-D10 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 496 E value 7.0e-64 Match length 137 93 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142807

LIB3168-019-P1-K1-D11 Seq. ID

Method BLASTN NCBI GI g2842474 BLAST score 50 2.0e-19 E value Match length 86 90 % identity

Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 NCBI Description

(ESSAII project)

Seq. No. 142808

Seq. ID LIB3168-019-P1-K1-D2

Method BLASTN NCBI GI g3212846 BLAST score 392 E value 0.0e + 00Match length 392 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic

sequence, complete sequence [Arabidopsis thaliana]

142809

Seq. No. Seq. ID LIB3168-019-P1-K1-D4

Method BLASTX g1628583 NCBI GI BLAST score 625

17551



2.0e-65 E value Match length 120 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142810

LIB3168-019-P1-K1-D5 Seq. ID

Method BLASTX g1628583 NCBI GI BLAST score 188 1.0e-14 E value Match length 61 % identity 61

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142811

Seq. ID LIB3168-019-P1-K1-E1

Method BLASTX NCBI GI g1628583 BLAST score 413 1.0e-40 E value Match length 99 83 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142812

LIB3168-019-P1-K1-E10 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 681 E value 6.0e-72 Match length 131 99 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142813

Seq. ID LIB3168-019-P1-K1-E11

Method BLASTX NCBI GI g1628583 BLAST score 246 E value 4.0e-21 Match length 72 % identity 67

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142814

Seq. ID LIB3168-019-P1-K1-E2

17552



BLASTX Method NCBI GI q1628583 329 BLAST score 1.0e-30 E value Match length 83 77 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 142815 LIB3168-019-P1-K1-E3 Seq. ID

Method BLASTX
NCBI GI g112681
BLAST score 304
E value 6.0e-28
Match length 92

% identity 66
NCRI Description 128 SEED STO

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142816

Seq. ID LIB3168-019-P1-K1-E4

Method BLASTX
NCBI GI g1628583
BLAST score 696
E value 1.0e-73
Match length 137
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142817

Seq. ID LIB3168-019-P1-K1-E5

Method BLASTX
NCBI GI g1628583
BLAST score 523
E value 1.0e-53
Match length 103
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142818

Seq. ID LIB3168-019-P1-K1-E7

Method BLASTX
NCBI GI g1628583
BLAST score 718
E value 3.0e-76
Match length 136
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis



thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

 Seq. No.
 142819

 Seq. ID
 LIB3168-019-P1-K1-E9

 Method
 BLASTX

 NCBI GI
 g112681

 BLAST score
 549

E value 2.0e-56 Match length 129 % identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142820

Seq. ID LIB3168-019-P1-K1-F1

Method BLASTX
NCBI GI g112681
BLAST score 596
E value 6.0e-62
Match length 138
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142821

Seq. ID LIB3168-019-P1-K1-F10

Method BLASTX
NCBI GI g112681
BLAST score 536
E value 6.0e-55
Match length 139
% identity 78

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142822

Seq. ID LIB3168-019-P1-K1-F11

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

NCBI Description



```
Seq. No.
                  142823
                  LIB3168-019-P1-K1-F12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1628583
BLAST score
                  629
                  7.0e-66
E value
                  125
Match length
% identity
                  97
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142824
Seq. No.
Seq. ID
                  LIB3168-019-P1-K1-F2
Method
                  BLASTN
                  q3868722
NCBI GI
BLAST score
                  393
E value
                  0.0e+00
Match length
                  409
                  99
% identity
                  Arabidopsis thaliana BAC T19G15, from chromosome V near
NCBI Description
                  60.5 cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  142825
Seq. ID
                  LIB3168-019-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                   634
E value
                   2.0e-66
Match length
                   127
                   98
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   142826
Seq. ID
                   LIB3168-019-P1-K1-F5
Method
                  BLASTX
NCBI GI
                   q1628583
BLAST score
                   625
E value
                   2.0e-65
                   120
Match length
                   100
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   142827
                   LIB3168-019-P1-K1-F6
Seq. ID
Method
                   BLASTX
                   g1628583
NCBI GI
                   455
BLAST score
                   1.0e-45
E value
                   92
Match length
% identity
                   96
```

(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

% identity

49



cruciferin seed storage protein [Arabidopsis thaliana]

```
Seq. No.
                  142828
                  LIB3168-019-P1-K1-F9
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  597
E value
                  4.0e-62
                  114
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142829
                  LIB3168-019-P1-K1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4691223
BLAST score
                  394
                  0.0e+00
E value
                  409
Match length
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
NCBI Description
                  (ESSA project)
                  142830
Seq. No.
Seq. ID
                  LIB3168-019-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
E value
                  2.0e-65
Match length
                  120
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142831
                  LIB3168-019-P1-K1-G11
Seq. ID
Method
                  BLASTX
                  q1628583
NCBI GI
                  187
BLAST score
                  1.0e-14
E value
Match length
                  65
% identity
                  65
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142832
Seq. ID
                  LIB3168-019-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q3075399
BLAST score
                  207
E value
                  2.0e-16
Match length
                  83
```



NCBI Description (AC004484) SF16-like protein [Arabidopsis thaliana]

Seq. No. 142833

Seq. ID LIB3168-019-P1-K1-G8

Method BLASTX
NCBI GI g1628583
BLAST score 619
E value 1.0e-64
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142834

Seq. ID LIB3168-019-P1-K1-G9

Method BLASTX
NCBI GI g1170939
BLAST score 570
E value 6.0e-59
Match length 114
% identity 95

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE

ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)

>gi_1084408_pir__S46540 methionine adenosyltransferase (EC

2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon

esculentum]

Seq. No. 142835

Seq. ID LIB3168-019-P1-K1-H1

Method BLASTX
NCBI GI g1628583
BLAST score 248
E value 4.0e-21
Match length 76
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142836

Seq. ID LIB3168-019-P1-K1-H11

Method BLASTX
NCBI GI g112737
BLAST score 554
E value 5.0e-57
Match length 134
% identity 81

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]



```
Seq. No.
                  142837
Seq. ID
                  LIB3168-019-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2252841
BLAST score
                  501
                  8.0e-51
E value
Match length
                  139
% identity
                  84
NCBI Description
                 (AF013293) No definition line found [Arabidopsis thaliana]
Seq. No.
                  142838
                  LIB3168-019-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  617
E value
                  2.0e-64
Match length
                  120
                  99
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142839
Seq. No.
Seq. ID
                  LIB3168-019-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g2388582
BLAST score
                  133
E value
                  4.0e-20
Match length
                  53
% identity
                  96
                  (AC000098) Contains similarity to Rattus O-GlcNAc
NCBI Description
                  transferase (gb_U76557). [Arabidopsis thaliana]
Seq. No.
                  142840
Seq. ID
                  LIB3168-019-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  394
E value
                  2.0e-38
Match length
                  104
% identity
                  75
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  142841
Seq. ID
                  LIB3168-019-P1-K1-H9
```

Method BLASTX
NCBI GI g112681
BLAST score 549
E value 2.0e-56
Match length 129
% identity 83



NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936 emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142842

Seq. ID LIB3168-020-P1-K1-A2

Method BLASTX
NCBI GI g1170939
BLAST score 529
E value 4.0e-54
Match length 111
% identity 92

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE

ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)

>gi 1084408 pir S46540 methionine adenosyltransferase (EC

2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon

esculentum]

Seq. No. 142843

Seq. ID LIB3168-020-P1-K1-A3

Method BLASTX
NCBI GI g1628583
BLAST score 325
E value 1.0e-30
Match length 72
% identity 90

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142844

Seq. ID LIB3168-020-P1-K1-A4

Method BLASTX
NCBI GI g4056467
BLAST score 662
E value 1.0e-69
Match length 128
% identity 99

NCBI Description (AC005990) Strong similarity to gb_AB006693 spermidine

synthase from Arabidopsis thaliana. ESTs gb_AA389822, gb_T41794, gb_N38455, gb_AI100106, gb_F14442 and gb_F14256

come from this gene. [Arabidopsis thaliana]

Seq. No. 142845

Seq. ID LIB3168-020-P1-K1-A5

Method BLASTX
NCBI GI g1628583
BLAST score 322
E value 8.0e-30
Match length 60
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]



```
142846
Seq. No.
```

Seq. ID LIB3168-020-P1-K1-A6

Method BLASTX NCBI GI g3334128 535 BLAST score 8.0e-55 E value Match length 113 99 % identity

BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE NCBI Description

PRECURSOR (BCCP) >gi_1066348 (U23155) acetyl-CoA carboxylase biotin-containing subunit [Arabidopsis

thaliana]

Seq. No.

142847

Seq. ID

LIB3168-020-P1-K1-A7

Method BLASTX g112737 NCBI GI BLAST score 446 2.0e-44E value Match length 112 77 % identity

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit

1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142848

LIB3168-020-P1-K1-A8 Seq. ID

Method BLASTN NCBI GI g4217996 BLAST score 219 1.0e-120 E value Match length 390 % identity 100

Arabidopsis thaliana chromosome II BAC F24H14 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 142849

Seq. ID LIB3168-020-P1-K1-B1

Method BLASTN NCBI GI q4581138 BLAST score 426 E value 0.0e + 00Match length 441 99 % identity

Arabidopsis thaliana chromosome II BAC F1011 genomic NCBI Description

sequence, complete sequence

142850 Seq. No.

Seq. ID LIB3168-020-P1-K1-B10

BLASTX Method NCBI GI g112682 BLAST score 537



```
E value
Match length
                   116
% identity
                   87
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
                   142851
Seq. No.
                   LIB3168-020-P1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1531762
BLAST score
                   195
                   6.0e-15
E value
Match length
                   51
                   75
 % identity
                   (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                   thalianal
                   142852
Seq. No.
                   LIB3168-020-P1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g112681
BLAST score
                   200
E value
                   6.0e-30
                   107
Match length
identity
                   73
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
 Seq. No.
                   142853
 Seq. ID
                   LIB3168-020-P1-K1-B2
Method
                   BLASTX
 NCBI GI
                   q1653767
 BLAST score
                   286
 E value
                   1.0e-25
Match length
                   133
                   42
 % identity
                  (D90916) oligopeptidase A [Synechocystis sp.]
 NCBI Description
 Seq. No.
                   142854
 Seq. ID
                   LIB3168-020-P1-K1-B3
 Method
                   BLASTX
 NCBI GI
                   g4678333
 BLAST score
                   602
```

9.0e-63 E value 125 Match length 92 % identity

(ALO49658) H+-transporting ATPase-like protein [Arabidopsis NCBI Description

thaliana]

142855 Seq. No.

LIB3168-020-P1-K1-B5 Seq. ID



```
Method BLASTX
NCBI GI g1628583
BLAST score 566
E value 2.0e-58
Match length 140
% identity 79
```

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142856

Seq. ID LIB3168-020-P1-K1-B6

Method BLASTX
NCBI GI g3169569
BLAST score 519
E value 6.0e-53
Match length 105
% identity 100

NCBI Description (AF062589) 3-keto-acyl-CoA thiolase 2 [Arabidopsis

thaliana] >gi 3220237 (AF062591) peroxisomal

3-keto-acyl-CoA thiolase 2 precursor [Arabidopsis thaliana]

Seq. No. 142857

Seq. ID LIB3168-020-P1-K1-B7

Method BLASTX
NCBI GI g1628583
BLAST score 674
E value 4.0e-71
Match length 144
% identity 92

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142858

Seq. ID LIB3168-020-P1-K1-B8

Method BLASTX
NCBI GI g2833389
BLAST score 169
E value 2.0e-12
Match length 38
% identity 84

NCBI Description SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS III)

>gi 1200154 emb CAA65065 (X95759) glycogen (starch)

synthase [Solanum tuberosum]

Seq. No. 142859

Seq. ID LIB3168-020-P1-K1-B9

Method BLASTX
NCBI GI g1628583
BLAST score 378
E value 6.0e-37
Match length 73
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]



```
Seq. No.
                  142860
Seq. ID
                  LIB3168-020-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  388
E value
                  1.0e-37
Match length
                  72
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142861
Seq. ID
                  LIB3168-020-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  730
E value
                  1.0e-77
Match length
                  141
                  97
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  142862
Seq. ID
                  LIB3168-020-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  620
                  9.0e-65
E value
Match length
                  120
                  99
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142863
Seq. No.
Seq. ID
                  LIB3168-020-P1-K1-C4
Method
                  BLASTN
                  g4159702
NCBI GI
BLAST score
                  323
E value
                  0.0e + 00
Match length
                  412
% identity
                  95
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K2N11, complete sequence
```

Seq. No. 142864

Seq. ID LIB3168-020-P1-K1-C5

Method BLASTX
NCBI GI g112681
BLAST score 718
E value 3.0e-76
Match length 140

17563



% identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142865

Seq. ID LIB3168-020-P1-K1-C6

Method BLASTX
NCBI GI g112682
BLAST score 583
E value 2.0e-60
Match length 136
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142866

Seq. ID LIB3168-020-P1-K1-C8

Method BLASTX
NCBI GI g4263771
BLAST score 318
E value 2.0e-29
Match length 82
% identity 70

NCBI Description (AC006218) putative nonspecific lipid-transfer protein

precursor [Arabidopsis thaliana]

>gi_4726121_gb_AAD28321.1_AC006436_12 (AC006436) putative
nonspecific lipid-transfer protein precursor [Arabidopsis

thaliana]

Seq. No. 142867

Seq. ID LIB3168-020-P1-K1-C9

Method BLASTX
NCBI GI g112681
BLAST score 614
E value 5.0e-64
Match length 141
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142868

Seq. ID LIB3168-020-P1-K1-D1

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 123
% identity 98



NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

 Seq. No.
 142869

 Seq. ID
 LIB3168-020-P1-K1-D10

 Method
 BLASTX

 NCBI CI
 ~1629593

NCBI GI g1628583 BLAST score 688 E value 9.0e-73 Match length 134 % identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142870

Seq. ID LIB3168-020-P1-K1-D2

Method BLASTX
NCBI GI g1628583
BLAST score 334
E value 3.0e-31
Match length 62
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142871

Seq. ID LIB3168-020-P1-K1-D3

Method BLASTX
NCBI GI 94220476
BLAST score 498
E value 2.0e-50
Match length 108
% identity 95

NCBI Description (AC006069) ribophorin I-like protein [Arabidopsis thaliana]

Seq. No. 142872

Seq. ID LIB3168-020-P1-K1-D4

Method BLASTX
NCBI GI g2062167
BLAST score 293
E value 2.0e-26
Match length 74
% identity 73

NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis

thaliana]

Seq. No. 142873

Seq. ID LIB3168-020-P1-K1-D5

Method BLASTX
NCBI GI g112681
BLAST score 533
E value 1.0e-54
Match length 141
% identity 79

17565



12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142874

NCBI Description

Seq. ID LIB3168-020-P1-K1-D6

Method BLASTX
NCBI GI g16245
BLAST score 173
E value 2.0e-12
Match length 49
% identity 78

NCBI Description (X51514) precursor acetolactate synthase (670 AA)

[Arabidopsis thaliana]

Seq. No. 142875

Seq. ID LIB3168-020-P1-K1-D7

Method BLASTX
NCBI GI g2315135
BLAST score 296
E value 5.0e-33
Match length 81
% identity 90

NCBI Description (AB003522) beta subunit of coupling factor one [Arabidopsis

thaliana]

Seq. No. 142876

Seq. ID LIB3168-020-P1-K1-D8

Method BLASTX
NCBI GI g1628583
BLAST score 562
E value 6.0e-58
Match length 142
% identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142877

Seq. ID LIB3168-020-P1-K1-D9

Method BLASTX
NCBI GI g112681
BLAST score 628
E value 1.0e-65
Match length 127
% identity 94

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsisthaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142878

Seq. ID LIB3168-020-P1-K1-E1

Method BLASTX

```
NCBI GI
                  q166570
BLAST score
                  198
                  3.0e-15
E value
                  97
Match length
                  44
% identity
                  (L04173) glycine rich protein [Arabidopsis thaliana]
NCBI Description
                  142879
Seq. No.
                  LIB3168-020-P1-K1-E10
Seq. ID
Method
                  BLASTX
                  g131336
NCBI GI
BLAST score
                  261
                  1.0e-22
E value
Match length
                  58
% identity
                  90
                  PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi 72715 pir F2NT0P
NCBI Description
                  photosystem II phosphoprotein psbH - common tobacco
                  chloroplast >gi 11857 emb CAA77374 (Z00044) PSII 10kD
                  phosphoprotein [Nicotiana tabacum]
                  >gi 225225 prf 1211235BG photosystem II 10kD
                  phosphoprotein [Nicotiana tabacum]
                  142880
Seq. No.
Seq. ID
                  LIB3168-020-P1-K1-E11
Method
                  BLASTN
                  g12283
                  39
                  6.0e-13
                  55
% identity
                  93
NCBI Description
                  Spinach plastid psbB operon with genes for 10 kD
                  phosphoprotein associated with photosystem II (psbH),
```

NCBI GI BLAST score E value Match length

apocytochrome b6 and subunit 4 (petD) of cytochrome b6f

complex

Seq. No. 142881

Seq. ID LIB3168-020-P1-K1-E2

Method BLASTX g3150404 NCBI GI BLAST score 166 2.0e-11 E value Match length 54 70 % identity

(AC004165) putative mitochondrial carrier protein NCBI Description

[Arabidopsis thaliana]

Seq. No. 142882

Seq. ID LIB3168-020-P1-K1-E3

Method BLASTX NCBI GI g1628583 BLAST score 581 E value 3.0e-60 Match length 143 % identity 80

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

142883 Seq. No.

Seq. ID LIB3168-020-P1-K1-E4

Method BLASTX q1708025 NCBI GI 582 BLAST score 2.0e-60 E value Match length 136 % identity 85

GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+] NCBI Description

>gi_840731_emb_CAA56125_ (X79677) glycerol-3-phosphate

dehydrogenase (NAD+) [Cuphea lanceolata]

Seq. No. 142884

LIB3168-020-P1-K1-E5 Seq. ID

Method BLASTX NCBI GI g112737 BLAST score 566 2.0e-58 E value Match length 136 81 % identity

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142885

LIB3168-020-P1-K1-E6 Seq. ID

Method BLASTX NCBI GI g112681 BLAST score 527 7.0e-54 E value Match length 126 82 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

142886 Seq. No.

Seq. ID LIB3168-020-P1-K1-E7

Method BLASTX NCBI GI q112681 BLAST score 621 E value 7.0e-65 Match length 141 % identity

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]



```
Seq. No.
                  142887
                  LIB3168-020-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  693
E value
                  2.0e-73
Match length
                  136
                  97
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142888
                  LIB3168-020-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  552
E value
                  8.0e-57
Match length
                  135
% identity
                  79
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >qi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710_emb_CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  142889
                  LIB3168-020-P1-K1-F10
Seq. ID
                  BLASTX
Method
                  q3413701
NCBI GI
                  123
BLAST score
                  1.0e-06
E value
                  78
Match length
% identity
                  19
                  (AC004747) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  142890
                  LIB3168-020-P1-K1-F2
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  625
                  2.0e-65
E value
Match length
                  120
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142891
```

Seq. ID LIB3168-020-P1-K1-F3

Method BLASTX
NCBI GI g1628583
BLAST score 484
E value 5.0e-49
Match length 103



% identity 94

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142892

Seq. ID LIB3168-020-P1-K1-F4

Method BLASTX
NCBI GI g1628583
BLAST score 363
E value 4.0e-35
Match length 75
% identity 95

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142893

Seq. ID LIB3168-020-P1-K1-F5

Method BLASTX
NCBI GI g1628583
BLAST score 624
E value 2.0e-65
Match length 121
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142894

Seq. ID LIB3168-020-P1-K1-F6

Method BLASTX
NCBI GI g112681
BLAST score 611
E value 1.0e-63
Match length 139
% identity 85

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142895

Seq. ID LIB3168-020-P1-K1-F7

Method BLASTN
NCBI GI g4388714
BLAST score 150
E value 1.0e-78
Match length 428
% identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC F5K7 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 142896

Seq. ID LIB3168-020-P1-K1-F8

Method BLASTN

NCBI Description



```
q2760168
NCBI GI
BLAST score
                  244
E value
                  1.0e-135
Match length
                  384
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MEE6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  142897
                  LIB3168-020-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                  622
E value
                  5.0e-65
Match length
                  118
                  100
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >qi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  142898
Seq. ID
                  LIB3168-020-P1-K1-G1
Method
                  BLASTN
NCBI GI
                  g2264311
BLAST score
                  70
E value
                  6.0e-31
Match length
                  183
                  92
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MLN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  142899
Seq. ID
                  LIB3168-020-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  112
E value
                  8.0e-31
Match length
                  98
                  77
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  142900
Seq. ID
                  LIB3168-020-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g112743
BLAST score
                  395
E value
                  1.0e-41
Match length
                  98
% identity
                  87
```

2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor -



Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_(AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seg. No. 142901

Seq. ID LIB3168-020-P1-K1-G12

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142902

Seq. ID LIB3168-020-P1-K1-G2

Method BLASTX
NCBI GI g112739
BLAST score 414
E value 1.0e-40
Match length 122
% identity 70

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 142903

Seq. ID LIB3168-020-P1-K1-G3

Method BLASTX
NCBI GI g1628583
BLAST score 620
E value 8.0e-65
Match length 119
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142904

Seq. ID LIB3168-020-P1-K1-G4

Method BLASTX
NCBI GI g112682
BLAST score 556
E value 3.0e-57
Match length 131
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis





thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 142905

Seq. ID LIB3168-020-P1-K1-G6

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142906

Seq. ID LIB3168-020-P1-K1-G7

Méthod BLASTX
NCBI GI g1628583
BLAST score 564
E value 3.0e-58
Match length 140
% identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142907

Seq. ID LIB3168-020-P1-K1-G8

Method BLASTX
NCBI GI g625977
BLAST score 618
E value 1.0e-64
Match length 121
% identity 99

NCBI Description p40 protein homolog - Arabidopsis thaliana >gi_402904

(U01955) laminin receptor-like protein [Arabidopsis

thaliana]

Seq. No. 142908

Seq. ID LIB3168-020-P1-K1-G9

Method BLASTX
NCBI GI g1628583
BLAST score 620
E value 9.0e-65
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142909

Seq. ID LIB3168-020-P1-K1-H1

Method BLASTN
NCBI GI g4757401
BLAST score 205
E value 1.0e-111



Match length 416 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MGH6, complete sequence

Seq. No. 142910

Seq. ID LIB3168-020-P1-K1-H10

Method BLASTX
NCBI GI g1628583
BLAST score 331
E value 5.0e-31
Match length 69
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142911

Seq. ID LIB3168-020-P1-K1-H11

Method BLASTN
NCBI GI g1628582
BLAST score 67
E value 2.0e-29
Match length 191
% identity 84

NCBI Description Arabidopsis thaliana 12S cruciferin seed storage protein

(ATCRU3) gene, complete cds

Seq. No. 142912

Seq. ID LIB3168-020-P1-K1-H12

Method BLASTX
NCBI GI g112737
BLAST score 533
E value 1.0e-54
Match length 115
% identity 88

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit

1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142913

Seq. ID LIB3168-020-P1-K1-H2

Method BLASTX
NCBI GI g418908
BLAST score 182
E value 2.0e-13
Match length 75
% identity 44

NCBI Description vicilin precursor - cacao

Seq. No. 142914

Seq. ID LIB3168-020-P1-K1-H4

Method BLASTX



NCBI GI g112682 BLAST score 609 E value 2.0e-63 Match length 140 % identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142915

Seq. ID LIB3168-020-P1-K1-H5

Method BLASTX
NCBI GI g1628583
BLAST score 509
E value 6.0e-52
Match length 99
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142916

Seq. ID LIB3168-020-P1-K1-H6

Method BLASTX
NCBI GI g1628583
BLAST score 621
E value 6.0e-65
Match length 136
% identity 89

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142917

Seq. ID LIB3168-020-P1-K1-H7

Method BLASTX
NCBI GI g112681
BLAST score 417
E value 4.0e-41
Match length 111
% identity 76

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142918

Seq. ID LIB3168-020-P1-K1-H8

Method BLASTX
NCBI GI g2245029
BLAST score 159
E value 2.0e-20
Match length 64
% identity 82



NCBI Description (Z97341) limonene cyclase homolog [Arabidopsis thaliana]

Seq. No. 142919

Seq. ID LIB3168-020-P1-K1-H9

Method BLASTX
NCBI GI g112682
BLAST score 678
E value 1.0e-71
Match length 140
% identity 92

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142920

Seq. ID LIB3168-021-P1-K1-A1

Method BLASTX
NCBI GI g112681
BLAST score 544
E value 6.0e-56
Match length 126
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142921

Seq. ID LIB3168-021-P1-K1-A10

Method BLASTN
NCBI GI g2351062
BLAST score 199
E value 1.0e-108
Match length 411
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAH20, complete sequence [Arabidopsis thaliana]

Seq. No. 142922

Seq. ID LIB3168-021-P1-K1-A11

Method BLASTX
NCBI GI g112682
BLAST score 559
E value 1.0e-57
Match length 132
% identity 80

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142923

Seq. ID LIB3168-021-P1-K1-A12



Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142924

Seq. ID LIB3168-021-P1-K1-A2

Method BLASTX
NCBI GI g112681
BLAST score 556
E value 3.0e-57
Match length 135
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604 pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142925

Seq. ID LIB3168-021-P1-K1-A3

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142926

Seq. ID LIB3168-021-P1-K1-A4

Method BLASTX
NCBI GI 94567249
BLAST score 500
E value 1.0e-50
Match length 109
% identity 86

NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No. 142927

Seq. ID LIB3168-021-P1-K1-A5

Method BLASTX
NCBI GI g1628583
BLAST score 672
E value 7.0e-71
Match length 133
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

% identity

NCBI Description

99



```
142928
Seq. No.
                  LIB3168-021-P1-K1-A6
Seq. ID
                  BLASTN
Method
                  g2924257
NCBI GI
                  41
BLAST score
                  1.0e-13
E value
                  157
Match length
% identity
                  89
NCBI Description Tobacco chloroplast genome DNA
                  142929
Seq. No.
                  LIB3168-021-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  570
                  6.0e-59
E value
                  133
Match length
                  83
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
                  142930
Seq. No.
                  LIB3168-021-P1-K1-B1
Seq. ID
                  BLASTX
Method
                  g1628583
NCBI GI
                   548
BLAST score
                   2.0e-56
E value
                   138
Match length
                   78
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   142931
                   LIB3168-021-P1-K1-B10
Seq. ID
Method
                  BLASTX
                   a21911
NCBI GI
                   233
BLAST score
E value
                   2.0e-19
                   96
Match length
                   44
% identity
NCBI Description (X62625) vicilin [Theobroma cacao]
                   142932
Seq. No.
Seq. ID
                   LIB3168-021-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   q1628583
BLAST score
                   703
                   2.0e-74
E value
Match length
                   134
```

17578

(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

Seq. ID

Method



cruciferin seed storage protein [Arabidopsis thaliana]

```
Seq. No.
                  142933
                  LIB3168-021-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  661
E value
                  1.0e-69
                  133
Match length
                  98
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  142934
Seq. No.
                  LIB3168-021-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  407
                  8.0e-40
E value
                  103
Match length
                  80
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142935
Seq. No.
                  LIB3168-021-P1-K1-B3
Seq. ID
Method
                  BLASTX
                  q1628583
NCBI GI
                  404
BLAST score
E value
                  2.0e-39
                  112
Match length
% identity
                  73
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   142936
                  LIB3168-021-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g112681
BLAST score
                   531
                   2.0e-54
E value
Match length
                  138
                   78
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
                   142937
Seq. No.
```

17579

LIB3168-021-P1-K1-B5

BLASTX



```
NCBI GI g1628583
BLAST score 276
E value 2.0e-33
Match length 113
% identity 73
NCBI Description (U66916)
```

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142938

Seq. ID LIB3168-021-P1-K1-B6

Method BLASTX
NCBI GI g1628583
BLAST score 626
E value 2.0e-65
Match length 125
% identity 96

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis 🐖

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142939

Seq. ID LIB3168-021-P1-K1-B7

Method BLASTX
NCBI GI g1628583
BLAST score 611
E value 9.0e-64
Match length 117
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142940

Seq. ID LIB3168-021-P1-K1-B8

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142941

Seq. ID LIB3168-021-P1-K1-B9

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]



```
142942
Seq. No.
                  LIB3168-021-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1628583
                   619
BLAST score
                   1.0e-64
E value
                   120
Match length
                   99
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   142943
                   LIB3168-021-P1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1628583
BLAST score
                   625
                   2.0e-65
E value
                   120
Match length
                   100
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   142944
Seq. No.
                   LIB3168-021-P1-K1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1628583
BLAST score
                   658
                   3.0e-69
E value
Match length
                   131
                   96
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   142945
Seq. ID
                   LIB3168-021-P1-K1-C12
                   BLASTX
Method
NCBI GI
                   a2369714
BLAST score
                   534
                   1.0e-54
E value
                   116
Match length
                   91
% identity
                   (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   142946
Seq. No.
Seq. ID
                   LIB3168-021-P1-K1-C2
Method
                   BLASTX
```

43.

Method BLASTX
NCBI GI g1628583
BLAST score 545
E value 5.0e-56
Match length 138
% identity 78

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

17581



```
142947
Seq. No.
                  LIB3168-021-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112739
                  432
BLAST score
                  9.0e-43
E value
                  124
Match length
% identity
                  71
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
                  142948
Seq. No.
                  LIB3168-021-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112743
BLAST score
                  500
                  4.0e-58
E value
                  130
Match length
                  76
% identity
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68856 pir__NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_
                  (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >gi 4490713 emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
Seq. No.
                  142949
                  LIB3168-021-P1-K1-C6
Seq. ID
Method
                  BLASTX
                  g4586265
NCBI GI
BLAST score
                  238
E value
                  5.0e-20
                  89
Match length
% identity
                  52
                  (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  142950
                  LIB3168-021-P1-K1-C7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4519183
BLAST score
                  88
E value
                  7.0e-42
Match length
                  120
% identity
                  93
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K15C23, complete sequence

Seq. No. 142951

Seq. ID LIB3168-021-P1-K1-C8

Method BLASTX

17582

```
g2190016
NCBI GI
                   302
BLAST score
                   2.0e-27
E value
                   129
Match length
% identity
                   43
NCBI Description (AB004269) alliinase [Allium tuberosum]
                   142952
Seq. No.
                   LIB3168-021-P1-K1-C9
Seq. ID
                   BLASTX
Method
                   g1628583
NCBI GI
                   568
BLAST score
                   1.0e-58
E value
Match length
                   136
% identity
                   81
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   142953
                   LIB3168-021-P1-K1-D1
Seq. ID
                   BLASTX
Method
                   g112682
NCBI GI
BLAST score
                   635
E value
                   1.0e-66
Match length
                   137
% identity
                   91
                   12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   142954
                   LIB3168-021-P1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3135013
                   154
BLAST score
                    4.0e-10
E value
Match length
                   116
% identity
                    36
                   (AJ005963) 100 kDa protein [Ajellomyces capsulatus]
NCBI Description
                    142955
Seq. No.
                   LIB3168-021-P1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                    g1628583
BLAST score
                    625
                    2.0e-65
E value
Match length
                    120
                    100
% identity
```

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

142956 Seq. No.

LIB3168-021-P1-K1-D2 Seq. ID



```
BLASTX
Method
                  q4249382
NCBI GI
                  484
BLAST score
                  7.0e-49
E value
Match length
                  113
% identity
                  (AC005966) Strong similarity to gi 3337350 F13P17.3
NCBI Description
                  putative permease from Arabidopsis thaliana BAC
                  gb AC004481. [Arabidopsis thaliana]
                  142957
Seq. No.
Seq. ID
                  LIB3168-021-P1-K1-D3
Method
                  BLASTX
                  q4204299
NCBI GI
                  468
BLAST score
E value
                  6.0e-47
Match length
                  92
% identity
                  100
                  (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  142958
                  LIB3168-021-P1-K1-D4
Seq. ID
                  BLASTX
Method
                  q1628583
NCBI GI
BLAST score
                  620
E value
                  8.0e-65
                  134
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                  142959
Seq. No.
                  LIB3168-021-P1-K1-D5
Seq. ID
                  BLASTX
Method
                   g1628583
NCBI GI
                   700
BLAST score
                   4.0e-74
E value
                   138
Match length
                   98
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   142960
Seq. No.
                   LIB3168-021-P1-K1-D6
Seq. ID
                   BLASTX
Method
                   g1628583
NCBI GI
                   621
```

BLAST score E value 6.0e-65 Match length 120 99 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

NCBI Description



```
142961
Seq. No.
                  LIB3168-021-P1-K1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3513294
BLAST score
                  327
                  2.0e-30
E value
                  133
Match length
                  49
% identity
NCBI Description (AC005591) PkB-like [Homo sapiens]
                  142962
Seq. No.
                  LIB3168-021-P1-K1-E10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4539290
BLAST score
                  354
                  0.0e + 00
E value
Match length
                  411
                  95
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19
                   (ESSA project)
                  142963
Seq. No.
                  LIB3168-021-P1-K1-E11
Seq. ID
                  BLASTX
Method
                  g112681
NCBI GI
                  506
BLAST score
                   2.0e-51
E value
                   136
Match length
                   79
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
                   142964
Seq. No.
                   LIB3168-021-P1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4249382
BLAST score
                   483
                   1.0e-48
E value
Match length
                   111
                   78
% identity
                   (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb_AC004481. [Arabidopsis thaliana]
                   142965
Seq. No.
Seq. ID
                   LIB3168-021-P1-K1-E2
                   BLASTX
Method
NCBI GI
                   g112682
BLAST score
                   544
                   7.0e-56
E value
Match length
                   116
% identity
                   88
```

17585

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana



>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
storage protein [Arabidopsis thaliana]

Seq. No. 142966

Seq. ID LIB3168-021-P1-K1-E3

Method BLASTX
NCBI GI g1628583
BLAST score 703
E value 2.0e-74
Match length 134
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142967

Seq. ID LIB3168-021-P1-K1-E4

Method BLASTX
NCBI GI g112737
BLAST score 550
E value 1.0e-56
Match length 133
% identity 80

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir_NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142968

Seq. ID LIB3168-021-P1-K1-E5

Method BLASTX
NCBI GI g112682
BLAST score 570
E value 6.0e-59
Match length 134
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142969

Seq. ID LIB3168-021-P1-K1-E6

Method BLASTX
NCBI GI g112681
BLAST score 592
E value 2.0e-61
Match length 136
% identity 85

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis





thaliana] >gi_808936_emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana]

142970 Seq. No. Seq. ID LIB3168-021-P1-K1-E8 Method BLASTX g1628583 NCBI GI BLAST score 692 3.0e-73E value 132 Match length % identity 99 (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 142971 LIB3168-021-P1-K1-F1 Seq. ID Method BLASTN q3337347 NCBI GI BLAST score 87 2.0e-41 E value Match length 91 99 % identity Arabidopsis thaliana chromosome II BAC F13P17 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 142972 Seq. ID LIB3168-021-P1-K1-F10 Method BLASTX NCBI GI g1628583 BLAST score 703 E value 2.0e-74 135 Match length 99 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 142973 LIB3168-021-P1-K1-F11 Seq. ID BLASTX Method q1628583 NCBI GI -625 BLAST score 2.0e-65 E value 120 Match length 100 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

142974 Seq. No.

LIB3168-021-P1-K1-F12 Seq. ID

Method BLASTX q3660471 NCBI GI BLAST score 351 E value 3.0e-33 Match length 64



% identity 100
NCBI Description (AJ001809) succinate dehydrogenase flavoprotein alpha
subunit [Arabidopsis thaliana]

Seq. No. 142975

Seq. ID LIB3168-021-P1-K1-F2

Method BLASTX
NCBI GI g112681
BLAST score 725
E value 4.0e-77
Match length 138
% identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__\$08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142976

Seq. ID LIB3168-021-P1-K1-F5

Method BLASTX
NCBI GI g1628583
BLAST score 551
E value 1.0e-56
Match length 139
% identity 78

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142977

Seq. ID LIB3168-021-P1-K1-F6

Method BLASTX
NCBI GI g1345973
BLAST score 313
E value 8.0e-29
Match length 58
% identity 100

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 142978

Seq. ID LIB3168-021-P1-K1-F7

Method BLASTX
NCBI GI g1628583
BLAST score 599
E value 2.0e-62
Match length 120
% identity 96

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis



thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142979

Seq. ID LIB3168-021-P1-K1-F8

Method BLASTX
NCBI GI g112681
BLAST score 144
E value 5.0e-09
Match length 123
% identity 76

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142980

Seq. ID LIB3168-021-P1-K1-F9

Method BLASTX
NCBI GI g112682
BLAST score 564
E value 3.0e-58
Match length 132
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142981

Seq. ID LIB3168-021-P1-K1-G1

Method BLASTN
NCBI GI g4220637
BLAST score 73
E value 8.0e-33
Match length 340
% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MIE1, complete sequence [Arabidopsis thaliana]

Seq. No. 142982

Seq. ID LIB3168-021-P1-K1-G10

Method BLASTX
NCBI GI g1628583
BLAST score 410
E value 2.0e-40
Match length 89
% identity 92

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142983

Seq. ID LIB3168-021-P1-K1-G11

Method BLASTX



NCBI GI g112737 BLAST score 540 E value 2.0e-55 Match length 131 % identity 80

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68853 pir_NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204 emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 142984

Seq. ID LIB3168-021-P1-K1-G12

Method BLASTX
NCBI GI g112681
BLAST score 586
E value 8.0e-61
Match length 136
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 142985

Seq. ID LIB3168-021-P1-K1-G2

Method BLASTX
NCBI GI g112741
BLAST score 749
E value 6.0e-80
Match length 136
% identity 99

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 142986

Seq. ID LIB3168-021-P1-K1-G4

Method BLASTX
NCBI GI g1628583
BLAST score 395
E value 2.0e-38
Match length 109
% identity 73

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142987

Seq. ID LIB3168-021-P1-K1-G5



Method BLASTX
NCBI GI g1628583
BLAST score 730
E value 1.0e-77
Match length 140
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142988

Seq. ID LIB3168-021-P1-K1-G6

Method BLASTX
NCBI GI g881615
BLAST score 715
E value 6.0e-76
Match length 138
% identity 100

NCBI Description (U29142) fatty acid elongase 1 [Arabidopsis thaliana]

>gi_3096921_emb_CAA18831.1_ (AL023094) fatty acid elongase

1 [Arabidopsis thaliana]

Seq. No. 142989

Seq. ID LIB3168-021-P1-K1-G7

Method BLASTX
NCBI GI g1628583
BLAST score 620
E value 8.0e-65
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142990

Seq. ID LIB3168-021-P1-K1-G9

Method BLASTX
NCBI GI g4115935
BLAST score 414
E value 1.0e-40
Match length 80
% identity 100

NCBI Description (AF118223) contains similarity to Helicobacter pylori

peptide methionine sulfoxide reductase (msrA) (GB:AE000542)

[Arabidopsis thaliana]

Seq. No. 142991

Seq. ID LIB3168-021-P1-K1-H1

Method BLASTX
NCBI GI g1628583
BLAST score 380
E value 1.0e-36
Match length 97
% identity 78

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]



```
142992
Seq. No.
Seq. ID
                  LIB3168-021-P1-K1-H10
Method
                  BLASTX
                  g119350
NCBI GI
                  553
BLAST score
                  6.0e-57
E value
                  116
Match length
% identity
                  94
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187
                  phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                  thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
                  [Arabidopsis thaliana]
                  >gi_4581151_gb_AAD24635.1 AC006919 13 (AC006919) enolase
                  (2-phospho-D-glycerate hydroylase); identical to P25696
                  [Arabidopsis thaliana]
                  142993
Seq. No.
                  LIB3168-021-P1-K1-H11
Seq. ID
Method
                  BLASTX
                  g1076331
NCBI GI
                  150
BLAST score
                  1.0e-09
E value
                  52
Match length
% identity
                  69
                  histidine transport protein - Arabidopsis thaliana
NCBI Description
                  >gi 510238_emb_CAA54634_ (X77503) oligopeptide transporter
                  1-1 [Arabidopsis thaliana] >gi 744157_prf__2014244A His
                  transporter [Arabidopsis thaliana]
                  142994
Seq. No.
                  LIB3168-021-P1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  665
E value
                  4.0e-70
Match length
                  131
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  142995
Seq. No.
Seq. ID
                  LIB3168-021-P1-K1-H2
                  BLASTX
Method
                  q1628583
NCBI GI
                   618
BLAST score
E value
                   1.0e-64
                   132
Match length
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
```

Seq. No. LIB3168-021-P1-K1-H3 Seq. ID

142996

cruciferin seed storage protein [Arabidopsis thaliana]



Method BLASTX
NCBI GI g2132930
BLAST score 327
E value 2.0e-30
Match length 137
% identity 47

NCBI Description probable membrane protein YOR262w - yeast (Saccharomyces cerevisiae) >gi_1420591_emb_CAA99484_ (Z75170) ORF YOR262w

[Saccharomyces cerevisiae]

Seq. No. 142997

Seq. ID LIB3168-021-P1-K1-H4

Method BLASTX
NCBI GI g1628583
BLAST score 278
E value 2.0e-30
Match length 86
% identity 80

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 142998

Seq. ID LIB3168-021-P1-K1-H6

Method BLASTN
NCBI GI 94406776
BLAST score 240
E value 1.0e-132
Match length 276
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F14H20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 142999

Seq. ID LIB3168-021-P1-K1-H7

Method BLASTX
NCBI GI g1628583
BLAST score 684
E value 3.0e-72
Match length 136
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143000

Seq. ID LIB3168-021-P1-K1-H8

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]



```
143001
Seq. No.
                  LIB3168-021-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  564
                  2.0e-58
E value
Match length
                  110
                  99
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  143002
Seq. No.
                  LIB3168-022-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567311
BLAST score
                  265
E value
                   4.0e-23
Match length
                  66
                  73
% identity
                  (AC005956) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   143003
                  LIB3168-022-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2129659
BLAST score
                   418
E value
                   4.0e-41
Match length
                   128
% identity
                   70
                  oleosin, isoform 21K - Arabidopsis thaliana >gi_725260
NCBI Description
                   (L40954) oleosin [Arabidopsis thaliana]
                   143004
Seq. No.
                   LIB3168-022-P1-K1-A2
Seq. ID
Method
                   BLASTX
                   g112681
NCBI GI
BLAST score
                   471
                   2.0e-47
E value
                   118
Match length
                   80
% identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81604_pir_ S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi 808936_emb_CAA32493_ (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   143005
                   LIB3168-022-P1-K1-A3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3540210
                   296
BLAST score
                   1.0e-166
```

E value Match length 400 % identity

Arabidopsis thaliana chromosome I BAC F5A8 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]



```
143006
Seq. No.
                  LIB3168-022-P1-K1-A4
Seq. ID
Method
                  BLASTX
                  q4204299
NCBI GI
                  658
BLAST score
                  3.0e-69
E value
                  130
Match length
                  98
% identity
                  (AC003027) lcl_prt seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
                  143007
Seq. No.
                  LIB3168-022-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q266693
BLAST score
                  247
                  5.0e-21
E value
                  122
Match length
% identity
                  50
                  OLEOSIN >gi_282875_pir__$22538 oleosin - Arabidopsis
NCBI Description
                  thaliana >gi 16405 emb CAA44225 (X62353) oleosin
                  [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_
                  (AL035523) oleosin, 18.5K [Arabidopsis thaliana]
Seq. No.
                  143008
                  LIB3168-022-P1-K1-A7
Seq. ID
                  BLASTX
Method
                  g112741
NCBI GI
                  67
BLAST score
                  6.0e-15
E value
                  62
Match length
                  60
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  143009
                  LIB3168-022-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  573
                  3.0e-59
E value
Match length
                  132
```

82 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>qi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143010

LIB3168-022-P1-K1-A9 Seq. ID



```
BLASTX
Method
                  q4406780
NCBI GI
BLAST score
                  556
                  2.0e-57
E value
Match length
                  105
% identity
                  99
NCBI Description (AC006532) putative multispanning membrane protein
                  [Arabidopsis thaliana]
                  143011
Seq. No.
                  LIB3168-022-P1-K1-B1
Seq. ID
                  BLASTX
Method
                  q112681
NCBI GI
BLAST score
                  611
                  1.0e-63
E value
Match length
                  139
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  143012
                  LIB3168-022-P1-K1-B11
Seq. ID
Method
                  BLASTX
                  g3980396
NCBI GI
BLAST score
                  565
E value
                  2.0e-58
Match length
                  107
% identity
                  99
                  (AC004561) putative C-4 sterol methyl oxidase [Arabidopsis
NCBI Description
                  thaliana]
                  143013
Seq. No.
                  LIB3168-022-P1-K1-B2
Seq. ID
                  BLASTX
Method
                  g112682
NCBI GI
```

BLAST score 662 1.0e-69 E value Match length 138 % identity 91

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

143014 Seq. No.

LIB3168-022-P1-K1-B3 Seq. ID

Method BLASTX NCBI GI q1628583 BLAST score 625 2.0e-65 E value Match length 120 100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

E value

Match length

% identity

126 77



thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

```
143015
Seq. No.
                  LIB3168-022-P1-K1-B4
Seq. ID
Method
                  BLASTX
                  g3808062
NCBI GI
BLAST score
                  231
                  3.0e-19
E value
                  136
Match length
% identity
                  38
NCBI Description (AB019195) PV100 [Cucurbita maxima]
Seq. No.
                  143016
                  LIB3168-022-P1-K1-B5
Seq. ID
                  BLASTX
Method
                  g112682
NCBI GI
                  584
BLAST score
                  1.0e-60
E value
Match length
                  120
% identity
                  91
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  143017
Seq. No.
                  LIB3168-022-P1-K1-B6
Seq. ID
Method
                  BLASTX
                  g4544445
NCBI GI
BLAST score
                  221
                  5.0e-18
E value
                  110
Match length
% identity
                  45
                  (AC006592) putative pyrophosphate--fructose 6-phosphate
NCBI Description
                  1-phosphotransferase [Arabidopsis thaliana]
                  143018
Seq. No.
                  LIB3168-022-P1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4531433
                   275
BLAST score
                  1.0e-153
E value
Match length
                  279
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome II P1 MFL8 genomic
                   sequence, complete sequence
                   143019
Seq. No.
Seq. ID
                  LIB3168-022-P1-K1-B9
                  BLASTX
Method
NCBI GI
                  q2244759
BLAST score
                   474
                   1.0e-47
```

```
NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]
                  143020
Seq. No.
Seq. ID
                  LIB3168-022-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g112743
BLAST score
                  632
                  3.0e-66
E value
                  133
Match length
                  89
% identity
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68856_pir_ NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi 166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi_395202_emb CAA80869
                  (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >gi_4490713_emb_CAB38847.1 (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
                  143021
Seq. No.
Seq. ID
                  LIB3168-022-P1-K1-C10
                  BLASTX
Method
NCBI GI
                  q1628583
                  537
BLAST score
                  4.0e-55
E value
                  116
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >qi 2842495 emb CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  143022
Seq. No.
```

Seq. ID LIB3168-022-P1-K1-C12

Method BLASTX
NCBI GI g3915961
BLAST score 300
E value 1.0e-27
Match length 91
% identity 65

NCBI Description HYPOTHETICAL 267 KD PROTEIN (ORF 2280)

>gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical

protein [Nicotiana tabacum]

Seq. No. 143023

Seq. ID LIB3168-022-P1-K1-C2

Method BLASTX
NCBI GI g1628583
BLAST score 145
E value 5.0e-09
Match length 80
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143024

Seq. ID LIB3168-022-P1-K1-C4

17598



Method BLASTN
NCBI GI g1223909
BLAST score 408
E value 0.0e+00
Match length 412
% identity 100

NCBI Description Arabidopsis thaliana chaperonin-60 alpha subunit gene, nuclear gene encoding plastid protein, complete cds

Seq. No. 143025

Seq. ID LIB3168-022-P1-K1-C5

Method BLASTX
NCBI GI g4204299
BLAST score 646
E value 8.0e-68
Match length 127
% identity 98

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 143026

Seq. ID LIB3168-022-P1-K1-C6

Method BLASTX
NCBI GI g3660471
BLAST score 635
E value 1.0e-66
Match length 136
% identity 88

NCBI Description (AJ001809) succinate dehydrogenase flavoprotein alpha

subunit [Arabidopsis thaliana]

Seq. No. 143027

Seq. ID LIB3168-022-P1-K1-C7

Method BLASTX
NCBI GI g1864017
BLAST score 548
E value 2.0e-56
Match length 104
% identity 100

NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No. 143028

Seq. ID LIB3168-022-P1-K1-C8

Method BLASTX
NCBI GI g112741
BLAST score 579
E value 4.0e-60
Match length 107
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68855 pir_NWMU3 2S albumin 3 precursor -

Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

NCBI Description



```
143029
Seq. No.
                  LIB3168-022-P1-K1-D1
Seq. ID
                  BLASTX
Method
                  g1628583
NCBI GI
                  374
BLAST score
                  6.0e-36
E value
Match length
                  69
                  100
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495 emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  143030
Seq. No.
Seq. ID
                  LIB3168-022-P1-K1-D10
                  BLASTN
Method
                  g3885325
NCBI GI
BLAST score
                  335
                   0.0e + 00
E value
Match length
                   406
                   98
% identity
                  Arabidopsis thaliana chromosome II BAC T20P8 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   143031
Seq. No.
                   LIB3168-022-P1-K1-D11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4204299
                   651
BLAST score
                   2.0e-68
E value
Match length
                   126
                   100
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   143032
Seq. No.
                   LIB3168-022-P1-K1-D12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1628583
BLAST score
                   359
                   3.0e-34
E value
Match length
                   66
                   100
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   143033
Seq. No.
                   LIB3168-022-P1-K1-D3
Seq. ID
                   BLASTX
Method
                   g3249096
NCBI GI
                   489
BLAST score
                   2.0e-49
E value
Match length
                   112
                   90
% identity
                   (AC003114) Match to mRNA for importin alpha-like protein 4
```

(impa4) gb_Y14616 from A. thaliana. ESTs gb_N96440, gb_N37503, gb_N37498 and gb_T42198 come from this gene.



[Arabidopsis thaliana]

 Seq. No.
 143034

 Seq. ID
 LIB3168-022-P1-K1-D4

 Method
 BLASTX

 NCBI GI
 a112682

NCBI GI g112682 BLAST score 574 E value 2.0e-59 Match length 137 % identity 80

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143035

Seq. ID LIB3168-022-P1-K1-D5

Method BLASTX
NCBI GI g1628583
BLAST score 301
E value 3.0e-27
Match length 91
% identity 73

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143036

Seq. ID LIB3168-022-P1-K1-D6

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143037

Seq. ID LIB3168-022-P1-K1-D7

Method BLASTX
NCBI GI g4679028
BLAST score 331
E value 6.0e-31
Match length 134
% identity 49

NCBI Description (AF077207) HSPC021 [Homo sapiens]

Seq. No. 143038

Seq. ID LIB3168-022-P1-K1-D8

Method BLASTX
NCBI GI g112737
BLAST score 363
E value 5.0e-35
Match length 85

17601



% identity NCBI Description

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No.

143039

Seq. ID

LIB3168-022-P1-K1-E1

Method BLASTX NCBI GI g112682 BLAST score 556 E value 3.0e-57 Match length 131

% identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>qi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.

143040

Seq. ID

LIB3168-022-P1-K1-E10

Method BLASTX NCBI GI q1628583 BLAST score 625 E value 2.0e-65 120 Match length % identity 100

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.

143041

Seq. ID

LIB3168-022-P1-K1-E11

Method BLASTX NCBI GI q112737 BLAST score 486 4.0e-49 E value Match length 121 79 % identity

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68853_pir__NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No.

143042

Seq. ID

LIB3168-022-P1-K1-E12

Method BLASTX NCBI GI g2529683 BLAST score 55 2.0e-54 E value



Match length 132 % identity 79

NCBI Description (AC002535) unknown protein [Arabidopsis thaliana]

Seq. No.

143043

Seq. ID Method LIB3168-022-P1-K1-E2

NCBI GI

BLASTX g1628583

BLAST score E value

357 5.0e-34

73

100

Match length % identity

NCBI Description

(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.

143044

Seq. ID

LIB3168-022-P1-K1-E3

Method BLASTN
NCBI GI g4580365
BLAST score 247
E value 1.0e-137
Match length 293

Match length 293 % identity 95

NCBI Description Arabi

Arabidopsis thaliana chromosome I BAC F3F20 genomic

sequence, complete sequence

Seq. No.

143045

143046

Seq. ID

LIB3168-022-P1-K1-E4

Method BLASTX
NCBI GI g1628583
BLAST score 647
E value 6.0e-68
Match length 135
% identity 93

NCBI Description

(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.

Seq. ID

LIB3168-022-P1-K1-E5

Method BLASTX
NCBI GI g1628583
BLAST score 506
E value 2.0e-51
Match length 137
% identity 72

NCBI Description

(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143047

Seq. ID LIB3168-022-P1-K1-E8

Method BLASTX
NCBI GI g4512675
BLAST score 556
E value 2.0e-57

17603



Match length % identity 97

NCBI Description (AC006931) putative citrate synthase [Arabidopsis thaliana]

143048 Seq. No.

Seq. ID LIB3168-022-P1-K1-E9

Method BLASTX NCBI GI g112681 BLAST score 702 E value 2.0e-74 Match length 132 % identity 100

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir \$08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143049

LIB3168-022-P1-K1-F1 Seq. ID

Method BLASTX NCBI GI g3335372 BLAST score 162 E value 4.0e-11 Match length 75 % identity 40

NCBI Description (AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No. 143050

LIB3168-022-P1-K1-F11 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 363 E value 7.0e-35 Match length 95 % identity 78

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143051

Seq. ID LIB3168-022-P1-K1-F12

Method BLASTN NCBI GI q4199934 BLAST score 281 E value 1.0e-157 Match length 303 % identity 100

Genomic sequence for Arabidopsis thaliana BAC T3P18, NCBI Description

complete sequence [Arabidopsis thaliana]

Seq. No. 143052

Seq. ID LIB3168-022-P1-K1-F2

Method BLASTX NCBI GI g112682 BLAST score 664 E value 6.0e-70



Match length 137 % identity 92

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143053

Seq. ID LIB3168-022-P1-K1-F3

Method BLASTN
NCBI GI g2477521
BLAST score 408
E value 0.0e+00
Match length 408
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 143054

Seq. ID LIB3168-022-P1-K1-F4

Method BLASTX
NCBI GI g112682
BLAST score 536
E value 6.0e-55
Match length 116
% identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143055

Seq. ID LIB3168-022-P1-K1-F6

Method BLASTX
NCBI GI g1628583
BLAST score 112
E value 3.0e-05
Match length 73
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_(AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143056

Seq. ID LIB3168-022-P1-K1-F9

Method BLASTX
NCBI GI g1628583
BLAST score 564
E value 2.0e-58
Match length 111
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]



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143057
Seq. No.
Seq. ID
                  LIB3168-022-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  162
                  4.0e-11
E value
Match length
                  73
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143058
Seq. ID
                  LIB3168-022-P1-K1-G10
Method
                  BLASTX
                  g1486472
NCBI GI
BLAST score
                  440
E value
                  1.0e-43
Match length
                  100
% identity
                  86
                  (X99853) oxoglutarate malate translocator [Solanum
NCBI Description
                  tuberosum]
Seq. No.
                  143059
Seq. ID
                  LIB3168-022-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g3513294
BLAST score
                  331
E value
                  6.0e-31
Match length
                  133
% identity
                  49
NCBI Description (AC005591) PkB-like [Homo sapiens]
Seq. No.
                  143060
Seq. ID
                  LIB3168-022-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  695
E value
                  1.0e-73
Match length
                  137
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143061
Seq. ID
                  LIB3168-022-P1-K1-G3
Method
                  BLASTN
NCBI GI
                  q4510392
BLAST score
                  408
```

E value 0.0e + 00Match length 412 % identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T17D12 genomic

sequence, complete sequence

Seq. No. 143062

17606



```
LIB3168-022-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  625
E value
                  2.0e-65
Match length
                  120
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143063
Seq. ID
                  LIB3168-022-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  q1246403
BLAST score
                  460
E value
                  5.0e-46
Match length
                  109
% identity
                  81
NCBI Description
                  (X94698) TINY [Arabidopsis thaliana] >gi 3406035 (AC005405)
                  TINY [Arabidopsis thaliana]
Seq. No.
                  143064
Seq. ID
                  LIB3168-022-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q112251
BLAST score
                  78
E value
                  3.0e-01
Match length
                  120
% identity
                  18
NCBI Description
                  polypyrimidine tract-binding protein 1 - rat
                  >gi 57002 emb CAA43202 (X60789) pyrimidine binding protein
                  1 [Rattus norvegicus]
Seq. No.
                  143065
Seq. ID
                  LIB3168-022-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  523
E value
                  2.0e-53
Match length
                  136
% identity
                  77
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  143066
Seq. ID
                  LIB3168-022-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  683
E value
                  3.0e-72
Match length
                  128
```

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17607

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

99

% identity



PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868 (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712 emb CAB38846.1 $_{-}$ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No. 143067

Seq. ID LIB3168-022-P1-K1-H1

Method BLASTX g600178 NCBI GI BLAST score 656 E value 5.0e-69 Match length 138 % identity 94

NCBI Description (L27074) acetyl-CoA carboxylase [Arabidopsis thaliana]

>gi 1090217 prf 2018327A Ac-CoA carboxylase [Arabidopsis

thaliana]

Seq. No. 143068

Seq. ID LIB3168-022-P1-K1-H11

Method BLASTX NCBI GI g112681 BLAST score 569 E value 8.0e-59 Match length 133 % identity 83

12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143069

Seq. ID LIB3168-022-P1-K1-H12

Method BLASTX NCBI GI q3395432 270 BLAST score 9.0e-24 E value Match length 91 % identity 56

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 143070

Seq. ID LIB3168-022-P1-K1-H2

Method BLASTX NCBI GI q1628583 BLAST score 607 E value 3.0e-63 Match length 116 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143071

Seq. ID LIB3168-022-P1-K1-H3



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Method
                   BLASTN
NCBI GI
                   q4159708
BLAST score
                   41
                   3.0e-14
E value
Match length
                   113
% identity
                   84
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MKP6, complete sequence
Seq. No.
                  143072
Seq. ID
                  LIB3168-022-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  g2947056
                   231
BLAST score
E value
                  1.0e-127
Match length
                   323
                   93
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20F6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  143073
Seq. ID
                  LIB3168-022-P1-K1-H6
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                   636
E value
                  1.0e-66
Match length
                  127
                   98
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143074
Seq. ID
                  LIB3168-022-P1-K1-H8
Method
                  BLASTN
NCBI GI
                  q2760165
BLAST score
                   197
E value
                  1.0e-107
Match length
                   410
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  143075
Seq. ID
                  LIB3168-022-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  335
E value
                  2.0e-31
Match length
                   62
```

100 % identity

2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712 emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

17609



precursor [Arabidopsis thaliana]

Seq. No. 143076 Seq. ID LIB3168-023-P1-K1-A1 Method BLASTX NCBI GI g1628583 BLAST score 625 E value 2.0e-65 Match length 120

% identity 100 NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143077

Seq. ID LIB3168-023-P1-K1-A10

Method BLASTX NCBI GI g112681 BLAST score 269 E value 2.0e-59 Match length 119 % identity 100

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143078

LIB3168-023-P1-K1-A11 Seq. ID

Method BLASTX NCBI GI q1628583 BLAST score 614 4.0e-64 E value 119 Match length % identity 99

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143079

Seq. ID LIB3168-023-P1-K1-A12

Method BLASTX NCBI GI q112681 BLAST score 576 E value 1.0e-59 Match length 133 84 % identity

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

143080 Seq. No.

Seq. ID LIB3168-023-P1-K1-A2

Method BLASTX



NCBI GI g112681 BLAST score 675 E value 4.0e-71 Match length 139 % identity 97

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__\$08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3168-023-P1-K1-A3

143081

Method BLASTX
NCBI GI g112681
BLAST score 315
E value 2.0e-56
Match length 139
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir \$08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143082

Seq. ID LIB3168-023-P1-K1-A4

Method BLASTX
NCBI GI g1628583
BLAST score 723
E value 7.0e-77
Match length 138
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143083

Seq. ID LIB3168-023-P1-K1-A5

Method BLASTX
NCBI GI g119143
BLAST score 690
E value 5.0e-73
Match length 131
% identity 99

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_81606_pir__S06724 translation elongation factor eEF-1
alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
(X16430) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1369927_emb_CAA34454_ (X16431) elongation factor
1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_
(X16431) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana]
>gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana]
>gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No. 143084



LIB3168-023-P1-K1-A6 Seq. ID

Method BLASTX NCBI GI g2117634 BLAST score 154 E value 3.0e-37 Match length 137 % identity 60

NCBI Description lipoxygenase (EC 1.13.11.12) - common tobacco

>qi 899344 emb CAA58859 (X84040) lipoxygenase [Nicotiana

143085 Seq. No.

Seq. ID LIB3168-023-P1-K1-A8

Method BLASTX NCBI GI g1628583 BLAST score 354 E value 1.0e-33 Match length 88 % identity 78

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143086

Seq. ID LIB3168-023-P1-K1-A9

Method BLASTX NCBI GI g112737 BLAST score 464 E value 1.0e-46 Match length 116 % identity 78

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

> PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143087

Seq. ID LIB3168-023-P1-K1-B1

Method BLASTX NCBI GI q1628583 BLAST score 625 E value 2.0e-65 Match length 120 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143088

Seq. ID LIB3168-023-P1-K1-B10

Method BLASTX NCBI GI g112682 BLAST score 686 E value 2.0e-72



Match length 142 % identity 92

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsīs thalianā

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143089

Seq. ID LIB3168-023-P1-K1-B11

Method BLASTX
NCBI GI g112681
BLAST score 603
E value 9.0e-63
Match length 138
% identity 85

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143090

Seq. ID LIB3168-023-P1-K1-B12

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143091

Seq. ID LIB3168-023-P1-K1-B2

Method BLASTX
NCBI GI g1628583
BLAST score 607
E value 3.0e-63
Match length 116
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143092

Seq. ID LIB3168-023-P1-K1-B3

Method BLASTX
NCBI GI g2129657
BLAST score 398
E value 1.0e-38
Match length 109
% identity 77

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin



[Arabidopsis thaliana]

 Seq. No.
 143093

 Seq. ID
 LIB3168-023-P1-K1-B4

 Method
 BLASTX

 NCBI GI
 g3334123

 BLAST score
 686

BLAST score 686 E value 2.0e-72 Match length 139 % identity 100

NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi 1655480 dbj BAA13599 (D88374) gamma subunit of

mitochondrial FI-ATPase [Arabidopsis thaliana] >gi 2924787

(AC002334) mitochondrial F1-ATPase, gamma subunit

[Arabidopsis thaliana]

Seq. No. 143094

Seq. ID LIB3168-023-P1-K1-B5

Method BLASTX
NCBI GI g1628583
BLAST score 527
E value 5.0e-54
Match length 103
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143095

Seq. ID LIB3168-023-P1-K1-B6

Method BLASTX
NCBI GI g1628583
BLAST score 374
E value 5.0e-36
Match length 69
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143096

Seq. ID LIB3168-023-P1-K1-B8

Method BLASTX
NCBI GI g1628583
BLAST score 619
E value 9.0e-65
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143097

Seq. ID LIB3168-023-P1-K1-B9

Method BLASTN NCBI GI g2182286 BLAST score 70



E value 8.0e-32 Match length 78 % identity 97

NCBI Description Sequence of BAC F20P5 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 143098

Seq. ID LIB3168-023-P1-K1-C11

Method BLASTX
NCBI GI g112682
BLAST score 595
E value 7.0e-62
Match length 138
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143099

Seq. ID LIB3168-023-P1-K1-C12

Method BLASTX
NCBI GI g1628583
BLAST score 620
E value 9.0e-65
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143100

Seq. ID LIB3168-023-P1-K1-C2

Method BLASTX
NCBI GI g3063451
BLAST score 662
E value 1.0e-69
Match length 129
% identity 99

NCBI Description (AC003981) F22013.13 [Arabidopsis thaliana]

Seq. No. 143101

Seq. ID LIB3168-023-P1-K1-C3

Method BLASTX
NCBI GI g1628583
BLAST score 601
E value 1.0e-62
Match length 119
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143102

Seq. ID LIB3168-023-P1-K1-C4

Method BLASTX



NCBI GI g1628583 BLAST score 386 5.0e-68 E value Match length 137 % identity 96

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143103

Seq. ID LIB3168-023-P1-K1-C5

Method BLASTX NCBI GI g1628583 BLAST score 625 E value 2.0e-65 Match length 120 100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143104

Seq. ID LIB3168-023-P1-K1-C6

Method BLASTX NCBI GI g1628583 BLAST score 637 E value 3.0e-71 Match length 138 % identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143105

Seq. ID LIB3168-023-P1-K1-C8

Method BLASTX NCBI GI g112741 BLAST score 56 E value 7.0e-70 Match length 132 % identity 100

2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi 68855_pir__NWMU3 2S albumin 3 precursor -

Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143106

Seq. ID LIB3168-023-P1-K1-C9

Method BLASTX g469467 NCBI GI BLAST score 671 E value 9.0e-71 Match length 124 % identity 99



NCBI Description (X77943) alcohol dehydrogenase [Arabidopsis thaliana] >gi_1944214_dbj_BAA19619_ (D84244) alcohol dehydrogenase [Arabidopsis thaliana] >gi_2570194_dbj_BAA22981_ (D63463) alcohol dehydrogenase [Arabidopsis thaliana] >gi_2829917 (AC002291) Alcohol Dehydrogenase [Arabidopsis thaliana]

Seq. No. 143107

Seq. ID LIB3168-023-P1-K1-D10

Method BLASTX
NCBI GI g112681
BLAST score 605
E value 5.0e-63
Match length 139
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143108

Seq. ID LIB3168-023-P1-K1-D11

Method BLASTX
NCBI GI g1628583
BLAST score 106
E value 2.0e-04
Match length 65
% identity 86

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143109

Seq. ID LIB3168-023-P1-K1-D2

Method BLASTX
NCBI GI g1628583
BLAST score 358
E value 5.0e-34
Match length 90
% identity 78

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143110

Seq. ID LIB3168-023-P1-K1-D3

Method BLASTX
NCBI GI g112682
BLAST score 641
E value 3.0e-67
Match length 141
% identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

17617



Seq. No. 143111

Seq. ID LIB3168-023-P1-K1-D4

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143112

Seq. ID LIB3168-023-P1-K1-D5

Method BLASTX
NCBI GI g112681
BLAST score 428
E value 3.0e-42
Match length 88
% identity 95

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143113

Seq. ID LIB3168-023-P1-K1-D6

Method BLASTX
NCBI GI g2129789
BLAST score 484
E value 8.0e-49
Match length 127
% identity 78

NCBI Description biotin carboxyl carrier protein precursor (clone BP4) -

rape >gi_1070006_emb_CAA62264_ (X90730) Biotin carboxyl
carrier protein [Brassica napus] >gi_1589043_prf__2210244D

Ac-CoA carboxylase:ISOTYPE=bp4 [Brassica napus]

Seq. No. 143114

Seq. ID LIB3168-023-P1-K1-D7

Method BLASTX
NCBI GI g4741191
BLAST score 204
E value 5.0e-16
Match length 42
% identity 100

NCBI Description (AL049746) ABC transporter-like protein [Arabidopsis

thaliana]

Seq. No. 143115

Seq. ID LIB3168-023-P1-K1-D8

Method BLASTN
NCBI GI g4589450
BLAST score 161
E value 3.0e-85



Match length 412 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

T31K7, complete sequence

Seq. No. 143116

Seq. ID LIB3168-023-P1-K1-D9

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143117

Seq. ID LIB3168-023-P1-K1-E1

Method BLASTX
NCBI GI g4249382
BLAST score 486
E value 4.0e-49
Match length 113
% identity 78

NCBI Description (AC005966) Strong similarity to gi 3337350 F13P17.3

putative permease from Arabidopsis thaliana BAC

gb AC004481. [Arabidopsis thaliana]

Seq. No. 143118

Seq. ID LIB3168-023-P1-K1-E10

Method BLASTX
NCBI GI g1628583
BLAST score 473
E value 1.0e-47
Match length 134
% identity 72

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143119

Seq. ID LIB3168-023-P1-K1-E11

Method BLASTN
NCBI GI g3402745
BLAST score 225
E value 1.0e-123
Match length 364
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5

(ESSAII project)

Seq. No. 143120

Seq. ID LIB3168-023-P1-K1-E12

Method BLASTX NCBI GI g112741 BLAST score 716



5.0e-76 E value Match length 133 % identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit

3 precursor [Arabidopsis thaliana] >qi 395201 emb CAA80868 (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143121

LIB3168-023-P1-K1-E2 Seq. ID

Method BLASTX NCBI GI g112739 BLAST score 425 E value 6.0e-42Match length 121 % identity 71

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >qi 68854 pir NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 143122

Seq. ID LIB3168-023-P1-K1-E3

Method BLASTX NCBI GI q1628583 BLAST score 625 2.0e-65 E value Match length 120 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143123

Seq. ID LIB3168-023-P1-K1-E4

Method BLASTX NCBI GI q1628583 BLAST score 625 E value 2.0e-65 Match length 120 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143124

Seq. ID LIB3168-023-P1-K1-E5

Method BLASTX NCBI GI g112681 BLAST score 709 E value 3.0e-75



Match length 136 % identity 98

% identity 98
NCBI Description 12S SEED STORAGE PROTEIN PRECURA

12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143125

Seq. ID LIB3168-023-P1-K1-E6

Method BLASTX
NCBI GI g3980407
BLAST score 262
E value 8.0e-23
Match length 110
% identity 48

NCBI Description (AC004561) putative receptor-like protein kinase

[Arabidopsis thaliana]

Seq. No. 143126

Seq. ID LIB3168-023-P1-K1-E7

Method BLASTX
NCBI GI g1628583
BLAST score 621
E value 6.0e-65
Match length 119
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143127

Seq. ID LIB3168-023-P1-K1-E8

Method BLASTX
NCBI GI g1791309
BLAST score 509
E value 8.0e-52
Match length 102
% identity 99

NCBI Description (U83500) cystathionine gamma-synthase [Arabidopsis

thaliana] >gi_2852454_dbj_BAA24699_ (AB010888)

cystathionine gamma-synthase [Arabidopsis thaliana]

Seq. No. 143128

Seq. ID LIB3168-023-P1-K1-E9

Method BLASTX
NCBI GI g3183454
BLAST score 236
E value 9.0e-20
Match length 103
% identity 44

NCBI Description HYPOTHETICAL 30.7 KD PROTEIN IN MCPC-KINA INTERGENIC REGION

>gi_2632217_emb_CAA10859_ (AJ222587) YkwC protein [Bacillus subtilis] >gi_2633767_emb_CAB13269_ (Z99111) similar to 3-hydroxyisobutyrate dehydrogenase [Bacillus subtilis]

Seq. No. 143129



LIB3168-023-P1-K1-F10 Seq. ID

Method BLASTX NCBI GI q112681 BLAST score 644 1.0e-67 E value 127 Match length % identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143130

Seq. ID LIB3168-023-P1-K1-F11

Method BLASTX NCBI GI q112741 BLAST score 331 E value 3.0e-31 Match length 86 % identity 77

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143131

LIB3168-023-P1-K1-F12 Seq. ID

Method BLASTX NCBI GI g112681 BLAST score 607 E value 3.0e-63 Match length 121 % identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143132

Seq. ID LIB3168-023-P1-K1-F2

Method BLASTX NCBI GI q1628583 BLAST score 162 E value 4.0e-11 Match length 60 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143133

Seq. ID LIB3168-023-P1-K1-F3



Method BLASTN NCBI GI g4581161 BLAST score 69 E value 5.0e-31 Match length 105 % identity 90

Arabidopsis thaliana chromosome II BAC T20G20 genomic NCBI Description

sequence, complete sequence

Seq. No. 143134

Seq. ID LIB3168-023-P1-K1-F4

Method BLASTX NCBI GI g112737 BLAST score 673 E value 5.0e-71 Match length 139 % identity 91

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >qi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143135

Seq. ID LIB3168-023-P1-K1-F5

Method BLASTX NCBI GI g112737 BLAST score 299 E value 4.0e-27 129 Match length % identity 52

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143136

Seq. ID LIB3168-023-P1-K1-F6

Method BLASTX NCBI GI g112682 BLAST score 284 6.0e-26 E value Match length 52 % identity 100

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143137

Seq. ID LIB3168-023-P1-K1-F7



Method BLASTX
NCBI GI g112681
BLAST score 442
E value 3.0e-47
Match length 141
% identity 77

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143138

Seq. ID LIB3168-023-P1-K1-F8

Method BLASTX
NCBI GI g112681
BLAST score 534
E value 9.0e-55
Match length 126
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143139

Seq. ID LIB3168-023-P1-K1-F9

Method BLASTX
NCBI GI g3023848
BLAST score 620
E value 9.0e-65
Match length 123
% identity 60

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis

thaliana]

Seq. No. 143140

Seq. ID LIB3168-023-P1-K1-G1

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143141

Seq. ID LIB3168-023-P1-K1-G10

Method BLASTX
NCBI GI g112682
BLAST score 518
E value 7.0e-53



Match length 111 87 % identity

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143142

Seq. ID LIB3168-023-P1-K1-G11

Method BLASTX NCBI GI g3860261 BLAST score 314 E value 7.0e-29 Match length 115 % identity 63

NCBI Description (AC005824) putative acidic ribosomal protein [Arabidopsis

thaliana]

Seq. No. 143143

LIB3168-023-P1-K1-G12 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 625 E value 2.0e-65 Match length 120 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143144

Seq. ID LIB3168-023-P1-K1-G2

Method BLASTX g112681 NCBI GI BLAST score 746 E value 2.0e-79 Match length 142 % identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143145

Seq. ID LIB3168-023-P1-K1-G3

Method BLASTX NCBI GI g2244749 BLAST score 325 E value 3.0e-54Match length 111 % identity

NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 143146

Seq. ID LIB3168-023-P1-K1-G4



Method BLASTX
NCBI GI g1628583
BLAST score 568
E value 1.0e-58
Match length 141
% identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143147

Seq. ID LIB3168-023-P1-K1-G5

Method BLASTX
NCBI GI g112682
BLAST score 612
E value 6.0e-64
Match length 116
% identity 100

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143148

Seq. ID LIB3168-023-P1-K1-G6

Method BLASTX
NCBI GI g1169476
BLAST score 633
E value 3.0e-66
Match length 121
% identity 100

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE

ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632)

vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No. 143149

Seq. ID LIB3168-023-P1-K1-H1

Method BLASTX
NCBI GI g1628583
BLAST score 569
E value 8.0e-59
Match length 141
% identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143150

Seq. ID LIB3168-023-P1-K1-H10

Method BLASTX
NCBI GI g1628583
BLAST score 212
E value 6.0e-17
Match length 78
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis



thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143151

Seq. ID LIB3168-023-P1-K1-H11

Method BLASTX
NCBI GI g4204277
BLAST score 684
E value 3.0e-72
Match length 126
% identity 100

NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 143152

Seq. ID LIB3168-023-P1-K1-H12

Method BLASTX
NCBI GI g2117937
BLAST score 521
E value 5.0e-56
Match length 128
% identity 83

NCBI Description UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose

pyrophosphorylase [Hordeum vulgare]

Seq. No. 143153

Seq. ID LIB3168-023-P1-K1-H3

Method BLASTX
NCBI GI g112682
BLAST score 556
E value 2.0e-57
Match length 125
% identity 85

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__\$08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143154

Seq. ID LIB3168-023-P1-K1-H4

Method BLASTX
NCBI GI g1345973
BLAST score 471
E value 3.0e-47
Match length 111
% identity 78

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

17627



Seq. No. 143155

Seq. ID LIB3168-023-P1-K1-H6

Method BLASTX
NCBI GI g112681
BLAST score 525
E value 1.0e-53
Match length 134
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143156

Seq. ID LIB3168-023-P1-K1-H8

Method BLASTX
NCBI GI g1172556
BLAST score 217
E value 2.0e-17
Match length 82
% identity 49

NCBI Description 36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN

(VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 36) >gi_629729_pir__ S46925 porin II, 36K - potato >gi_1076681_pir__ B55364 porin (clone pPOM 36.2) - potato mitochondrion >gi 515360 emb CAA56600 (X80387) 36kDA porin

II [Solanum tuberosum]

Seq. No. 143157

Seq. ID LIB3168-024-P1-K1-A11

Method BLASTN
NCBI GI g4512656
BLAST score 406
E value 0.0e+00
Match length 406
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic

sequence, complete sequence

Seq. No. 143158

Seq. ID LIB3168-024-P1-K1-A12

Method BLASTX
NCBI GI g112682
BLAST score 574
E value 2.0e-59
Match length 134
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143159

Seq. ID LIB3168-024-P1-K1-A2

Method BLASTN



NCBI GI q3402695 BLAST score 259 1.0e-144 E value Match length 400 % identity 100 NCBI Description Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 143160 Seq. ID LIB3168-024-P1-K1-A3 Method BLASTX NCBI GI g112681 BLAST score 689 E value 7.0e-73 Match length 137

% identity 99 NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir \$08509 cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143161 Seq. ID LIB3168-024-P1-K1-A4 Method BLASTX NCBI GI q2708750 BLAST score 310 E value 2.0e-28

Match length 128 % identity 54

NCBI Description (AC003952) putative physical impedence protein [Arabidopsis

thaliana]

Seq. No. 143162

Seq. ID LIB3168-024-P1-K1-A5

Method BLASTX NCBI GI g112681 BLAST score 581 E value 3.0e-60 Match length 134 % identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143163

Seq. ID LIB3168-024-P1-K1-A6

Method BLASTN NCBI GI g1813353 BLAST score 206 1.0e-112 E value Match length 290 % identity 98

NCBI Description Arabidopsis thaliana AtCR20-1 mRNA

% identity

NCBI Description

95

fragment No



```
Seq. No.
                  143164
Seq. ID
                  LIB3168-024-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g2769642
BLAST score
                  554
E value
                  4.0e-57
Match length
                  131
% identity
                  77
NCBI Description
                  (Z97215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon
                  esculentum]
Seq. No.
                  143165
Seq. ID
                  LIB3168-024-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  625
E value
                  2.0e-65
Match length
                  120
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143166
Seq. ID
                  LIB3168-024-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g2129657
BLAST score
                  315
E value
                  4.0e-29
Match length
                  93
% identity
                  73
NCBI Description
                  oleosin isoform - Arabidopsis thaliana
                  >gi 987014 emb_CAA90877_ (Z54164) oleosin [Arabidopsis
                  thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin
                   [Arabidopsis thaliana]
Seq. No.
                  143167
Seq. ID
                  LIB3168-024-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q4589972
BLAST score
                  228
                  7.0e-19
E value
Match length
                  95
% identity
                  67
NCBI Description
                   (AC007195) putative indole-3 acetic acid induced protein
                   (ARG7) [Arabidopsis thaliana]
Seq. No.
                  143168
Seq. ID
                  LIB3168-024-P1-K1-B10
Method
                  BLASTN
NCBI GI
                  g2244991
BLAST score
                  322
E value
                  0.0e+00
Match length
                  402
```

17630

Arabidopsis thaliana DNA chromosome 4, ESSA I contig



```
Seq. No.
                  143169
Seq. ID
                  LIB3168-024-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g1350768
BLAST score
                  452
                  4.0e-45
E value
Match length
                  105
% identity
                  86
NCBI Description 60S RIBOSOMAL PROTEIN L7A
                  143170
Seq. No.
Seq. ID
                  LIB3168-024-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g1399277
BLAST score
                  479
                  2.0e-48
E value
Match length
                  92
                  99
% identity
NCBI Description
                  (U31836) calmodulin-domain protein kinase CDPK isoform 7
                  [Arabidopsis thaliana]
Seq. No.
                  143171
                  LIB3168-024-P1-K1-B2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3172156
BLAST score
                  278
                  1.0e-155
E value
Match length
                  282
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome 1 BAC T22J18 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  143172
Seq. ID
                  LIB3168-024-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g82426
BLAST score
                  522
                  3.0e-53
E value
Match length
                  106
% identity
                  46
NCBI Description
                  ubiquitin precursor - barley (fragment)
                  >gi_755763_emb_CAA27751_ (X04133) ubiquitin polyprecursor
                  (171 aa) [Hordeum vulgare]
Seq. No.
                  143173
Seq. ID
                  LIB3168-024-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g3150407
BLAST score
                  511
E value
                  5.0e-52
                  97
Match length
% identity
                  100
NCBI Description (AC004165) hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 143174

Seq. ID LIB3168-024-P1-K1-B5



```
Method BLASTX
NCBI GI g1628583
BLAST score 649
E value 4.0e-68
Match length 131
% identity 95
NCBI Description (U66916) thaliana
```

ription (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

NCBI GI g112741
BLAST score 685
E value 2.0e-72
Match length 128
% identity 99

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -

Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143176

Seq. ID LIB3168-024-P1-K1-B9

Method BLASTX
NCBI GI g2961390
BLAST score 541
E value 1.0e-55
Match length 101
% identity 99

NCBI Description (AL022141) beta-galactosidase like protein [Arabidopsis

thaliana]

Seq. No. 143177

Seq. ID LIB3168-024-P1-K1-C1

Method BLASTX
NCBI GI g2499298
BLAST score 321
E value 4.0e-30
Match length 65
% identity 100

NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 6, CHLOROPLAST

>gi_1619279_emb_CAA67670_ (X99278) ndhG [Arabidopsis

thaliana]

Seq. No. 143178

Seq. ID LIB3168-024-P1-K1-C11

Method BLASTX
NCBI GI g1107501
BLAST score 404
E value 2.0e-39
Match length 99
% identity 82



NCBI Description (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)

Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from

this gene. [Arabidopsis thaliana]

Seq. No. 143179

Seq. ID LIB3168-024-P1-K1-C12

Method BLASTX
NCBI GI g3023848
BLAST score 604
E value 6.0e-63
Match length 119
% identity 59

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis

thaliana]

Seq. No. 143180

Seq. ID LIB3168-024-P1-K1-C3

Method BLASTN
NCBI GI g2924257
BLAST score 60
E value 5.0e-25
Match length 88
% identity 92

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 143181

Seq. ID LIB3168-024-P1-K1-C4

Method BLASTX
NCBI GI g112681
BLAST score 560
E value 9.0e-58
Match length 131
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143182

Seq. ID LIB3168-024-P1-K1-C5

Method BLASTX
NCBI GI g1628583
BLAST score 533
E value 1.0e-54
Match length 136
% identity 78

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143183

Seq. ID LIB3168-024-P1-K1-C8

Method BLASTX



NCBI GI q1628583 BLAST score 437 E value 2.0e-43 Match length 106 % identity 82

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143184

Seq. ID LIB3168-024-P1-K1-C9

Method BLASTX NCBI GI g112681 BLAST score 560 E value 9.0e-58 Match length 131 % identity 83

12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir \$08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143185

LIB3168-024-P1-K1-D1 Seq. ID

Method BLASTX NCBI GI g117238 BLAST score 374 E value 6.0e-36 Match length 115 % identity 71

MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN NCBI Description

CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE)

>gi 81656 pir S12785 protein ch-42 precursor, chloroplast - Arabidopsis thaliana >gi_1020100_emb_CAA62754 (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi 2832653 emb CAA16728 (AL021710) protein ch-42

precursor, chloroplast [Arabidopsis thaliana]

>gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein
[Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene

[Euglena gracilis]

Seq. No. 143186

Seq. ID LIB3168-024-P1-K1-D11

Method BLASTN g4103953 NCBI GI BLAST score 405 E value 0.0e + 00Match length 405 % identity 100

NCBI Description Arabidopsis thaliana A37 (A37) gene, complete cds

Seq. No. 143187

Seq. ID LIB3168-024-P1-K1-D12

Method BLASTX NCBI GI g1628583 BLAST score 540



E value 2.0e-55
Match length 135
% identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143188

Seq. ID LIB3168-024-P1-K1-D2

Method BLASTX
NCBI GI g112681
BLAST score 506
E value 2.0e-51
Match length 136
% identity 78

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143189

Seq. ID LIB3168-024-P1-K1-D4

Method BLASTX
NCBI GI g133841
BLAST score 403
E value 2.0e-39
Match length 90
% identity 91

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S18 >gi_71016_pir__R3NT18

ribosomal protein S18 - common tobacco chloroplast
>gi_11851_emb_CAA77371_ (Z00044) ribosomal protein S18
[Nicotiana tabacum] >gi_225220_prf__1211235BB ribosomal

protein S18 [Nicotiana tabacum]

Seq. No. 143190

Seq. ID LIB3168-024-P1-K1-D5

Method BLASTX
NCBI GI g112737
BLAST score 554
E value 5.0e-57
Match length 134
% identity 81

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143191

Seq. ID LIB3168-024-P1-K1-D6

Method BLASTX
NCBI GI g1628583
BLAST score 601
E value 1.0e-62



Match length 124 % identity 93

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143192

Seq. ID LIB3168-024-P1-K1-D7

Method BLASTX
NCBI GI g3142300
BLAST score 371
E value 1.0e-35
Match length 134
% identity 55

NCBI Description (AC002411) Contains similarity to pre-mRNA processing

protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this

gene. [Arabidopsis thaliana]

Seq. No. 143193

Seq. ID LIB3168-024-P1-K1-E1

Method BLASTX
NCBI GI g4678299
BLAST score 646
E value 8.0e-68
Match length 126
% identity 100

NCBI Description (AL049655) cysteine proteinase precursor-like protein

[Arabidopsis thaliana]

Seq. No. 143194

Seq. ID LIB3168-024-P1-K1-E10

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143195

Seq. ID LIB3168-024-P1-K1-E11

Method BLASTX
NCBI GI g625509
BLAST score 612
E value 7.0e-64
Match length 123
% identity 25

NCBI Description ubiquitin precursor - Arabidopsis thaliana (fragment)

Seq. No. 143196

Seq. ID LIB3168-024-P1-K1-E12

Method BLASTX NCBI GI g3150414 BLAST score 485

17636



E value 6.0e-49 Match length 111 % identity 89

NCBI Description (AC004165) AtRanBPlb protein [Arabidopsis thaliana]

Seq. No. 143197

Seq. ID LIB3168-024-P1-K1-E2

Method BLASTX
NCBI GI g112743
BLAST score 580
E value 4.0e-60
Match length 126
% identity 87

NCBI Description 2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_

(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4

precursor [Arabidopsis thaliana]

Seq. No. 143198

Seq. ID LIB3168-024-P1-K1-E3

Method BLASTX
NCBI GI g2129657
BLAST score 437
E value 2.0e-43
Match length 117
% identity 79

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
thaliana] >gi 987016_emb_CAA90878_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 143199

Seq. ID LIB3168-024-P1-K1-E4

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143200

Seq. ID LIB3168-024-P1-K1-E5

Method BLASTX
NCBI GI g4388826
BLAST score 200
E value 1.0e-15
Match length 82
% identity 51

NCBI Description (AC006528) hypothetical protein [Arabidopsis thaliana]

Seq. No. 143201



Seq. ID LIB3168-024-P1-K1-E6 Method BLASTX

NCBI GI g1628583 BLAST score 420 E value 2.0e-41 Match length 79 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143202

Seq. ID LIB3168-024-P1-K1-E7

Method BLASTN
NCBI GI g2832639
BLAST score 191
E value 1.0e-103
Match length 338
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12

(ESSAII project)

Seq. No. 143203

Seq. ID LIB3168-024-P1-K1-E9

Method BLASTX
NCBI GI g112741
BLAST score 411
E value 5.0e-44
Match length 100
% identity 90

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__ NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143204

Seq. ID LIB3168-024-P1-K1-F1

Method BLASTX
NCBI GI g3123188
BLAST score 661
E value 1.0e-69
Match length 129
% identity 98

NCBI Description CATALASE 3 >gi 2347178 (U43147) catalase 3 [Arabidopsis

thaliana] >gi 2511726 (AF021937) catalase 3 [Arabidopsis

thaliana]

Seq. No. 143205

Seq. ID LIB3168-024-P1-K1-F10

Method BLASTX
NCBI GI g112682
BLAST score 564
E value 3.0e-58
Match length 132



>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143206

Seq. ID LIB3168-024-P1-K1-F11

Method BLASTX
NCBI GI g112741
BLAST score 691
E value 4.0e-73
Match length 128
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868_

÷.

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143207

Seq. ID LIB3168-024-P1-K1-F12

Method BLASTX
NCBI GI g1628583
BLAST score 569
E value 8.0e-59
Match length 120
% identity 92

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143208

Seq. ID LIB3168-024-P1-K1-F2

Method BLASTN
NCBI GI g4220643
BLAST score 239
E value 1.0e-132
Match length 300
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 143209

Seq. ID LIB3168-024-P1-K1-F3

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]



Seq. No. 143210

LIB3168-024-P1-K1-F4 Seq. ID

Method BLASTX g1628583 NCBI GI 625 BLAST score 2.0e-65 E value 120 Match length 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143211

Seq. ID LIB3168-024-P1-K1-F6

Method BLASTX q1628583 NCBI GI BLAST score 442 3.0e-63 E value Match length 137 % identity 89

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495 emb_CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143212

LIB3168-024-P1-K1-F8 Seq. ID

BLASTX Method NCBI GI q112741 BLAST score 682 5.0e-72 E value Match length 127 99 % identity

2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi 68855 pir_NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143213

LIB3168-024-P1-K1-G1 Seq. ID

BLASTX Method g112739 NCBI GI BLAST score 425 E value 6.0e-42121 Match length 71 % identity

2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]



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143214
Seq. No.
                  LIB3168-024-P1-K1-G10
Seq. ID
Method
                  BLASTX
                                                      Ť.
                  g166570
NCBI GI
                  253
BLAST score
                  9.0e-22
E value
                  107
Match length
                  50
% identity
                  (L04173) glycine rich protein [Arabidopsis thaliana]
NCBI Description
                  143215
Seq. No.
                  LIB3168-024-P1-K1-G2
Seq. ID
                  BLASTX
Method
                  g112681
NCBI GI
BLAST score
                  592
                  2.0e-70
E value
                  134
Match length
                  99
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  143216
Seq. No.
                  LIB3168-024-P1-K1-G3
Seq. ID
                  BLASTX
Method
                  g112682
NCBI GI
BLAST score
                  545
                  5.0e-56
E value
                  129
Match length
                  81
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  143217
Seq. ID
                  LIB3168-024-P1-K1-G4
Method
                  BLASTN
NCBI GI
                  q16472
BLAST score
                   399
                  0.0e + 00
E value
Match length
                   407
                  100
% identity
NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type
Seq. No.
                   143218
Seq. ID
                  LIB3168-024-P1-K1-G5
Method
                  BLASTX
```

Method BLASTX
NCBI GI g112737
BLAST score 566
E value 2.0e-58
Match length 136
% identity 81

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE



PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No. 143219

Seq. ID LIB3168-024-P1-K1-G6

Method BLASTX
NCBI GI g3096920
BLAST score 644
E value 1.0e-67
Match length 126
% identity 100

NCBI Description (AL023094) putative ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 143220

Seq. ID LIB3168-024-P1-K1-G7

Method BLASTX
NCBI GI g1628583
BLAST score 512
E value 4.0e-52
Match length 132
% identity 77

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143221

Seq. ID LIB3168-024-P1-K1-G8

Method BLASTN
NCBI GI g419934
BLAST score 277
E value 1.0e-154
Match length 319
% identity 98

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 143222

Seq. ID LIB3168-024-P1-K1-H1

Method BLASTX
NCBI GI g112737
BLAST score 537
E value 5.0e-55
Match length 131
% identity 79

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No.



```
Seq. No.
                  143223
                  LIB3168-024-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832625
BLAST score
                  226
                  1.0e-18
E value
Match length
                  66
                  62
% identity
NCBI Description
                  (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  143224
                  LIB3168-024-P1-K1-H11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  504
E value
                  3.0e-51
Match length
                  111
% identity
                  87
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143225
                  LIB3168-024-P1-K1-H12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4199934
BLAST score
                  357
                  0.0e + 00
E value
Match length
                  409
                  97
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
                  143226
Seq. No.
                  LIB3168-024-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169476
BLAST score
                  585
E value
                  1.0e-60
Match length
                  119
% identity
                  95
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
NCBI Description
                  ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)
                  vitronectin-like adhesion protein [Nicotiana tabacum]
Seq. No.
                  143227
                  LIB3168-024-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4008006
BLAST score
                  282
E value
                  4.0e-25
Match length
                  128
% identity
NCBI Description
                  (AF084034) receptor-like protein kinase [Arabidopsis
```

17643

thaliana]

143228



```
LIB3168-024-P1-K1-H4
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  44
                  4.0e-60
E value
Match length
                  120
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143229
                  LIB3168-024-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
E value
                  2.0e-65
Match length
                  120
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143230
                  LIB3168-024-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  682
E value
                  4.0e-72
Match length
                  132
% identity
                  98
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143231
                  LIB3168-024-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3859607
BLAST score
                  496
E value
                  3.0e-50
```

Match length 116 84 % identity

(AF104919) contains similarity to cysteine proteases (Pfam: NCBI Description

PF00112, E=.21, N=1) [Arabidopsis thaliana]

Seq. No. 143232

Seq. ID LIB3168-024-P1-K1-H8

Method BLASTX NCBI GI q1628583 BLAST score 252 E value 1.0e-21 Match length 71 99 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]



```
143233
Seq. No.
Seq. ID
                  LIB3168-024-P1-K1-H9
Method
                  BLASTX
                  g112681
NCBI GI
BLAST score
                  718
                  3.0e-76
E value
Match length
                  135
% identity
                  99
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__$08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  143234
                  LIB3168-025-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  481
                  2.0e-48
E value
Match length
                  90
                  100
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143235
                  LIB3168-025-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  686
E value
                  1.0e-72
Match length
                  130
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143236
Seq. ID
                  LIB3168-025-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g4587529
BLAST score
                  46
                  7.0e-33
E value
Match length
                  97
% identity
                  77
NCBI Description
                  (AC007060) Strong similarity to F19I3.2 gi_3033375 putative
                  berberine bridge enzyme from Arabidopsis thaliana BAC
```

gb_AC004238. EST gb_H76902 comes from this gene

Seq. No.

Seq. ID LIB3168-025-P1-K1-A2

143237

Method BLASTX
NCBI GI g1628583
BLAST score 541
E value 2.0e-55



Match length 103 % identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143238

Seq. ID LIB3168-025-P1-K1-A5

Method BLASTX
NCBI GI g1628583
BLAST score 350
E value 1.0e-33
Match length 70
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143239

Seq. ID LIB3168-025-P1-K1-A6

Method BLASTX
NCBI GI g1628583
BLAST score 502
E value 4.0e-51
Match length 113
% identity 86

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143240

Seq. ID LIB3168-025-P1-K1-A7

Method BLASTX
NCBI GI g112682
BLAST score 575
E value 2.0e-59
Match length 133
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143241

Seq. ID LIB3168-025-P1-K1-A8

Method BLASTX
NCBI GI g2996096
BLAST score 527
E value 5.0e-54
Match length 101
% identity 99

NCBI Description (AF030517) translation elongation factor-1 alpha; EF-1

alpha [Oryza sativa]

Seq. No. 143242

Seq. ID LIB3168-025-P1-K1-A9



Method BLASTX
NCBI GI g2959781
BLAST score 683
E value 3.0e-72
Match length 133
% identity 96

NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No. 143243

Seq. ID LIB3168-025-P1-K1-B1

Method BLASTX
NCBI GI g3915866
BLAST score 187
E value 6.0e-14
Match length 57
% identity 77

NCBI Description GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)

>gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine

synthetase [Lupinus luteus]

Seq. No. 143244

Seq. ID LIB3168-025-P1-K1-B10

Method BLASTX
NCBI GI g112681
BLAST score 652
E value 1.0e-68
Match length 132
% identity 98

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143245

Seq. ID LIB3168-025-P1-K1-B11

Method BLASTN
NCBI GI g16231
BLAST score 191
E value 1.0e-103
Match length 211
% identity 98

NCBI Description Arabidopsis CRA1 gene for 12S seed storage protein

>qi 166675 gb M37247 ATHCRA1AA A.thaliana 12S storage

protein CRA1 gene, exons 1-4

Seq. No. 143246

Seq. ID LIB3168-025-P1-K1-B12

Method BLASTN
NCBI GI g3540210
BLAST score 254
E value 1.0e-141
Match length 372
% identity 98

NCBI Description Arabidopsis thaliana chromosome I BAC F5A8 genomic

sequence, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                     143247
                     LIB3168-025-P1-K1-B3
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     g112741
  BLAST score
                     680
  E value
                     8.0e-72
  Match length
                     126
                     100
   % identity
NCBI Description
                     2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                     PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                     Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                     3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                     (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                     >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                     precursor [Arabidopsis thaliana]
   Seq. No.
                     143248
                     LIB3168-025-P1-K1-B4
   Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g1628583
  BLAST score
                     571
                     8.0e-63
  E value
  Match length
                     127
                     98
   % identity
  NCBI Description
                     (U66916) 12S cruciferin seed storage protein [Arabidopsis
                     thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                     cruciferin seed storage protein [Arabidopsis thaliana]
  Seq. No.
                     143249
  Seq. ID
                     LIB3168-025-P1-K1-B5
  Method
                     BLASTX
  NCBI GI
                     g112681
  BLAST score
                     517
  E value
                     1.0e-52
  Match length
                     133
  % identity
                     80
  NCBI Description
                     12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                     cruciferin precursor (CRA1) - Arabidopsis thaliana
                     >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                     thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                     storage protein [Arabidopsis thaliana]
  Seq. No.
                     143250
  Seq. ID
                     LIB3168-025-P1-K1-B6
  Method
                     BLASTX
  NCBI GI
                     g4006897
  BLAST score
                     567
  E value
                     1.0e-58
```

Match length 119 % identity

NCBI Description (Z99708) globulin-like protein [Arabidopsis thaliana]

Seq. No.

143251

Seq. ID LIB3168-025-P1-K1-B7

Method BLASTX NCBI GI g1628583 BLAST score 398



E value 7.0e-39 Match length 112 % identity 72

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143252

Seq. ID LIB3168-025-P1-K1-B8

Method BLASTX
NCBI GI g1628583
BLAST score 196
E value 4.0e-15
Match length 70
% identity 94

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143253

Seq. ID LIB3168-025-P1-K1-B9

Method BLASTX
NCBI GI g1628583
BLAST score 444
E value 3.0e-44
Match length 94
identity 91

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143254

Seq. ID LIB3168-025-P1-K1-C1

Method BLASTX
NCBI GI g1143511
BLAST score 429
E value 2.0e-42
Match length 82
% identity 96

NCBI Description (Z47076) Ser/Thr protein phosphatase homologous to PPX

[Malus domestica] >gi_1586034_prf__2202340A Ser/Thr protein

phosphatase [Malus domestica]

Seq. No. 143255

Seq. ID LIB3168-025-P1-K1-C11

Method BLASTN
NCBI GI g4589409
BLAST score 173
E value 2.0e-92
Match length 398
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F17P19, complete sequence

Seq. No. 143256

Seq. ID LIB3168-025-P1-K1-C2

Method BLASTX



```
NCBI GI
                  g112739
BLAST score
                  429
E value
                  2.0e-42
Match length
                  122
% identity
                  71
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) > gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >qi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  143257
Seq. ID
                  LIB3168-025-P1-K1-C3
Method
                  BLASTX
                  g2914710
NCBI GI
BLAST score
                  709
                  3.0e-75
E value
Match length
                  135
% identity
                  100
                  (AC003974) putative beta-D-galactosidase [Arabidopsis
NCBI Description
                  thaliana]
                  143258
Seq. No.
Seq. ID
                  LIB3168-025-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  334
                  2.0e-31
E value
                  95
Match length
                  73
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  143259
Seq. ID
                  LIB3168-025-P1-K1-C5
```

Method BLASTX

g112737 NCBI GI BLAST score 605 E value 5.0e-63 Match length 129 % identity 89 NCBI Description

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143260

Seq. ID LIB3168-025-P1-K1-C6

Method BLASTX



```
NCBI GI
                   g1865677
BLAST score
                   683
E value
                   3.0e-72
Match length
                   133
                   100
% identity
                   (Y08568) trehalose-6-phosphate synthase [Arabidopsis
NCBI Description
                   thaliana]
                   143261
Seq. No.
                   LIB3168-025-P1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   581
E value
                   3.0e-60
Match length
                   110
                   100
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   143262
                   LIB3168-025-P1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g633890
BLAST score
                   290
E value
                   4.0e-26
Match length
                   98
% identity
                   61
NCBI Description
                   (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
                   vulgare]
                   143263
Seq. No.
                   LIB3168-025-P1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g112741
BLAST score
                   680
E value
                   8.0e-72
Match length
                   126
% identity
                   100
NCBI Description
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                   PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                   Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
Seq. No.
                   143264
Seq. ID
                   LIB3168-025-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g1526424
BLAST score
                   170
```

E value 5.0e-12 59 Match length % identity 33

NCBI Description (D64140) LEA protein in group 3 [Arabidopsis thaliana]



Seq. No. 143265

Seq. ID LIB3168-025-P1-K1-D2

Method BLASTX
NCBI GI g112681
BLAST score 573
E value 3.0e-59
Match length 117
% identity 93

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143266

Seq. ID LIB3168-025-P1-K1-D3

Method BLASTX
NCBI GI g1628583
BLAST score 668
E value 2.0e-70
Match length 128
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143267

Seq. ID LIB3168-025-P1-K1-D4

Method BLASTX
NCBI GI g112682
BLAST score 553
E value 6.0e-57
Match length 118
% identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143268

Seq. ID LIB3168-025-P1-K1-D5

Method BLASTX
NCBI GI g1628583
BLAST score 590
E value 3.0e-61
Match length 129
% identity 88

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143269

Seq. ID LIB3168-025-P1-K1-D6

Method BLASTX
NCBI GI g3322615
BLAST score 155



```
E value 3.0e-10
Match length 130
% identity 32
```

NCBI Description (AE001213) folylpolyglutamate synthetase (folC) [Treponema

pallidum]

NCBI GI g112682
BLAST score 389
E value 6.0e-38
Match length 88
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143271

Seq. ID LIB3168-025-P1-K1-D8

Method BLASTX
NCBI GI g112743
BLAST score 322
E value 4.0e-30
Match length 77
% identity 79

NCBI Description 2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi 395202 emb_CAA80869_

(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]

>gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4

precursor [Arabidopsis thaliana]

Seq. No. 143272

Seq. ID LIB3168-025-P1-K1-D9

Method BLASTX
NCBI GI g112681
BLAST score 560
E value 9.0e-58
Match length 131
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143273

Seq. ID LIB3168-025-P1-K1-E1

Method BLASTN
NCBI GI g3449331
BLAST score 40
E value 4.0e-13
Match length 429



% identity 37
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
MNC17, complete sequence [Arabidopsis thaliana]

 Seq. No.
 143274

 Seq. ID
 LIB3168-025-P1-K1-E10

 Method
 BLASTX

 NCBI GI
 g1628583

 PLACE - 2002
 300

BLAST score 388
E value 1.0e-37
Match length 77
% identity 96

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143275

Seq. ID LIB3168-025-P1-K1-E12

Method BLASTX
NCBI GI g112681
BLAST score 534
E value 1.0e-54
Match length 127
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143276

Seq. ID LIB3168-025-P1-K1-E2

Method BLASTX
NCBI GI g1628583
BLAST score 644
E value 1.0e-67
Match length 129
% identity 96

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143277

Seq. ID LIB3168-025-P1-K1-E3

Method BLASTX
NCBI GI g4204298
BLAST score 533
E value 1.0e-54
Match length 120
% identity 86

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 143278

Seq. ID LIB3168-025-P1-K1-E4

Method BLASTX NCBI GI g112682

17654



BLAST score 501 E value 5.0e-51 Match length 106 % identity 89

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143279

Seq. ID LIB3168-025-P1-K1-E5

Method BLASTX
NCBI GI g112740
BLAST score 213
E value 4.0e-17
Match length 108
% identity 47

NCBI Description NAPIN 2 PRECURSOR (1.7S SEED STORAGE PROTEIN)

>gi 81691 pir A25997 napin precursor (napA) - rape

>gi_167153 (J02586) prepronapin [Brassica napus] >gi_167155

(J02798) napin [Brassica napus]

Seq. No. 143280

Seq. ID LIB3168-025-P1-K1-E6

Method BLASTX
NCBI GI g112681
BLAST score 302
E value 1.0e-27
Match length 71
% identity 80

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143281

Seq. ID LIB3168-025-P1-K1-E7

Method BLASTN
NCBI GI g16473
BLAST score 257
E value 1.0e-142
Match length 300
% identity 45

NCBI Description Arabidopsis thaliana 25S-18S ribosomal DNA spacer

Seq. No. 143282

Seq. ID LIB3168-025-P1-K1-E8

Method BLASTX
NCBI GI g112737
BLAST score 479
E value 3.0e-48
Match length 103
% identity 88

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -



Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

143283 Seq. No. LIB3168-025-P1-K1-E9 Seq. ID Method BLASTX NCBI GI g112681 BLAST score 464 2.0e-46 E value Match length 116

79

% identity NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143284

Seq. ID LIB3168-025-P1-K1-F1

Method BLASTX NCBI GI q1800307 BLAST score 170 E value 5.0e-12 Match length 108 % identity 24

NCBI Description (U83883) pl05 coactivator [Rattus norvegicus]

Seq. No. 143285

LIB3168-025-P1-K1-F12 Seq. ID

Method BLASTN NCBI GI g3282170 BLAST score 146 E value 2.0e-76 Match length 388 % identity 95

NCBI Description Arabidopsis thaliana chromosome 1 BAC F8K4 sequence,

complete sequence [Arabidopsis thaliana]

143286 Seq. No.

Seq. ID LIB3168-025-P1-K1-F2

Method BLASTX NCBI GI q1628583 BLAST score 493 E value 4.0e-50 Match length 101 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

> thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143287

Seq. ID LIB3168-025-P1-K1-F3

Method BLASTX NCBI GI g1628583



```
BLAST score 511
E value 5.0e-52
Match length 133
% identity 77
```

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143288

Seq. ID LIB3168-025-P1-K1-F5

Method BLASTX
NCBI GI g1628583
BLAST score 461
E value 3.0e-46
Match length 120
% identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143289

Seq. ID LIB3168-025-P1-K1-F6

Method BLASTX
NCBI GI g1628583
BLAST score 669
E value 1.0e-70
Match length 129
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143290

Seq. ID LIB3168-025-P1-K1-F7

Method BLASTX
NCBI GI g112737
BLAST score 536
E value 6.0e-55
Match length 130
% identity 80

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__ NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143291

Seq. ID LIB3168-025-P1-K1-F9

Method BLASTX
NCBI GI 94204299
BLAST score 399
E value 5.0e-39
Match length 81
% identity 98

NCBI Description (AC003027) lcl prt seq No definition line found



[Arabidopsis thaliana]

```
Seq. No.
                  143292
Seq. ID
                  LIB3168-025-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
E value
                  2.0e-65
Match length
                  120
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143293
Seq. ID
                  LIB3168-025-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  509
E value
                  8.0e-52
Match length
                  131
% identity
                  78
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143294
                  LIB3168-025-P1-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3510347
BLAST score
                  397
E value
                  0.0e + 00
Match length
                  401
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSJ11, complete sequence [Arabidopsis thaliana]
                  143295
Seq. No.
Seq. ID
                  LIB3168-025-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g4204299
BLAST score
                  702
                  2.0e-74
E value
Match length
                  133
                  100
% identity
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  143296
Seq. No.
Seq. ID
                  LIB3168-025-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  58
                  7.0e-42
E value
Match length
                  125
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
```

NCBI GI

E value

BLAST score

Match length

% identity

g112681

1.0e-58

567

131

84



thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143297 LIB3168-025-P1-K1-G4 Seq. ID Method BLASTN g4097693 NCBI GI 87 BLAST score E value 3.0e-41 Match length 155 % identity 90 Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete NCBI Description Seq. No. 143298 LIB3168-025-P1-K1-G5 Seq. ID Method BLASTN q3985949 NCBI GI BLAST score 84 E value 2.0e-39 236 Match length 95 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana] 143299 Seq. No. LIB3168-025-P1-K1-G6 Seq. ID BLASTX Method NCBI GI g1628583 BLAST score 618 E value 1.0e-64 120 Match length 99 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143300 LIB3168-025-P1-K1-G7 Seq. ID Method BLASTX q1628583 NCBI GI BLAST score 597 E value 4.0e-62 Match length 114 % identity 100 (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143301 Seq. ID LIB3168-025-P1-K1-G8 Method BLASTX

17659



12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 143302 LIB3168-025-P1-K1-G9 Seq. ID Method BLASTX NCBI GI g112681 BLAST score 530 E value 3.0e-54Match length 127 % identity 82 NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 143303 LIB3168-025-P1-K1-H10 Seq. ID Method BLASTN NCBI GI g4199934 BLAST score 277 E value 1.0e-154 Match length 366 % identity 90 NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana] Seq. No. 143304 Seq. ID LIB3168-025-P1-K1-H11 Method BLASTX NCBI GI g1628583 BLAST score 625 2.0e-65 E value Match length 120 % identity 100 NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143305 Seq. ID LIB3168-025-P1-K1-H12 Method BLASTN NCBI GI g3449331 BLAST score 295

E value 1.0e-165 Match length 342 % identity 28

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNC17, complete sequence [Arabidopsis thaliana]

Seq. No. 143306

Seq. ID LIB3168-025-P1-K1-H2

Method BLASTX



NCBI GI g1628583 BLAST score 356 E value 8.0e-34 Match length 66 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143307

Seq. ID LIB3168-025-P1-K1-H3

Method BLASTX
NCBI GI g1628583
BLAST score 179
E value 4.0e-13
Match length 70
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143308

Seq. ID LIB3168-025-P1-K1-H4

Method BLASTX
NCBI GI g112741
BLAST score 680
E value 9.0e-72
Match length 126
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >qi 395201 emb CAA80868

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143309

Seq. ID LIB3168-025-P1-K1-H5

Method BLASTX
NCBI GI g112682
BLAST score 544
E value 7.0e-56
Match length 116
% identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605_pir__\$08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143310

Seq. ID LIB3168-025-P1-K1-H6

Method BLASTN
NCBI GI g3236234
BLAST score 359
E value 0.0e+00



Match length 375 % identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 143311

Seq. ID LIB3168-025-P1-K1-H8

Method BLASTX
NCBI GI g112741
BLAST score 655
E value 6.0e-69
Match length 125
% identity 98

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143312

Seq. ID LIB3168-025-P1-K1-H9

Method BLASTX
NCBI GI g112682
BLAST score 544
E value 7.0e-56
Match length 116
% identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143313

Seq. ID LIB3168-026-P1-K1-A10

Method BLASTX
NCBI GI g112737
BLAST score 526
E value 9.0e-54
Match length 129
% identity 79

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143314

Seq. ID LIB3168-026-P1-K1-A11

Method BLASTX NCBI GI g112741 BLAST score 680 E value 8.0e-72



```
Match length
                  126
% identity
                  100
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  143315
                  LIB3168-026-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  611
                  9.0e-64
E value
Match length
                  117
                  100
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143316
                  LIB3168-026-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  216
E value
                  1.0e-17
Match length
                  72
% identity
                  62
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  143317
Seq. ID
                  LIB3168-026-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g2129659
BLAST score
                  485
E value
                  6.0e-49
Match length
                  127
                  79
% identity
                  oleosin, isoform 21K - Arabidopsis thaliana >gi_725260
NCBI Description
                   (L40954) oleosin [Arabidopsis thaliana]
Seq. No.
                  143318
Seq. ID
                  LIB3168-026-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  371
```

6.0e-36 E value 75 Match length % identity 96

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S





cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143319 Seq. ID LIB3168-026-P1-K1-A5 Method BLASTX NCBI GI g112737 BLAST score 513 E value 3.0e-52 Match length 127 % identity 79 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana] Seq. No. 143320 Seq. ID LIB3168-026-P1-K1-A6 Method BLASTX NCBI GI q1628583 BLAST score 390 E value 4.0e-41 Match length 99 87 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143321 LIB3168-026-P1-K1-A7 Seq. ID BLASTX Method NCBI GI g112682 BLAST score 326 E value 2.0e-30 101 Match length % identity 66 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 NCBI Description cruciferin precursor (CRB) - Arabidopsis thaliana >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 143322 Seq. ID LIB3168-026-P1-K1-A8 Method BLASTX NCBI GI g1628583 BLAST score 375 E value 2.0e-42 Match length 102 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

Seq. No. 143323

cruciferin seed storage protein [Arabidopsis thaliana]



Seq. ID LIB3168-026-P1-K1-A9

Method BLASTX
NCBI GI g1628583
BLAST score 365
E value 5.0e-35
Match length 108
% identity 68

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143324

Seq. ID LIB3168-026-P1-K1-B1

Method BLASTX
NCBI GI g112682
BLAST score 564
E value 3.0e-58
Match length 132
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143325

Seq. ID LIB3168-026-P1-K1-B10

Method BLASTX
NCBI GI g112737
BLAST score 495
E value 4.0e-50
Match length 107
% identity 88

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143326

Seq. ID LIB3168-026-P1-K1-B11

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143327

Seq. ID LIB3168-026-P1-K1-B12

Method BLASTX NCBI GI g112681



BLAST score 489 E value 2.0e-49 Match length 134 % identity 78

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936 emb_CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143328

Seq. ID LIB3168-026-P1-K1-B2

Method BLASTX
NCBI GI g21112
BLAST score 225
E value 2.0e-18
Match length 48
% identity 85

NCBI Description (X59805) cruciferin [Raphanus sativus]

Seq. No. 143329

Seq. ID LIB3168-026-P1-K1-B3

Method BLASTX
NCBI GI g112681
BLAST score 457
E value 9.0e-46
Match length 118
% identity 76

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143330

Seq. ID LIB3168-026-P1-K1-B4

Method BLASTN
NCBI GI g2244950
BLAST score 244
E value 1.0e-135
Match length 345
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 143331

Seq. ID LIB3168-026-P1-K1-B5

Method BLASTX
NCBI GI g2058280
BLAST score 559
E value 1.0e-57
Match length 120
% identity 88

NCBI Description (X97381) atran3 [Arabidopsis thaliana]

Seq. No. 143332

Seq. ID LIB3168-026-P1-K1-B6

17666



Method BLASTX g112739 NCBI GI 461 -BLAST score E value 4.0e-46 Match length 117 -% identity 77 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >qi 68854 pir NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >qi 166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi 395205 emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2
precursor [Arabidopsis thaliana]

Seq. No. 143333

Seq. ID LIB3168-026-P1-K1-B7

Method BLASTX
NCBI GI g112681
BLAST score 570
E value 6.0e-59
Match length 133
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143334

Seq. ID LIB3168-026-P1-K1-B9

Method BLASTX
NCBI GI g1628583
BLAST score 639
E value 5.0e-67
Match length 129
% identity 95

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143335

Seq. ID LIB3168-026-P1-K1-C1

Method BLASTX
NCBI GI g1628583
BLAST score 620
E value 8.0e-65
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143336

Seq. ID LIB3168-026-P1-K1-C10

Method BLASTX
NCBI GI g1628583
BLAST score 557



E value 2.0e-57
Match length 107
% identity 97

NCBI Description (U66916) 125 cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143337

Seq. ID LIB3168-026-P1-K1-C11

Method BLASTX
NCBI GI g112681
BLAST score 538
E value 3.0e-55
Match length 127
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143338

Seq. ID LIB3168-026-P1-K1-C12

Method BLASTX
NCBI GI g1628583
BLAST score 631
E value 4.0e-66
Match length 125
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143339

Seq. ID LIB3168-026-P1-K1-C2

Method BLASTX
NCBI GI g112737
BLAST score 480
E value 2.0e-48
Match length 108
% identity 84

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143340

Seq. ID LIB3168-026-P1-K1-C3

Method BLASTX
NCBI GI 94468804
BLAST score 226
E value 7.0e-19
Match length 78
% identity 49



NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

143341 Seq. No. LIB3168-026-P1-K1-C5 Seq. ID Method BLASTX NCBI GI g112681 BLAST score 709 E value 3.0e-75 Match length 134 99 % identity

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

, r

storage protein [Arabidopsis thaliana]

Seq. No. 143342

Seq. ID LIB3168-026-P1-K1-C6

Method BLASTX
NCBI GI g1628583
BLAST score 638
E value 6.0e-67
Match length 125
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143343

Seq. ID LIB3168-026-P1-K1-C7

Method BLASTX
NCBI GI g112737
BLAST score 205
E value 4.0e-16
Match length 100
% identity 46

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__ NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143344

Seq. ID LIB3168-026-P1-K1-C9

Method BLASTX
NCBI GI g1628583
BLAST score 597
E value 3.0e-62
Match length 117
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143345

NCBI Description



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LIB3168-026-P1-K1-D1
Seq. ID
Method
                  BLASTX
                  g112681
NCBI GI
BLAST score
                  408
E value
                  6.0e-40
Match length
                  82
                  99
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  143346
Seq. ID
                  LIB3168-026-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g2317913
BLAST score
                  539
E value
                  2.0e-55
Match length
                  106
% identity
                  99
                  (U89959) cathepsin B-like cysteine proteinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  143347
Seq. ID
                  LIB3168-026-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g3273751
BLAST score
                  441
E value
                  8.0e-44
Match length
                  124
% identity
                  69
                  (AF061518) manganese superoxide dismutase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  143348
                  LIB3168-026-P1-K1-D12
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  366
E value
                  5.0e-35
Match length
                  99
                  75
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143349
Seq. ID
                  LIB3168-026-P1-K1-D2
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  654
E value
                  8.0e-69
Match length
                  127
% identity
                  98
```

(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S



cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143350 Seq. ID LIB3168-026-P1-K1-D3 Method BLASTN NCBI GI q4510392 BLAST score 201 E value 1.0e-109 Match length 217 % identity 98 NCBI Description Arabidopsis thaliana chromosome II BAC T17D12 genomic sequence, complete sequence

Seq. No. 143351

Seq. ID LIB3168-026-P1-K1-D4

Method BLASTX
NCBI GI g1628583
BLAST score 435
E value 2.0e-43
Match length 92
% identity 92

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143352

Seq. ID LIB3168-026-P1-K1-D5

Method BLASTX
NCBI GI g112741
BLAST score 556
E value 3.0e-57
Match length 125
% identity 86

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143353

Seq. ID LIB3168-026-P1-K1-D6

Method BLASTX
NCBI GI g112739
BLAST score 420
E value 2.0e-41
Match length 122
% identity 70

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]



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Seq. No.
                  143354
Seq. ID
                  LIB3168-026-P1-K1-D7
Method .
                 BLASTX
```

NCBI GI q112741 BLAST score 655 E value 7.0e-69 Match length 124 % identity 98

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

143355 Seq. No.

LIB3168-026-P1-K1-D8 Seq. ID

Method BLASTX g112682 NCBI GI BLAST score 615 E value 3.0e-64 133 Match length % identity

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >qi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143356

Seq. ID LIB3168-026-P1-K1-D9

Method BLASTX g112681 NCBI GI 558 BLAST score E value 2.0e-57 Match length 131 % identity 83

12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143357

Seq. ID LIB3168-026-P1-K1-E1

Method BLASTX NCBI GI q1628583 BLAST score 553 5.0e-57 E value Match length 115 % identity 95

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143358

Match length

% identity

100



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LIB3168-026-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  333
                  9.0e-32
E value
Match length
                  71
% identity
                  92
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143359
                  LIB3168-026-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  550
E value
                  1.0e-56
                  130
Match length
% identity
                  82
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir $08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  143360
Seq. ID
                  LIB3168-026-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g2829898
BLAST score
                  373
E value
                  8.0e-36
Match length
                  93
                  76
% identity
NCBI Description (AC002311) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  143361
Seq. ID
                  LIB3168-026-P1-K1-E2
Method
                  BLASTX
                  g112681
NCBI GI
BLAST score
                  589
E value
                  4.0e-61
Match length
                  121
% identity
                  93
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__$08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  143362
Seq. ID
                  LIB3168-026-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g1628583
                  522
BLAST score
E value
                  3.0e-53
```



NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein Arabidopsis thaliana]

Seq. No. 143363

Seq. ID LIB3168-026-P1-K1-E4

Method BLASTX
NCBI GI g112681
BLAST score 499
E value 1.0e-50
Match length 132
% identity 77

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143364

Seq. ID LIB3168-026-P1-K1-E5

Method BLASTX
NCBI GI g1628583
BLAST score 663
E value 7.0e-70
Match length 127
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143365

Seq. ID LIB3168-026-P1-K1-E6

Method BLASTN
NCBI GI 94589437
BLAST score 383
E value 0.0e+00
Match length 395
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MPN9, complete sequence

Seq. No. 143366

Seq. ID LIB3168-026-P1-K1-E7

Method BLASTX
NCBI GI g3242328
BLAST score 461
E value 4.0e-46
Match length 114
% identity 76

NCBI Description (X98083) cinnamoyl-CoA reductase [Zea mays]

Seq. No. 143367

Seq. ID LIB3168-026-P1-K1-E9

Method BLASTX
NCBI GI g1628583
RLAST score 72

BLAST score 72 E value 7.0e-61



Match length 123 % identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143368

Seq. ID LIB3168-026-P1-K1-F1

Method BLASTX
NCBI GI g1628583
BLAST score 519
E value 5.0e-53
Match length 120
% identity 85

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143369

Seq. ID LIB3168-026-P1-K1-F10

Method BLASTX
NCBI GI g1628583
BLAST score 610
E value 1.0e-63
Match length 124
% identity 95

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143370

Seq. ID LIB3168-026-P1-K1-F11

Method BLASTN
NCBI GI g4544365
BLAST score 329
E value 0.0e+00
Match length 395
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC F26H6 genomic

sequence, complete sequence

Seq. No. 143371

Seq. ID LIB3168-026-P1-K1-F12

Method BLASTX
NCBI GI g1628583
BLAST score 692
E value 3.0e-73
Match length 132
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143372

Seq. ID LIB3168-026-P1-K1-F2

Method BLASTX NCBI GI g2129657



BLAST score 446 E value 2.0e-44 Match length 120

% identity 78

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi 987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 143373

Seq. ID LIB3168-026-P1-K1-F3

Method BLASTN
NCBI GI g2244788
BLAST score 275
E value 1.0e-153
Match length 318
% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 143374

Seq. ID LIB3168-026-P1-K1-F6

Method BLASTX
NCBI GI g112743
BLAST score 513
E value 3.0e-52
Match length 119
% identity 83

NCBI Description 2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_

(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]

>gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4

precursor [Arabidopsis thaliana]

Seq. No. 143375

Seq. ID LIB3168-026-P1-K1-F7

Method BLASTN
NCBI GI g3033373
BLAST score 280
E value 1.0e-156
Match length 402
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F19I3 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 143376

Seq. ID LIB3168-026-P1-K1-F8

Method BLASTX
NCBI GI g1628583
BLAST score 493
E value 4.0e-50
Match length 102
% identity 93

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S



cruciferin seed storage protein [Arabidopsis thaliana]

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Seq. No.
                  143377
                                                         dia-
                  LIB3168-026-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1169476
BLAST score
                  568
                  1.0e-58
E value
Match length
                  112
% identity
                  97
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
NCBI Description
                  ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)
                  vitronectin-like adhesion protein [Nicotiana tabacum]
Seq. No.
                  143378
Seq. ID
                  LIB3168-026-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g2190554
BLAST score
                  464
E value
                  2.0e-46
Match length
                  109
% identity
                  77
                  (AC001229) Similar to Arabidopsis cytochrome P450 CYP90
NCBI Description
                  (gb X87367). [Arabidopsis thaliana]
Seq. No.
                  143379
Seq. ID
                  LIB3168-026-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  635
E value
                  1.0e-66
Match length
                  123
                  99
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143380
Seq. ID
                  LIB3168-026-P1-K1-G11
Method
                  BLASTN
NCBI GI
                  g4519195
BLAST score
                  155
E value
                  9.0e-82
Match length
                  355
% identity
                  95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MQC12, complete sequence
Seq. No.
                  143381
                  LIB3168-026-P1-K1-G12
Seq. ID
Method
                  BLASTX
                  q1628583
NCBI GI
BLAST score
                  674
E value
                  4.0e-71
Match length
                  129
% identity
                  100
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis
```



thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143382

Seq. ID LIB3168-026-P1-K1-G2

Method BLASTN
NCBI GI g4539309
BLAST score 340
E value 0.0e+00
Match length 379
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22

(ESSA project)

Seq. No. 143383

Seq. ID LIB3168-026-P1-K1-G3

Method BLASTX
NCBI GI g4538979
BLAST score 186
E value 6.0e-14
Match length 98
% identity 52

NCBI Description (AL049487) putative protein [Arabidopsis thaliana]

Seq. No. 143384

Seq. ID LIB3168-026-P1-K1-G4

Method BLASTX
NCBI GI g2129657
BLAST score 329
E value 1.0e-30
Match length 97
% identity 73

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 143385

Seq. ID LIB3168-026-P1-K1-G5

Method BLASTN
NCBI GI g3335170
BLAST score 115
E value 5.0e-58
Match length 290
% identity 97

NCBI Description Arabidopsis thaliana embryo-specific protein 3 (ATS3) gene,

complete cds

Seq. No. 143386

Seq. ID LIB3168-026-P1-K1-G6

Method BLASTX
NCBI GI g1628583
BLAST score 64
E value 1.0e-51
Match length 118
% identity 87

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis



thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

143387 Seq. No. LIB3168-026-P1-K1-G7 Seq. ID Method BLASTX NCBI GI q1864017 BLAST score 573 E value 3.0e-59 Match length 110 99 % identity (D63396) elongation factor-1 alpha [Nicotiana tabacum] NCBI Description 143388 Seq. No. Seq. ID LIB3168-026-P1-K1-G8 Method BLASTX NCBI GI g1628583 BLAST score 638 6.0e-67 E value Match length 125 % identity 98 (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143389 LIB3168-026-P1-K1-G9 Seq. ID Method BLASTX NCBI GI g3687228 BLAST score 269 7.0e-24 E value Match length 54 93 % identity (AC005169) putative malate dehydrogenase [Arabidopsis NCBI Description thaliana] Seq. No. 143390 Seq. ID LIB3168-026-P1-K1-H1 Method BLASTX NCBI GI g1628583 BLAST score 625 E value 2.0e-65 Match length 120 100 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143391 LIB3168-026-P1-K1-H10 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g2129639
BLAST score 347
E value 3.0e-33
Match length 69
% identity 99

NCBI Description luminal binding protein (BiP) - Arabidopsis thaliana

Seq. No.

Seq. ID

Method

NCBI GI

BLAST score

143396

BLASTX

529

g1628583

LIB3168-026-P1-K1-H6





>gi_1303695_dbj_BAA12348_ (D84414) luminal binding protein
(BiP) [Arabidopsis thaliana]

```
Seq. No.
                  143392
Seq. ID
                  LIB3168-026-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2129659
BLAST score
                  156
E value
                  2.0e-10
Match length
                  55
                  60
% identity
NCBI Description
                  oleosin, isoform 21K - Arabidopsis thaliana >gi 725260
                  (L40954) oleosin [Arabidopsis thaliana]
Seq. No.
                  143393
Seq. ID
                  LIB3168-026-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g21112
BLAST score
                  215
                  3.0e-17
E value
Match length
                  48
% identity
                  83
NCBI Description (X59805) cruciferin [Raphanus sativus]
Seq. No.
                  143394
                  LIB3168-026-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  675
E value
                  3.0e-71
Match length
                  131
                  98
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143395
Seq. ID
                  LIB3168-026-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  215
E value
                  3.0e-17
                  99
Match length
% identity
                  48
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi_4490710_emb_CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
```



E value 3.0e-54
Match length 103
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143397

Seq. ID LIB3168-026-P1-K1-H7

Method BLASTX
NCBI GI g1370186
BLAST score 470
E value 3.0e-47
Match length 93
% identity 98

NCBI Description (Z73942) RAB7C [Lotus japonicus]

Seq. No. 143398

Seq. ID LIB3168-026-P1-K1-H8

Method BLASTN
NCBI GI g2765441
BLAST score 267
E value 1.0e-148
Match length 298
% identity 97

NCBI Description Arabidopsis thaliana mRNA for ethylene-regulated transcript

Seq. No. 143399

Seq. ID LIB3168-026-P1-K1-H9

Method BLASTX
NCBI GI g1628583
BLAST score 551
E value 2.0e-67
Match length 132
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143400

Seq. ID LIB3168-027-P1-K1-A1

Method BLASTX
NCBI GI g112681
BLAST score 330
E value 3.0e-52
Match length 132
% identity 76

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143401

Seq. ID LIB3168-027-P1-K1-A10

Method BLASTX NCBI GI g1628583



BLAST score 625 E value 3.0e-65 Match length 120

% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

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Seq. No. 143402

Seq. ID LIB3168-027-P1-K1-A11

Method BLASTN
NCBI GI 94263774
BLAST score 189
E value 1.0e-102
Match length 475
% identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC T20F21 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 143403

Seq. ID LIB3168-027-P1-K1-A12

Method BLASTN
NCBI GI g2828180
BLAST score 234
E value 1.0e-129
Match length 451
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDK4, complete sequence [Arabidopsis thaliana]

Seq. No. 143404

Seq. ID LIB3168-027-P1-K1-A3

Method BLASTX
NCBI GI g1628583
BLAST score 357
E value 3.0e-56
Match length 117
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143405

Seq. ID LIB3168-027-P1-K1-A4

Method BLASTX
NCBI GI g112682
BLAST score 648
E value 5.0e-68
Match length 150
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143406



```
LIB3168-027-P1-K1-A5
Seq. ID
Method
                  BLASTX
                  g2129657
NCBI GI
BLAST score
                  398
E value
                  1.0e-38
Match length
                  109
                  77
% identity
                  oleosin isoform - Arabidopsis thaliana
NCBI Description
                  >gi 987014 emb CAA90877 (Z54164) oleosin [Arabidopsis
                  thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin
                   [Arabidopsis thaliana]
                  143407
Seq. No.
                  LIB3168-027-P1-K1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3869071
BLAST score
                  86
                  2.0e-40
E value
Match length
                  118
% identity
                  94
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MIL23, complete sequence [Arabidopsis thaliana]
Seq. No.
                  143408
                  LIB3168-027-P1-K1-A7
Seq. ID
Method
                  BLASTN
                  g2244829
NCBI GI
BLAST score
                  77
                  8.0e-36
E value
Match length
                  92
% identity
                  97
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                   143409
Seq. No.
                  LIB3168-027-P1-K1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1628583
BLAST score
                   648
E value
                   4.0e-68
Match length
                   125
                   99
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   143410
                   LIB3168-027-P1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2829893
BLAST score
                   494
```

3.0e-50 E value Match length 96 % identity 98

NCBI Description (AC002311) phosphoglucomutase [Arabidopsis thaliana]

143411 Seq. No.



Seq. ID LIB3168-027-P1-K1-B10

Method BLASTX
NCBI GI g112743
BLAST score 680
E value 9.0e-72
Match length 145
% identity 88

NCBI Description 2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi 395202 emb CAA80869

(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]

>gi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4

precursor [Arabidopsis thaliana]

Seq. No. 143412

Seq. ID LIB3168-027-P1-K1-B12

Method BLASTX
NCBI GI g1628583
BLAST score 272
E value 4.0e-24
Match length 88
% identity 62

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143413

Seq. ID LIB3168-027-P1-K1-B2

Method BLASTX
NCBI GI g112741
BLAST score 525
E value 9.0e-54
Match length 98
% identity 99

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143414

Seq. ID LIB3168-027-P1-K1-B3

Method BLASTX
NCBI GI g3335171
BLAST score 72
E value 2.0e-11
Match length 61

% identity 65

NCBI Description (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]

Seq. No. 143415

Seq. ID LIB3168-027-P1-K1-B4

Method BLASTX NCBI GI g1628583



BLAST score E value 4.0e-76 Match length 138 % identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143416

LIB3168-027-P1-K1-B5 Seq. ID

Method BLASTX NCBI GI q1628583 BLAST score 541 E value 2.0e-55 Match length 120 % identity 88

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143417

LIB3168-027-P1-K1-B8 Seq. ID

Method BLASTX NCBI GI g2924258 BLAST score 168 E value 2.0e-12 Match length 50 64

% identity

NCBI Description (Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]

Seq. No. 143418

LIB3168-027-P1-K1-B9 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 621 E value 8.0e-65 Match length 120 % identity 99

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143419

LIB3168-027-P1-K1-C1 Seq. ID

Method BLASTX NCBI GI q1628583 BLAST score 532 E value 2.0e-54 Match length 100 100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143420

Seq. ID LIB3168-027-P1-K1-C10

Method BLASTX



NCBI GI g112737 BLAST score 381 E value 9.0e-37 Match length 68 % identity 100

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143421

Seq. ID LIB3168-027-P1-K1-C11

Method BLASTX
NCBI GI g4490295
BLAST score 594
E value 1.0e-61
Match length 137
% identity 81

NCBI Description (AL035678) hypothetical protein [Arabidopsis thaliana]

Seq. No. 143422

Seq. ID LIB3168-027-P1-K1-C12

Method BLASTX
NCBI GI g112682
BLAST score 650
E value 3.0e-68
Match length 148
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143423

Seq. ID LIB3168-027-P1-K1-C2

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143424

Seq. ID LIB3168-027-P1-K1-C5

Method BLASTX
NCBI GI 94539005
BLAST score 728
E value 2.0e-77
Match length 148
% identity 99



NCBI Description (AL049481) putative oxidoreductase [Arabidopsis thaliana]

Seq. No. 143425

Seq. ID LIB3168-027-P1-K1-C6

Method BLASTX
NCBI GI g135858
BLAST score 375
E value 6.0e-36
Match length 76
% identity 97

NCBI Description TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)

>gi_99760_pir__S22201 tonoplast intrinsic protein alpha Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551)
tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
[Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast

intrinsic protein alpha [Arabidopsis thaliana]

Seq. No. 143426

Seq. ID LIB3168-027-P1-K1-C7

Method BLASTX
NCBI GI g1628583
BLAST score 791
E value 9.0e-85
Match length 153
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143427

Seq. ID LIB3168-027-P1-K1-C9

Method BLASTX
NCBI GI g1628583
BLAST score 403
E value 3.0e-39
Match length 112
% identity 73

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143428

Seq. ID LIB3168-027-P1-K1-D1

Method BLASTX
NCBI GI g112681
BLAST score 644
E value 1.0e-67
Match length 147
% identity 85

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143429



```
LIB3168-027-P1-K1-D10
Seq. ID
Method
                  BLASTX
                  g3292816
NCBI GI
BLAST score
                  479
                  3.0e-48
E value
                  111
Match length
% identity
                  (AL031018) putative fizzy-related protein [Arabidopsis
NCBI Description
                  thaliana]
                  143430
Seq. No.
                  LIB3168-027-P1-K1-D11
Seq. ID
                  BLASTX
Method
                  q1628583
NCBI GI
BLAST score
                  440
E value
                  1.0e-43
Match length
                  118
                  75
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  143431
Seq. No.
                  LIB3168-027-P1-K1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  625
E value
                  2.0e-65
                  120
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143432
                  LIB3168-027-P1-K1-D2
Seq. ID
                  BLASTN
Method
                  g2842474
NCBI GI
BLAST score
                  196
E value
                  1.0e-106
Match length
                  280
                  93
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
NCBI Description
                   (ESSAII project)
Seq. No.
                  143433
                  LIB3168-027-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                   661
E value
                  2.0e-69
                  151
Match length
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604_pir__S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
```

17688

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936 emb_CAA32493 (X14312) 12S seed

BLAST score E value

1.0e-42



storage protein [Arabidopsis thaliana]

```
Seq. No.
                  143434
Seq. ID
                  LIB3168-027-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                   685
E value
                  2.0e-72
Match length
                  138
% identity
                   94
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  143435
Seq. No.
Seq. ID
                  LIB3168-027-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q4204298
BLAST score
                  573
E value
                   3.0e-59
Match length
                  144
% identity
                  78
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   143436
Seq. ID
                  LIB3168-027-P1-K1-D7
Method
                  BLASTX
NCBI GI
                   g1628583
BLAST score
                   562
                   6.0e-58
E value
Match length
                   120
                   90
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   143437
Seq. ID
                  LIB3168-027-P1-K1-D8
Method
                  BLASTX
                   g4586047
NCBI GI
BLAST score
                   254
E value
                   2.0e-22
Match length
                   110
% identity
                   55
                   (AC007020) putative ferritin protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4588004 gb_AAD25945.1_AF085279_18 (AF085279)
                  hypothetical ferritin subunit [Arabidopsis thaliana]
Seq. No.
                   143438
                  LIB3168-027-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4678285
```



Match length % identity 53

(AL049660) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

143439

Seq. ID

LIB3168-027-P1-K1-E10

Method NCBI GI BLASTN g4159702

BLAST score

226

E value Match length 1.0e-124

% identity

392 96

NCBI Description

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K2N11, complete sequence

Seq. No.

143440

Seq. ID

LIB3168-027-P1-K1-E11

Method NCBI GI BLASTX q1628583

BLAST score E value

625 3.0e-65

Match length % identity

120 100

NCBI Description

(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495 emb_CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.

143441

Seq. ID Method

LIB3168-027-P1-K1-E2 BLASTX

NCBI GI BLAST score

g112681 665

E value Match length

5.0e-70 151

85

% identity NCBI Description

12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.

143442

Seq. ID

LIB3168-027-P1-K1-E4

Method BLASTX NCBI GI g1628583 BLAST score 625 E value 2.0e-65

Match length 120 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.

143443

Seq. ID

LIB3168-027-P1-K1-E5

Method NCBI GI BLASTX g1345973



BLAST score 567 E value 2.0e-58 Match length 122 % identity 85

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 143444

Seq. ID LIB3168-027-P1-K1-E6

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143445

Seq. ID LIB3168-027-P1-K1-E7

Method BLASTX
NCBI GI g112681
BLAST score 588
E value 5.0e-61
Match length 149
% identity 80

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143446

Seq. ID LIB3168-027-P1-K1-E8

Method BLASTX
NCBI GI g112681
BLAST score 644
E value 2.0e-67
Match length 147
% identity 85

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

charanaj vgi 000930 emb CAA32493 (X14312)

storage protein [Arabidopsis thaliana]

Seq. No. 143447

Seq. ID LIB3168-027-P1-K1-E9

Method BLASTN



```
g4455348
NCBI GI
BLAST score
                  98
E value
                  3.0e-48
Match length
                  122
% identity
                  96
                 Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8
NCBI Description
                  (ESSAII project)
                  143448
Seq. No.
                  LIB3168-027-P1-K1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112737
                  624
BLAST score
                  3.0e-65
E value
Match length
                  146
% identity
                  82
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  143449
Seq. No.
                  LIB3168-027-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3355477
BLAST score
                  641
                  3.0e-67
E value
Match length
                  149
% identity
                  46
                  (AC004218) putative P-glycoprotein, pgp1 [Arabidopsis
NCBI Description
                  thaliana]
                  143450
Seq. No.
                  LIB3168-027-P1-K1-F2
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  625
E value
                  3.0e-65
Match length
                  120
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  143451
Seq. No.
Seq. ID
                  LIB3168-027-P1-K1-F3
Method
                  BLASTX
```

Method BLASTX
NCBI GI g136739
BLAST score 355
E value 1.0e-33
Match length 112
% identity 63

NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE

PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU

Method

NCBI GI BLAST score

E value

g112737

3.0e-65

624



UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) potato >qi 218001 dbj BAA00570 (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No. 143452 LIB3168-027-P1-K1-F4 Seq. ID Method BLASTN q2656031 NCBI GI BLAST score 324 E value 0.0e+00Match length 424 96 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description Seq. No. 143453 LIB3168-027-P1-K1-F5 Seq. ID Method BLASTX NCBI GI q1628583 BLAST score 541 E value 2.0e-55 Match length 120 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143454 LIB3168-027-P1-K1-F6 Seq. ID BLASTX Method q2494320 NCBI GI BLAST score 470 4.0e-47 E value 150 Match length 67 % identity EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) NCBI Description >gi 1806575 emb_CAA67868_ (X99517) Eukaryotic initiation factor-5 [Zea mays] Seq. No. 143455 Seq. ID LIB3168-027-P1-K1-F7 BLASTX Method NCBI GI g1628583 BLAST score 232 E value 3.0e-19 Match length 87 100 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143456 Seq. ID LIB3168-027-P1-K1-F8 BLASTX



Match length 82

% identity NCBI Description

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68853_pir NWMU1 2S albumin 1 precursor Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

143457 Seq. No.

Seq. ID LIB3168-027-P1-K1-G1

Method BLASTX g1628583 NCBI GI BLAST score 756 1.0e-80 E value Match length 149 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

143458 Seq. No.

Seq. ID LIB3168-027-P1-K1-G11

Method BLASTX NCBI GI g112681 BLAST score 635 2.0e-66 E value Match length 145

% identity 85

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604_pir__S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143459

LIB3168-027-P1-K1-G12 Seq. ID

Method BLASTX NCBI GI g112682 BLAST score 646 E value 9.0e-68 Match length 147 83 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143460

Seq. ID LIB3168-027-P1-K1-G2

BLASTX Method NCBI GI g2160146 BLAST score 418 5.0e-41 E value 137 Match length



% identity (AC000375) Strong similarity to Arabidopsis NCBI Description gb X91953, F21M12.3, F21M12.1. EST gb H36326 comes from this gene. [Arabidopsis thaliana] 143461 Seq. No. LIB3168-027-P1-K1-G3 Seq. ID Method BLASTX NCBI GI g81546 BLAST score 243 E value 2.0e-20 Match length 153 % identity alpha-globulin type B precursor (tandem 1) - upland cotton NCBI Description (fragment) 143462 Seq. No. Seq. ID LIB3168-027-P1-K1-G4 Method BLASTX q1628583 NCBI GI 687 BLAST score 1.0e-72 E value Match length 151 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143463 LIB3168-027-P1-K1-G5 Seq. ID Method BLASTX NCBI GI g4469003 BLAST score 690 E value 6.0e-73 Match length 150 % identity 87 (AL035602) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 143464 LIB3168-027-P1-K1-G6 Seq. ID BLASTX Method q112737 NCBI GI 340 BLAST score E value 4.0e-32 Match length 84

81

% identity NCBI Description

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

143465 Seq. No.

Seq. ID LIB3168-027-P1-K1-G8

Method BLASTX



NCBI GI g1628583 BLAST score 625 E value 2.0e-65 Match length 120 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143466

Seq. ID LIB3168-027-P1-K1-G9

Method BLASTX
NCBI GI g112681
BLAST score 756
E value 1.0e-80
Match length 148
% identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143467

Seq. ID LIB3168-027-P1-K1-H1

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143468

Seq. ID LIB3168-027-P1-K1-H10

Method BLASTX
NCBI GI g2605714
BLAST score 464
E value 2.0e-46
Match length 112
% identity 83

NCBI Description (AF026275) beta-tonoplast intrinsic protein [Arabidopsis

thaliana]

Seq. No. 143469

Seq. ID LIB3168-027-P1-K1-H11

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.

143475



```
143470
Seq. No.
                  LIB3168-027-P1-K1-H2
Seq. ID
Method
                  BLASTX
                  g2444180
NCBI GI
                  560
BLAST score
                  9.0e-58
E value
Match length
                  136
% identity
                  84
NCBI Description (U94785) unconventional myosin [Helianthus annuus]
                  143471
Seq. No.
                  LIB3168-027-P1-K1-H3
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  620
                  1.0e-64
E value
                  120
Match length
                  99
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  143472
Seq. No.
Seq. ID
                  LIB3168-027-P1-K1-H6
                  BLASTX
Method
NCBI GI
                  g3879811
                  148
BLAST score
                  2.0e-09
E value
Match length
                  45
% identity
                   56
                  (Z66524) Homology with Squid retinal-binding protein (PIR
NCBI Description
                  Acc. No. A53057) [Caenorhabditis elegans]
Seq. No.
                  143473
                  LIB3168-027-P1-K1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4581161
BLAST score
                   269
E value
                  1.0e-149
                   423
Match length
                   95
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T20G20 genomic
                   sequence, complete sequence
                   143474
Seq. No.
                  LIB3168-028-P1-K1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                   q2656026
BLAST score
                   281
E value
                   1.0e-157
Match length
                   362
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDF20
```

Seq. ID

LIB3168-028-P1-K1-A10

```
Method
                  BLASTX
NCBI GI
                  q4204277
                  687
BLAST score
                  1.0e-72
E value
                  128
Match length
% identity
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  143476
Seq. No.
Seq. ID
                  LIB3168-028-P1-K1-A11
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  562
                  6.0e-58
E value
Match length
                  141
                  79
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  143477
Seq. No.
Seq. ID
                  LIB3168-028-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g112739
BLAST score
                  493
                  7.0e-50
E value
Match length
                  127
% identity
                  78
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  143478
Seq. ID
                  LIB3168-028-P1-K1-A4
Method
                  BLASTN
NCBI GI
                  q4757403
BLAST score
                  240
E value
                  1.0e-132
Match length
                  416
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MJL12, complete sequence
                  143479
Seq. No.
                  LIB3168-028-P1-K1-A5
Seq. ID
                  BLASTX
Method
                  g3600031
NCBI GI
BLAST score
                  533
E value
                  1.0e-54
                  130
Match length
                  84
% identity
NCBI Description (AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic
```

NCBI GI BLAST score

E value



acid aldolases [Arabidopsis thaliana]

```
143480
Seq. No.
                  LIB3168-028-P1-K1-A6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4314374
BLAST score
                  348
                  0.0e + 00
E value
Match length
                  364
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC F10A12 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  143481
                  LIB3168-028-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  591
                  2.0e-61
E value
                  137
Match length
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__ S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  143482
Seq. No.
Seq. ID
                  LIB3168-028-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                   699
E value
                   5.0e-74
Match length
                  138
                   96
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                   143483
Seq. No.
Seq. ID
                  LIB3168-028-P1-K1-A9
                  BLASTX
Method
NCBI GI
                   g3169172
                   416
BLAST score
                   5.0e-41
E value
Match length
                   112
% identity
                   68
                   (AC004401) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                   thaliana] >gi 3445214 (AC004786) putative serine
                   carboxypeptidase I [Arabidopsis thaliana]
                   143484
Seq. No.
Seq. ID
                   LIB3168-028-P1-K1-B1
                   BLASTX
Method
```

17699

g112681

6.0e-45



```
Match length
% identity
                  81
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  143485
Seq. No.
                  LIB3168-028-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  618
                  2.0e-64
E value
                  120
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  143486
Seq. No.
                  LIB3168-028-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1497987
BLAST score
                  393
E value
                  4.0e-38
Match length
                  140
                  57
% identity
NCBI Description
                  (U62798) SCARECROW [Arabidopsis thaliana]
Seq. No.
                  143487
Seq. ID
                  LIB3168-028-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g3914468
BLAST score
                  312
E value
                  1.0e-28
Match length
                  114
% identity
                   56
                  26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
NCBI Description
                  >qi 478411 pir JQ2257 nuclear antigen 21D7 - carrot
                  >qi 217911 dbj BAA02696 (D13434) 21D7 antigen [Daucus
                   carota]
Seq. No.
                  143488
Seq. ID
                  LIB3168-028-P1-K1-B6
Method
                  BLASTX
NCBI GI
                   q1628583
BLAST score
                   318
                  2.0e-29
E value
```

Match length 60 98 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

143489 Seq. No.

Seq. ID LIB3168-028-P1-K1-B9



```
BLASTN
Method
NCBI GI
                  g2564047
BLAST score
                  34
                  1.0e-09
E value
Match length
                  130
                  79
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJB21, complete sequence [Arabidopsis thaliana]
Seq. No.
                  143490
Seq. ID
                  LIB3168-028-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  q4204299
                  199
BLAST score
E value
                  6.0e-37
Match length
                  86
% identity
                  95
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  143491
Seq. ID
                  LIB3168-028-P1-K1-C11
Method
                  BLASTN
NCBI GI
                  q3461834
BLAST score
                  44
E value
                  7.0e-16
                  102
Match length
% identity
                  93
                  Arabidopsis thaliana chromosome II BAC T9I4 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  143492
Seq. ID
                  LIB3168-028-P1-K1-C12
                  BLASTX
Method
NCBI GI
                  g1628583
                  619
BLAST score
                  1.0e-64
E value
Match length
                  126
                   98
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143493
Seq. ID
                  LIB3168-028-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g2190554
BLAST score
                  169
                   4.0e-14
E value
Match length
                  78
% identity
                   50
                   (ACO01229) Similar to Arabidopsis cytochrome P450 CYP90
NCBI Description
```

(gb_X87367). [Arabidopsis thaliana]

143494 Seq. No.

Seq. ID LIB3168-028-P1-K1-C4

Method BLASTX

Method NCBI GI



```
NCBI GI
                  q401169
BLAST score
                  203
                  3.0e-16
E value
Match length
                  43
% identity
                  93
NCBI Description
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
Seq. No.
                  143495
                  LIB3168-028-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129657
BLAST score
                  335
E value
                  2.0e-31
Match length
                  97
% identity
NCBI Description
                  oleosin isoform - Arabidopsis thaliana
                  >gi 987014 emb CAA90877 (Z54164) oleosin [Arabidopsis
                   thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin
                   [Arabidopsis thaliana]
Seq. No.
                   143496
Seq. ID
                  LIB3168-028-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q21112
BLAST score
                   265
E value
                   4.0e-23
Match length
                   60
                   83
% identity
NCBI Description
                  (X59805) cruciferin [Raphanus sativus]
Seq. No.
                   143497
                   LIB3168-028-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1628583
BLAST score
                   578
                   6.0e-60
E value
Match length
                   112
% identity
                   98
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   143498
Seq. No.
Seq. ID
                   LIB3168-028-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   q2853090
BLAST score
                   442
                   6.0e-44
E value
                  91
Match length
                   98
% identity
                   (AL021768) small GTP-binding protein-like [Arabidopsis
NCBI Description
                   thaliana]
                   143499
Seq. No.
                  LIB3168-028-P1-K1-D3
Seq. ID
```

17702

BLASTN

g4589409



```
BLAST score 231
E value 1.0e-127
Match length 360
% identity 32
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F17P19, complete sequence

 Seq. No.
 143500

 Seq. ID
 LIB3168-028-P1-K1-D4

 Method
 BLASTX

 NCBI GI
 g112741

 BLAST score
 630

 E value
 6.0e-66

E value 6.0e-Match length 117 % identity 98

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143501

Seq. ID LIB3168-028-P1-K1-D5

Method BLASTX
NCBI GI g529353
BLAST score 169
E value 4.0e-38
Match length 110
% identity 64

NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No. 143502

Seq. ID LIB3168-028-P1-K1-D6

Method BLASTX 92982440
BLAST score 236
E value 3.0e-40
Match length 122
% identity 73

NCBI Description (AL022224) terpene cyclase like protein [Arabidopsis

thaliana]

Seq. No. 143503

Seq. ID LIB3168-028-P1-K1-D7

Method BLASTX
NCBI GI g112682
BLAST score 547
E value 3.0e-56
Match length 131
% identity 80

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

NCBI GI

BLAST score



```
143504
Seq. No.
Seq. ID
                  LIB3168-028-P1-K1-D8
                  BLASTX
Method
NCBI GI
                  g112737
                  220
BLAST score
                  4.0e-18
E value
                  52
Match length
                  85
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  143505
Seq. No.
Seq. ID
                  LIB3168-028-P1-K1-D9
Method
                  BLASTN
                  g4589409
NCBI GI
BLAST score
                  34
                  1.0e-09
E value
Match length
                  69
% identity
                  27
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  F17P19, complete sequence
                  143506
Seq. No.
Seq. ID
                  LIB3168-028-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g629602
BLAST score
                  118
E value
                  2.0e-19
Match length
                  86
                  53
% identity
                  probable imbibition protein - wild cabbage
NCBI Description
                  >gi 488787 emb CAA55893 (X79330) putative imbibition
                  protein [Brassica oleracea]
                  143507
Seq. No.
Seq. ID
                  LIB3168-028-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g3335169
BLAST score
                  736
E value
                  2.0e-78
                  136
Match length
                  100
% identity
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
                  >qi 4455197 emb CAB36520.1 (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                  143508
                  LIB3168-028-P1-K1-E3
Seq. ID
Method
                  BLASTN
```

17704

q1313927



E value 4.0e-16 Match length 191 % identity 82

NCBI Description B.oleracea mRNA for IFA binding protein (sp10)

Seq. No. 143509

Seq. ID LIB3168-028-P1-K1-E4

Method BLASTX
NCBI GI g1628583
BLAST score 493
E value 3.0e-60
Match length 123
% identity 95

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143510

Seq. ID LIB3168-028-P1-K1-E5

Method BLASTN
NCBI GI g166569
BLAST score 234
E value 1.0e-129
Match length 238
% identity 100

NCBI Description Arabidopsis thaliana glycine rich protein (RAB18) gene,

complete cds

Seq. No. 143511

Seq. ID LIB3168-028-P1-K1-E6

Method BLASTX
NCBI GI g1628583
BLAST score 426
E value 3.0e-42
Match length 97
% identity 86

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143512

Seq. ID LIB3168-028-P1-K1-E9

Method BLASTX
NCBI GI g120675
BLAST score 434
E value 5.0e-43
Match length 106
% identity 80

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844 (X04301) GAPDH (aa 1-338) [Sinapis

alba]

Seq. No. 143513

Seq. ID LIB3168-028-P1-K1-F1

Method BLASTN



```
NCBI GI
                   q3128139
                   149
BLAST score
                   4.0e-78
E value
Match length
                   418
                   100
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MIK19, complete sequence [Arabidopsis thaliana]
Seq. No.
                   143514
Seq. ID
                   LIB3168-028-P1-K1-F10
Method
                   BLASTN
NCBI GI
                   g3319359
BLAST score
                   296
E value
                   1.0e-166
                   355
Match length
                   95
% identity
NCBI Description Arabidopsis thaliana BAC T7M24
                   143515
Seq. No.
Seq. ID
                   LIB3168-028-P1-K1-F11
Method
                   BLASTX
                   q112741
NCBI GI
BLAST score
                   704
E value
                   1.0e-74
Match length
                   133
% identity
                   98
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                   3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                    (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >gi_4490712_emb_CAB38846.1 (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
Seq. No.
                   143516
                   LIB3168-028-P1-K1-F12
Seq. ID
Method
                   BLASTN
NCBI GI
                    g166609
BLAST score
                    175
E value
                    1.0e-93
Match length
                    427
% identity
                    82
                   A.thaliana at 2S1 gene encoding albumin 2S subunit 1,
NCBI Description
                    complete cds
                    143517
Seq. No.
                   LIB3168-028-P1-K1-F2
Seq. ID
Method
                    BLASTN
                    q3056579
NCBI GI
BLAST score
                    407
                    0.0e + 00
E value
                    427
Match length
                    99
% identity
                   Arabidopsis thaliana BAC T1F9 chromosome 1, complete
NCBI Description
```

Seq. No. 143518

sequence [Arabidopsis thaliana]



```
LIB3168-028-P1-K1-F4
Seq. ID
                  BLASTX
Method
                  g1628583
NCBI GI
                  486
BLAST score
E value
                  5.0e-49
                  127
Match length
                  76
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143519
                  LIB3168-028-P1-K1-F5
Seq. ID
                  BLASTX
Method
                  g3080427
NCBI GI
                  147
BLAST score
E value
                  1.0e-15
Match length
                  91
% identity
                  54
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
Seq. No.
                  143520
                  LIB3168-028-P1-K1-F6
Seq. ID
                  BLASTX
Method
                  q112741
NCBI GI
                  712
BLAST score
                 1.0e-75
E value
Match length
                  134
                  99
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  143521
Seq. No.
Seq. ID
                  LIB3168-028-P1-K1-F7
                  BLASTX
Method
NCBI GI
                  g112739
BLAST score
                  354
E value
                  8.0e-34
Match length
                  88
% identity
                  81
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >qi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
```

Seq. No. 143522

Seq. ID LIB3168-028-P1-K1-F8

Method BLASTX NCBI GI g112681



BLAST score 714 E value 8.0e-76 Match length 140 % identity 96

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143523

Seq. ID LIB3168-028-P1-K1-G1

Method BLASTX
NCBI GI g1628583
BLAST score 554
E value 5.0e-57
Match length 120
% identity 90

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143524

Seq. ID LIB3168-028-P1-K1-G11

Method BLASTN
NCBI GI g4159712
BLAST score 65
E value 4.0e-28
Match length 113
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence

Seq. No. 143525

Seq. ID LIB3168-028-P1-K1-G12

Method BLASTX
NCBI GI g1628583
BLAST score 559
E value 1.0e-57
Match length 141
% identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143526

Seq. ID LIB3168-028-P1-K1-G2

Method BLASTX
NCBI GI g2702272
BLAST score 581
E value 3.0e-60
Match length 140
% identity 35

NCBI Description (AC003033) hypothetical protein [Arabidopsis thaliana]

Seq. No. 143527

Seq. ID LIB3168-028-P1-K1-G3

17708



```
Method
                  BLASTX
NCBI GI
                  q4758340
BLAST score
                  163
                  3.0e-11
E value
                  130
Match length
                  33
% identity
                  phenylalanine-tRNA synthetase-like >gi 2102679 (U07424)
NCBI Description
                  putative tRNA synthetase-like protein [Homo sapiens]
                  >qi 4104935 gb AAD02221 (AF042347) putative
                  phenylalanyl-tRNA synthetase alpha-subunit; PheHA [Homo
                  sapiens]
Seq. No.
                  143528
                  LIB3168-028-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
                  607
BLAST score
E value
                  3.0e-63
                  120
Match length
                  97
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  143529
Seq. No.
                  LIB3168-028-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  623
E value
                  3.0e-65
Match length
                  121
                  98
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   143530
                  LIB3168-028-P1-K1-G7
Seq. ID
Method
                  BLASTX
                  g729479
NCBI GI
                   235
BLAST score
                   9.0e-20
E value
                   91
Match length
                   58
% identity
                  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi 551131
NCBI Description
                   (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]
Seq. No.
                   143531
                   LIB3168-028-P1-K1-G9
Seq. ID
                  BLASTX
Method
                   g112682
NCBI GI
                   582
BLAST score
```

3.0e-60 E value 137 Match length 81 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana



>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
storage protein [Arabidopsis thaliana]

 Seq. No.
 143532

 Seq. ID
 LIB3168-028-P1-K1-H1

 Method
 BLASTX

 NCBI GI
 g1628583

 BLAST score
 562

E value 5.0e-58 Match length 120 % identity 90

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143533

Seq. ID LIB3168-028-P1-K1-H10

Method BLASTX
NCBI GI g112682
BLAST score 682
E value 5.0e-72
Match length 140
% identity 91

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143534

Seq. ID LIB3168-028-P1-K1-H11

Method BLASTX
NCBI GI g1628583
BLAST score 414
E value 1.0e-40
Match length 120
% identity 74

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143535

Seq. ID LIB3168-028-P1-K1-H2

Method BLASTX
NCBI GI g112682
BLAST score 585
E value 1.0e-60
Match length 140
% identity 80

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143536

```
Seq. ID LIB3168-028-P1-K1-H3 Method BLASTX
```

NCBI GI g1402904 BLAST score 673 E value 5.0e-71

Match length 130 % identity 98

NCBI Description (X98313) peroxidase [Arabidopsis thaliana]

Seq. No. 143537

Seq. ID LIB3168-028-P1-K1-H4

Method BLASTX
NCBI GI g1628583
BLAST score 618
E value 2.0e-64
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143538

Seq. ID LIB3168-028-P1-K1-H5

Method BLASTX
NCBI GI g112682
BLAST score 563
E value 5.0e-58
Match length 134
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsīs thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143539

Seg. ID LIB3168-028-P1-K1-H6

Method BLASTX
NCBI GI g1628583
BLAST score 431
E value 7.0e-43
Match length 87
% identity 94

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143540

Seq. ID LIB3168-028-P1-K1-H9

Method BLASTN
NCBI GI g395203
BLAST score 176
E value 3.0e-94
Match length 346
% identity 67

NCBI Description A.thaliana 2S albumin gene isoforms 1 and 2, complete CDS's



Seq. No. 143541

Seq. ID LIB3168-029-P1-K1-A1

Method BLASTX
NCBI GI g112737
BLAST score 571
E value 5.0e-59
Match length 137
% identity 81

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143542

Seq. ID LIB3168-029-P1-K1-A10

Method BLASTN
NCBI GI g3293582
BLAST score 105
E value 5.0e-52
Match length 117
% identity 98

NCBI Description Arabidopsis thaliana BAC T15F16

Seq. No. 143543

Seq. ID LIB3168-029-P1-K1-A11

Method BLASTX
NCBI GI g1628583
BLAST score 820
E value 4.0e-88
Match length 156
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143544

Seq. ID LIB3168-029-P1-K1-A12

Method BLASTX
NCBI GI g112682
BLAST score 669
E value 2.0e-70
Match length 152
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143545

Seq. ID LIB3168-029-P1-K1-A2

Method BLASTX
NCBI GI g1628583
BLAST score 564



E value 4.0e-58 Match length 119 % identity 91

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143546

Seq. ID LIB3168-029-P1-K1-A3

Method BLASTX
NCBI GI g112681
BLAST score 662
E value 1.0e-69
Match length 150
% identity 85

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143547

Seq. ID LIB3168-029-P1-K1-A4

Method BLASTX
NCBI GI g2129641
BLAST score 751
E value 5.0e-80
Match length 136
% identity 100

NCBI Description major latex protein type 1 - Arabidopsis thaliana

>gi 1107493 emb CAA63026 (X91960) major latex protein

typel [Arabidopsis thaliana]

Seq. No. 143548

Seq. ID LIB3168-029-P1-K1-A5

Method BLASTX
NCBI GI g112682
BLAST score 194
E value 5.0e-15
Match length 38
% identity 100

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605 pir_ \$08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi_808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143549

Seq. ID LIB3168-029-P1-K1-A6

Method BLASTX
NCBI GI g1621268
BLAST score 585
E value 1.0e-60
Match length 128
% identity 88

NCBI Description (Z81012) unknown [Ricinus communis]



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Seq. No.
                  143550
Seq. ID
                  LIB3168-029-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  682
E value
                  6.0e-72
Match length
                  156
                  83
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  143551
Seq. ID
                  LIB3168-029-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  618
E value
                  2.0e-64
Match length
                  120
% identity
                  99
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143552
Seq. ID
                  LIB3168-029-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g2492953
BLAST score
                  197
E value
                  3.0e-15
Match length
                  86
                  48
% identity
                  CHORISMATE SYNTHASE 2 PRECURSOR
NCBI Description
                   (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 2)
                  >gi 542027 pir S40409 chorismate synthase (EC 4.6.1.4) 2
                  precursor - tomato >gi 410484 emb CAA79854 (Z21791)
                  chorismate synthase 2 [Lycopersicon esculentum]
Seq. No.
                  143553
Seq. ID
                  LIB3168-029-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  q4582411
BLAST score
                  419
E value
                  0.0e + 00
Match length
                  486
```

99 % identity

NCBI Description Arabidopsis thaliana chromosome 1 BAC T23K8 sequence,

complete sequence

Seq. No. 143554

Seq. ID LIB3168-029-P1-K1-B3

Method BLASTX NCBI GI q4204298



BLAST score 1.0e-52 E value Match length 116 % identity 85

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 143555

Seq. ID LIB3168-029-P1-K1-B5

Method BLASTX q4755193 NCBI GI BLAST score 597 5.0e-62 E value Match length 122 % identity 99

NCBI Description (AC007018) putative ribosomal protein S17 [Arabidopsis

thaliana]

Seq. No. 143556

Seq. ID LIB3168-029-P1-K1-B6

Method BLASTX NCBI GI q4454013 BLAST score 743 E value 4.0e-79 Match length 145 % identity 100

NCBI Description (AL035396) putative protein [Arabidopsis thaliana]

Seq. No. 143557

Seq. ID LIB3168-029-P1-K1-B7

Method BLASTX NCBI GI q112681 BLAST score 522 E value 2.0e-53 Match length 124 % identity 82

12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143558

Seq. ID LIB3168-029-P1-K1-B9

Method BLASTX NCBI GI g1628583 BLAST score 642 E value 3.0e-67 123 Match length 100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

143559

Seq. No. Seq. ID LIB3168-029-P1-K1-C12

Method BLASTN



NCBI GI g4589425 BLAST score 187 E value 1.0e-101 Match length 228 % identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBA10, complete sequence

Seq. No. 143560

Seq. ID LIB3168-029-P1-K1-C2

Method BLASTX
NCBI GI g1628583
BLAST score 621
E value 8.0e-65
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143561

Seq. ID LIB3168-029-P1-K1-C4

Method BLASTX
NCBI GI g2739046
BLAST score 377
E value 3.0e-36
Match length 123
% identity 54

NCBI Description (AF024652) polyphosphoinositide binding protein Ssh2p

[Glycine max]

Seq. No. 143562

Seq. ID LIB3168-029-P1-K1-C6

Method BLASTN
NCBI GI g2262135
BLAST score 354
E value 0.0e+00
Match length 382
% identity 98

NCBI Description Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15

cM, complete sequence

Seq. No. 143563

Seq. ID LIB3168-029-P1-K1-C8

Method BLASTX
NCBI GI g1628583
BLAST score 642
E value 3.0e-67
Match length 123
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495 emb_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143564

Seq. ID LIB3168-029-P1-K1-C9

Method BLASTX



```
NCBI GI
                   q2129532
BLAST score
                   421
                  2.0e-41
E value
Match length
                  110
% identity
                  75
NCBI Description
                  acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) -
                  Arabidopsis thaliana >gi_1107507_emb_CAA63746_ (X93461)
                  acyl-[acyl-carrier protein] desaturase [Arabidopsis
                  thaliana]
Seq. No.
                  143565
Seq. ID
                  LIB3168-029-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g2244906
BLAST score
                  542
E value
                  1.0e-55
Match length
                  154
% identity
                  70
NCBI Description
                   (Z97339) indole-3-acetate beta-glucosyltransferase
                   [Arabidopsis thaliana]
Seq. No.
                  143566
Seq. ID
                  LIB3168-029-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g1009234
BLAST score
                  717
E value
                  4.0e-76
Match length
                  154
% identity
                  84
NCBI Description
                  (L38829) SUP2 gene product [Nicotiana tabacum]
Seq. No.
                  143567
Seq. ID
                  LIB3168-029-P1-K1-D2
Method
                  BLASTN
NCBI GI
                  q4006885
BLAST score
                  324
E value
                  0.0e + 00
Match length
                  453
                  98
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                  fragment No
Seq. No.
                  143568
Seq. ID
                  LIB3168-029-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q4678299
BLAST score
                  816
E value
                  1.0e-87
Match length
                  158
% identity
                  99
NCBI Description
                  (AL049655) cysteine proteinase precursor-like protein
                  [Arabidopsis thaliana]
```

Seq. No. 143569

Seq. ID LIB3168-029-P1-K1-D4

Method BLASTX NCBI GI g3941412



BLAST score 505 E value 3.0e-51 Match length 91 % identity 99

NCBI Description (AF062860) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 143570

Seq. ID LIB3168-029-P1-K1-D5

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120

% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143571

Seq. ID LIB3168-029-P1-K1-D6

Method BLASTN
NCBI GI g3985932
BLAST score 247
E value 1.0e-137
Match length 251
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K22J17, complete sequence [Arabidopsis thaliana]

Seq. No. 143572

Seq. ID LIB3168-029-P1-K1-D7

Method BLASTX
NCBI GI g1628583
BLAST score 403
E value 3.0e-39
Match length 78
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143573

Seq. ID LIB3168-029-P1-K1-D8

Method BLASTX
NCBI GI g112681
BLAST score 668
E value 2.0e-70
Match length 150
% identity 86

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143574



Seq. ID LIB3168-029-P1-K1-D9 Method BLASTN

NCBI GI g4314374 BLAST score 50

E value 1.0e-19
Match length 70
% identity 12

NCBI Description Arabidopsis thaliana chromosome II BAC F10A12 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 143575

Seq. ID LIB3168-029-P1-K1-E1

Method BLASTX
NCBI GI g3540201
BLAST score 613
E value 7.0e-64
Match length 152
% identity 81

NCBI Description (AC004260) Putative nuclear protein [Arabidopsis thaliana]

Seq. No. 143576

Seq. ID LIB3168-029-P1-K1-E10

Method BLASTX
NCBI GI g2924779
BLAST score 687
E value 1.0e-72
Match length 136
% identity 100

NCBI Description (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis

thaliana] >gi_2981616_dbj_BAA25248_ (AB008854)
3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
>gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA

thiolase [Arabidopsis thaliana]

Seq. No. 143577

Seq. ID LIB3168-029-P1-K1-E12

Method BLASTX
NCBI GI g2586125
BLAST score 351
E value 1.0e-33
Match length 79
% identity 91

NCBI Description (U89512) b-keto acyl reductase [Arabidopsis thaliana]

Seq. No. 143578

Seq. ID LIB3168-029-P1-K1-E2

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143579



```
Seq. ID
                   LIB3168-029-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   g1076442
BLAST score
                   802
E value
                   5.0e-86
Match length
                   155
% identity
                   98
                  beta-glucosidase (EC 3.2.1.21) - rape
NCBI Description
                   >gi 757740 emb_CAA57913_ (X82577) beta-glucosidase
                   [Brassica napus]
                  143580
Seq. No.
Seq. ID
                  LIB3168-029-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g1174852
BLAST score
                   696
E value
                  1.0e-73
Match length
                  129
% identity
                  100
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-19 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) (TAYO29)
                  >gi_2129757_pir__S46656 ubiquitin carrier protein E2 (clone
                  TAY029) - Arabidopsis thaliana >gi_600389_emb_CAA51200_
                   (X72625) ubiquitin conjugating enzyme E2 [Arabidopsis
                   thaliana] >gi_992708 (U33759) UBC14 [Arabidopsis thaliana]
Seq. No.
                  143581
Seq. ID
                  LIB3168-029-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g1742961
BLAST score
                  477
E value
                  5.0e-48
Match length
                  93
% identity
                  100
NCBI Description
                  (X94756) cystathionine gamma-synthase [Arabidopsis
                  thaliana]
Seq. No.
                  143582
Seq. ID
                  LIB3168-029-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g2129657
BLAST score
                  396
E value
                  2.0e-38
Match length
                  110
% identity
                  76
NCBI Description
                  oleosin isoform - Arabidopsis thaliana
                  >gi 987014 emb CAA90877_ (Z54164) oleosin [Arabidopsis
                  thaliana] \overline{>}gi_{987016_{emb}} CAA90878_ (Z54165) oleosin
                  [Arabidopsis thaliana]
```

Seq. No. 143583

Seq. ID LIB3168-029-P1-K1-E8

Method BLASTX NCBI GI q119143 BLAST score 715 E value 8.0e-76 Match length 138



% identity S NCBI Description B

ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_81606_pir__S06724 translation elongation factor eEF-1
alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
(X16430) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1369927_emb_CAA34454_ (X16431) elongation factor
1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_
(X16431) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana]
>gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana]
>gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No. 143584

Seq. ID LIB3168-029-P1-K1-E9

Method BLASTX
NCBI GI g1628583
BLAST score 639
E value 1.0e-66
Match length 131
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143585

Seq. ID LIB3168-029-P1-K1-F1

Method BLASTX
NCBI GI g2244896
BLAST score 810
E value 5.0e-87
Match length 157
% identity 98

NCBI Description (Z97338) similar to HSR201 protein N.tabacum [Arabidopsis

thaliana]

Seq. No. 143586

Seq. ID LIB3168-029-P1-K1-F10

Method BLASTX
NCBI GI g112681
BLAST score 635
E value 2.0e-66
Match length 145
% identity 85

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604 pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143587

Seq. ID LIB3168-029-P1-K1-F11

Method BLASTX
NCBI GI g1628583
BLAST score 620
E value 1.0e-64
Match length 120
% identity 99

17721



NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143588 Seq. ID LIB3168-029-P1-K1-F2 BLASTX

Method NCBI GI g2984353 BLAST score 395 E value 2.0e-38 94 Match length 74 % identity

(AE000775) hypothetical protein [Aquifex aeolicus] NCBI Description

Seq. No. 143589 Seq. ID

LIB3168-029-P1-K1-F3

Method BLASTX NCBI GI g2583125 BLAST score 423 E value 1.0e-41 Match length 117 % identity 69

(AC002387) putative transketolase precursor [Arabidopsis NCBI Description

thaliana]

Seq. No. 143590

Seq. ID LIB3168-029-P1-K1-F4

Method BLASTX NCBI GI g4193388 BLAST score 453 E value 4.0e-45 Match length 122 % identity 74

NCBI Description (AF091455) translationally controlled tumor protein [Hevea

brasiliensis]

Seq. No. 143591

Seq. ID LIB3168-029-P1-K1-F6

Method BLASTX NCBI GI g1628583 BLAST score 400 E value 6.0e-39 Match length 110 % identity 74

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143592

LIB3168-029-P1-K1-F7 Seq. ID

Method BLASTN NCBI GI q4454447 BLAST score 444 E value 0.0e + 00Match length 465 % identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F5H14 genomic

Match length

% identity

156

89



sequence, complete sequence [Arabidopsis thaliana]

143593 Seq. No. Seq. ID LIB3168-029-P1-K1-F8 Method BLASTX NCBI GI g112681 BLAST score 812 3.0e-87 E value 154 Match length 99 % identity NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 143594 Seq. ID LIB3168-029-P1-K1-F9 Method BLASTX NCBI GI q4678952 BLAST score 664 E value 7.0e-70 Match length 125 99 % identity NCBI Description (AL049711) putative protein [Arabidopsis thaliana] Seq. No. 143595 Seq. ID LIB3168-029-P1-K1-G10 Method BLASTX NCBI GI g1628583 BLAST score 619 E value 1.0e-64 Match length 120 % identity 99 NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143596 Seq. ID LIB3168-029-P1-K1-G12 Method BLASTN NCBI GI g2109292 BLAST score 359 E value 0.0e + 00Match length 367 % identity 99 NCBI Description Arabidopsis thaliana serine/threonine protein kinase mRNA, complete cds Seq. No. 143597 Seq. ID LIB3168-029-P1-K1-G2 Method BLASTX NCBI GI g131143 BLAST score 752 E value 3.0e-80

17723

NCBI Description PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A1 >gi 72670_pir _A1NTP7 photosystem I P700 apoprotein A1 common tobacco chloroplast >gi_11830_emb_CAA77352 (Z00044) PSI P700 apoprotein Al [Nicotiana tabacum] >gi_225198 prf 1211235AC photosystem I P700 apoprotein A1 [Nicotiana tabacum] Seq. No. 143598 Seq. ID LIB3168-029-P1-K1-G3 Method BLASTN q4589428 NCBI GI BLAST score 178 E value 2.0e-95 Match length 415 % identity 96 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence Seq. No. 143599 Seq. ID LIB3168-029-P1-K1-G4 Method BLASTN NCBI GI g2494110 BLAST score 33 E value 8.0e-10 Match length 58 12 Sequence of BAC T1G11 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

% identity NCBI Description

Seq. No. 143600 Seq. ID LIB3168-029-P1-K1-G5 Method BLASTX NCBI GI g3334323

BLAST score 486 E value 5.0e-49 Match length 129 % identity 75

GTP-BINDING PROTEIN SAR1A >gi_1314860 (U56929) Sar1 homolog NCBI Description

[Arabidopsis thaliana] >gi 2104532 gb AAC78700.1

(AF001308) SAR1/GTP-binding secretory factor [Arabidopsis thaliana] >gi_2104550 (AF001535) AGAA.4 [Arabidopsis

thaliana]

Seq. No. 143601

LIB3168-029-P1-K1-G6 Seq. ID

Method BLASTX NCBI GI q1628583 BLAST score 378 E value 2.0e-36 Match length 78 % identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143602

Seq. ID LIB3168-029-P1-K1-G7

17724



Method BLASTX
NCBI GI g1628583
BLAST score 491
E value 1.0e-49
Match length 101
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143603

Seq. ID LIB3168-029-P1-K1-G8

Method BLASTX
NCBI GI g2828296
BLAST score 670
E value 1.0e-70
Match length 149
% identity 82

NCBI Description (AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No. 143604

Seq. ID LIB3168-029-P1-K1-G9

Method BLASTX
NCBI GI g2262113
BLAST score 629
E value 8.0e-66
Match length 148
% identity 82

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 143605

Seq. ID LIB3168-029-P1-K1-H1

Method BLASTX
NCBI GI g3193301
BLAST score 500
E value 1.0e-50
Match length 150
% identity 73

NCBI Description (AF069298) Arabidopsis putative chloroplast outer envelope

86-like protein T10P11.19 (GB: AC002330) [Arabidopsis

thaliana]

Seq. No. 143606

Seq. ID LIB3168-029-P1-K1-H10

Method BLASTX
NCBI GI g2498731
BLAST score 764
E value 1.0e-81
Match length 144
% identity 99

NCBI Description PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1

>gi_1362013_pir__S57611 zeta-crystallin homolog Arabidopsis thaliana >gi_886428_emb_CAA89838 (Z49768)

zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No. 143607

Seq. ID LIB3168-029-P1-K1-H11



Method BLASTN
NCBI GI g1628582
BLAST score 44
E value 1.0e-15
Match length 80
% identity 89

NCBI Description Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No. 143608

Seq. No. 143608 Seq. ID LIB3168-029-P1-K1-H3

Method BLASTX
NCBI GI g112682
BLAST score 680
E value 1.0e-71
Match length 153
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143609

Seq. ID LIB3168-029-P1-K1-H4

Method BLASTX
NCBI GI g1628583
BLAST score 619
E value 1.0e-64
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143610

Seq. ID LIB3168-029-P1-K1-H5

Method BLASTX
NCBI GI g2129657
BLAST score 398
E value 1.0e-38
Match length 109
% identity 77

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
thaliana] >gi 987016_emb CAA90878 (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 143611

Seq. ID LIB3168-029-P1-K1-H7

Method BLASTX
NCBI GI g112682
BLAST score 645
E value 1.0e-67
Match length 148
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

-



cruciferin precursor (CRB) - Arabidopsis thaliana
>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 143612

Seq. ID LIB3168-029-P1-K1-H8

Method BLASTN
NCBI GI g2213606
BLAST score 392
E value 0.0e+00
Match length 464
% identity 96

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F21J9,

complete sequence [Arabidopsis thaliana]

Seq. No. 143613

Seq. ID LIB3168-029-P1-K1-H9

Method BLASTX
NCBI GI g1628583
BLAST score 642
E value 3.0e-67
Match length 123
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143614

Seq. ID LIB3168-030-P1-K1-A1

Method BLASTX
NCBI GI g1628583
BLAST score 662
E value 1.0e-69
Match length 128
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143615

Seq. ID LIB3168-030-P1-K1-A11

Method BLASTX
NCBI GI g1071913
BLAST score 288
E value 7.0e-26
Match length 120
% identity 57

NCBI Description cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial

- spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine

synthase [Spinacia oleracea]

Seq. No. 143616

Seq. ID LIB3168-030-P1-K1-A12

Method BLASTX NCBI GI g112739 BLAST score 425



E value 6.0e-42
Match length 121
% identity 71
NCBI Description 2S SEED S

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -

Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205 emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi 4490711 emb CAB38845.1_ (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 143617

Seq. ID LIB3168-030-P1-K1-A3

Method BLASTX
NCBI GI g4115356
BLAST score 574
E value 2.0e-59
Match length 112
% identity 98

NCBI Description (AC005957) putative thionin variant protein [Arabidopsis

thaliana]

Seq. No. 143618

Seq. ID LIB3168-030-P1-K1-A4

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143619

Seq. ID LIB3168-030-P1-K1-A5

Method BLASTX
NCBI GI g1628583
BLAST score 544
E value 7.0e-56
Match length 137
% identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143620

Seq. ID LIB3168-030-P1-K1-A6

Method BLASTX
NCBI GI g112682
BLAST score 562
E value 5.0e-58
Match length 120
% identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis



thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 143621

Seq. ID LIB3168-030-P1-K1-A7

Method BLASTX
NCBI GI g1628583
BLAST score 665
E value 4.0e-70
Match length 128
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143622

Seq. ID LIB3168-030-P1-K1-A8

Method BLASTX
NCBI GI g2129532
BLAST score 460
E value 5.0e-46
Match length 116
% identity 77

NCBI Description acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) -

Arabidopsis thaliana >gi_1107507_emb_CAA63746_ (X93461) acyl-[acyl-carrier protein] desaturase [Arabidopsis

thaliana]

Seq. No. 143623

Seq. ID LIB3168-030-P1-K1-B1

Method BLASTX
NCBI GI g1628583
BLAST score 179
E value 2.0e-13
Match length 52
% identity 65

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_(AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143624

Seq. ID LIB3168-030-P1-K1-B10

Method BLASTX
NCBI GI g112682
BLAST score 610
E value 1.0e-63
Match length 135
% identity 87

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir \$08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143625

Seq. ID LIB3168-030-P1-K1-B11

Method BLASTX



NCBI GI g1628583 BLAST score 454 E value 2.0e-45 Match length 117 % identity 65

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143626

Seq. ID LIB3168-030-P1-K1-B12

Method BLASTN
NCBI GI g2842474
BLAST score 236
E value 1.0e-130

E value 1.0e-130 Match length 240 % identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009

(ESSAII project)

Seq. No. 143627

Seq. ID LIB3168-030-P1-K1-B2

Method BLASTN
NCBI GI g4757411
BLAST score 408
E value 0.0e+00
Match length 412
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MXC7, complete sequence

Seq. No. 143628

Seq. ID LIB3168-030-P1-K1-B3

Method BLASTX
NCBI GI g3355477
BLAST score 580
E value 4.0e-60
Match length 135
% identity 46

NCBI Description (AC004218) putative P-glycoprotein, pgpl [Arabidopsis

thaliana]

Seq. No. 143629

Seq. ID LIB3168-030-P1-K1-B4

Method BLASTX
NCBI GI g112682
BLAST score 592
E value 1.0e-61
Match length 125
% identity 89

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143630



Seq. ID LIB3168-030-P1-K1-B5

Method BLASTX
NCBI GI g1628583
BLAST score 195
E value 6.0e-52
Match length 137
% identity 80

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143631

Seq. ID LIB3168-030-P1-K1-B6

Method BLASTN
NCBI GI g1699056
BLAST score 361
E value 0.0e+00
Match length 373
% identity 99

NCBI Description Arabidopsis thaliana 27 kDa unknown protein mRNA, complete

cds

Seq. No. 143632

Seq. ID LIB3168-030-P1-K1-B7

Method BLASTX
NCBI GI g112682
BLAST score 569
E value 8.0e-59
Match length 133
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143633

Seq. ID LIB3168-030-P1-K1-B9

Method BLASTX
NCBI GI g112681
BLAST score 564
E value 3.0e-58
Match length 132
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143634

Seq. ID LIB3168-030-P1-K1-C10

Method BLASTN
NCBI GI g4106339
BLAST score 280
E value 1.0e-156
Match length 304



% identity 97
NCBI Description Arabidopsis thaliana protein phosphatase 2A regulatory
subunit isoform B' delta mRNA, complete cds

Seq. No. 143635

Seq. ID LIB3168-030-P1-K1-C11

Method BLASTX
NCBI GI g2829896
BLAST score 296
E value 8.0e-27
Match length 105
% identity 56

NCBI Description (AC002311) highly similar to auxin-regulated protein GH3,

gp X60033 18591 [Arabidopsis thaliana]

Seq. No. 143636

Seq. ID LIB3168-030-P1-K1-C12

Method BLASTX
NCBI GI g1171978
BLAST score 322
E value 7.0e-30
Match length 100
% identity 63

NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)

(PABP 2) >gi_304109 (L19418) poly(A)-binding protein

[Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)

poly(A)-binding protein [Arabidopsis thaliana]

Seq. No. 143637

Seq. ID LIB3168-030-P1-K1-C2

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143638

Seq. ID LIB3168-030-P1-K1-C3

Method BLASTX
NCBI GI g542157
BLAST score 550
E value 1.0e-56
Match length 126
% identity 83

NCBI Description ribosomal 5S RNA-binding protein - Rice

Seq. No. 143639

Seq. ID LTB3168-030-P1-K1-C4

Method BLASTX
NCBI GI g112681
BLAST score 504
E value 3.0e-51
Match length 136

17732



% identity 78

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143640

Seq. ID LIB3168-030-P1-K1-C5

Method BLASTX
NCBI GI g1628583
BLAST score 669
E value 2.0e-70
Match length 131
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143641

Seq. ID LIB3168-030-P1-K1-C7

Method BLASTX
NCBI GI g1628583
BLAST score 156
E value 2.0e-10
Match length 72
% identity 96

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143642

Seq. ID LIB3168-030-P1-K1-D1

Method BLASTN
NCBI GI g1209632
BLAST score 158
E value 1.0e-83
Match length 266
% identity 95

NCBI Description Arabidopsis thaliana pattern-formation (GNOM) gene,

complete cds

Seq. No. 143643

Seq. ID LIB3168-030-P1-K1-D10

Method BLASTX
NCBI GI g112737
BLAST score 540
E value 2.0e-55
Match length 131
% identity 80

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204 emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]



```
Seq. No.
                   143644
Seq. ID
                   LIB3168-030-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g4191794
BLAST score
                   383
                   5.0e-37
E value
Match length
                   71
% identity
                   97
NCBI Description
                   (AC005917) putative zinc finger-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   143645
Seq. ID
                   LIB3168-030-P1-K1-D12
Method
                   BLASTN
NCBI GI
                   q2262135
BLAST score
                   398
                   0.0e+00
E value
Match length
                   406
% identity
                   100
NCBI Description Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
                   cM, complete sequence
Seq. No.
                   143646
Seq. ID
                   LIB3168-030-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   g112741
BLAST score
                   691
E value
                   4.0e-73
Match length
                   128
% identity
                   100
NCBI Description
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                   PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                   3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
Seq. No.
                   143647
Seq. ID
                   LIB3168-030-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   621
E value
                   6.0e-65
Match length
                   120
% identity
                   99
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
```

Seq. No. 143648

Seq. ID LIB3168-030-P1-K1-D5

Method BLASTX
NCBI GI g1628583
BLAST score 314
E value 6.0e-29



Match length % identity 98

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143649

Seq. ID LIB3168-030-P1-K1-D6

Method BLASTX NCBI GI q4204299 BLAST score 551 E value 1.0e-56 Match length 111

% identity 98

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 143650

Seq. ID LIB3168-030-P1-K1-D7

Method BLASTX NCBI GI q1628583 BLAST score 118 E value 6.0e-06 Match length 72 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143651

Seq. ID LIB3168-030-P1-K1-E1

Method BLASTX NCBI GI g1628583 BLAST score 542 1.0e-55 E value Match length 137 79 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143652

Seq. ID LIB3168-030-P1-K1-E10

Method BLASTX NCBI GI g1491615 BLAST score 606 4.0e-63 E value Match length 136 % identity

NCBI Description (X99923) male sterility 2-like protein [Arabidopsis

thaliana]

Seq. No. 143653

Seq. ID LIB3168-030-P1-K1-E11

Method BLASTX NCBI GI g1169598 BLAST score 432



E value 9.0e-43 Match length 91 % identity 87

NCBI Description OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

(DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12

desaturase [Arabidopsis thaliana]

Seq. No. 143654

Seq. ID LIB3168-030-P1-K1-E12

Method BLASTX
NCBI GI g1628583
BLAST score 335
E value 2.0e-31
Match length 84
% identity 77

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143655

Seq. ID LIB3168-030-P1-K1-E2

Method BLASTX
NCBI GI g21112
BLAST score 277
E value 1.0e-24
Match length 59
% identity 86

NCBI Description (X59805) cruciferin [Raphanus sativus]

Seq. No. 143656

Seq. ID LIB3168-030-P1-K1-E3

Method BLASTX
NCBI GI g1628583
BLAST score 620
E value 8.0e-65
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143657

Seq. ID LIB3168-030-P1-K1-E4

Method BLASTN
NCBI GI g457401
BLAST score 143
E value 1.0e-74
Match length 143
% identity 100

NCBI Description Arabidopsis thaliana mRNA for MAP kinase, complete cds

Seq. No. 143658

Seq. ID LIB3168-030-P1-K1-E5

Method BLASTX
NCBI GI g1628583
BLAST score 686
E value 2.0e-72

17736



Match length 133 % identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143659

Seq. ID LIB3168-030-P1-K1-E6

Method BLASTN
NCBI GI g4371278
BLAST score 365
E value 0.0e+00
Match length 373
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T2N18 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 143660

Seq. ID LIB3168-030-P1-K1-F1

Method BLASTN
NCBI GI g166612
BLAST score 52
E value 3.0e-21
Match length 64
% identity 95

NCBI Description A.thaliana at 254 gene encoding albumin 25 subunit 4,

complete cds

Seq. No. 143661

Seq. ID LIB3168-030-P1-K1-F11

Method BLASTX
NCBI GI g1628583
BLAST score 687
E value 1.0e-72
Match length 135
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143662

Seq. ID LIB3168-030-P1-K1-F12

Method BLASTX
NCBI GI g1628583
BLAST score 619
E value 1.0e-64
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143663

Seq. ID LIB3168-030-P1-K1-F2

Method BLASTX NCBI GI g2739366 BLAST score 232



E value 3.0e-19 Match length 77

% identity 51

NCBI Description (AC002505) SF16 like protein [Arabidopsis thaliana]

Seq. No. 143664

Seq. ID LIB3168-030-P1-K1-F3

Method BLASTX
NCBI GI g112682
BLAST score 555
E value 4.0e-57
Match length 133
% identity 80

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143665

Seq. ID LIB3168-030-P1-K1-F4

Method BLASTX
NCBI GI g1628583
BLAST score 713
E value 1.0e-75
Match length 135
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143666

Seq. ID LIB3168-030-P1-K1-F5

Method BLASTX
NCBI GI g112682
BLAST score 578
E value 7.0e-60
Match length 135
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143667

Seq. ID LIB3168-030-P1-K1-F6

Method BLASTX
NCBI GI g4586249
BLAST score 457
E value 1.0e-45
Match length 135
% identity 62

NCBI Description (AL049640) putative pollen surface protein [Arabidopsis

thaliana]

Seq. No. 143668



Seq. ID LIB3168-030-P1-K1-F8 Method BLASTX NCBI GI a2736155 BLAST score 505 3.0e-51 E value Match length 118 % identity 86 NCBI Description (AF022082) sulfolipid biosynthesis protein [Arabidopsis thaliana] >gi_3688184_emb_CAA21212_ (AL031804) sulfolipid biosynthesis protein SQD1 [Arabidopsis thaliana] Seq. No. 143669 Seq. ID LIB3168-030-P1-K1-F9 Method BLASTX NCBI GI q2129657 BLAST score 333 E value 4.0e-31 Match length 99 ž % identity 73 NCBI Description oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877 (Z54164) oleosin [Arabidopsis thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin [Arabidopsis Thaliana] Seq. No. 143670 Seq. ID LIB3168-030-P1-K1-G10 Method BLASTX NCBI GI g4006924 BLAST score 726 E value 3.0e-77 Match length 135 % identity 100 NCBI Description (Z99708) beta-galactosidase like protein [Arabidopsis thaliana] 143671 Seq. No. Seq. ID LIB3168-030-P1-K1-G12 Method BLASTX NCBI GI q112681 BLAST score 710 E value 2.0e-75 Match length 135 % identity 99 NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 143672 Seq. ID LIB3168-030-P1-K1-G2 Method BLASTX NCBI GI q1628583

Method BLASTX
NCBI GI g1628583
BLAST score 606
E value 4.0e-63
Match length 120
% identity 97

17739



NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143673

Seq. ID LIB3168-030-P1-K1-G3

Method BLASTX
NCBI GI g112741
BLAST score 680
E value 8.0e-72
Match length 126
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143674

Seq. ID LIB3168-030-P1-K1-G4

Method BLASTX
NCBI GI g4006924
BLAST score 259
E value 2.0e-22
Match length 67
% identity 76

NCBI Description (Z99708) beta-galactosidase like protein [Arabidopsis

thaliana]

Seq. No. 143675

Seq. ID LIB3168-030-P1-K1-G5

Method BLASTX
NCBI GI g543841
BLAST score 534
E value 1.0e-54
Match length 106
% identity 97

NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875

ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236 2 (AC007236)

ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No. 143676

Seq. ID LIB3168-030-P1-K1-G6

Method BLASTN
NCBI GI g4165340
BLAST score 382
E value 0.0e+00
Match length 407
% identity 82

NCBI Description Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]



Seq. No.

Seq. ID LIB3168-030-P1-K1-G7

96

Method BLASTX NCBI GI g1628583 BLAST score 513 E value 2.0e-52 Match length 104

% identity NCBI Description

(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143678

Seq. ID LIB3168-030-P1-K1-G8

Method BLASTX NCBI GI g1174779 BLAST score 396 1.0e-38 E value Match length 84 % identity 93

NCBI Description TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi_166894

(M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana] >gi_4490703_emb_CAB38837.1_ (AL035680) tryptophan

synthase beta-subunit (TSB2) [Arabidopsis thaliana]

Seq. No. 143679

Seq. ID LIB3168-030-P1-K1-H1

Method BLASTX NCBI GI g1628583 BLAST score 524 2.0e-53 E value Match length 134 % identity 78

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143680

Seq. ID LIB3168-030-P1-K1-H11

Method BLASTX NCBI GI g1628583 BLAST score 727 2.0e-77 E value Match length 141 % identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143681

Seq. ID LIB3168-030-P1-K1-H3

Method BLASTX NCBI GI g1628583 BLAST score 620 8.0e-65 E value Match length 126 % identity



NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143682

Seq. ID LIB3168-030-P1-K1-H4

Method BLASTN
NCBI GI g3128136
BLAST score 285
E value 1.0e-159
Match length 350
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K1F13, complete sequence [Arabidopsis thaliana]

Seq. No. 143683

Seq. ID LIB3168-030-P1-K1-H6

Method BLASTX
NCBI GI g3935150
BLAST score 289
E value 6.0e-26
Match length 104
% identity 64

NCBI Description (AC005106) T25N20.14 [Arabidopsis thaliana]

Seq. No. 143684

Seq. ID LIB3168-030-P1-K1-H7

Method BLASTX
NCBI GI g2660673
BLAST score 244
E value 1.0e-20
Match length 112
% identity 25

NCBI Description (AC002342) unknown protein [Arabidopsis thaliana]

Seq. No. 143685

Seq. ID LIB3168-030-P1-K1-H8

Method BLASTX
NCBI GI g112681
BLAST score 654
E value 9.0e-69
Match length 134
% identity 93

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143686

Seq. ID LIB3168-030-P1-K1-H9

Method BLASTX
NCBI GI g112682
BLAST score 656
E value 5.0e-69
Match length 135
% identity 92



NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsīs thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143687

Seq. ID LIB3168-031-P1-K1-A1

Method BLASTX
NCBI GI g112741
BLAST score 667
E value 3.0e-70
Match length 128
% identity 98

% identity 98
NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143688

Seq. ID LIB3168-031-P1-K1-A10

Method BLASTX
NCBI GI g119143
BLAST score 271
E value 1.0e-41
Match length 108
% identity 85

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_81606_pir__S06724 translation elongation factor eEF-1
alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
(X16430) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1369927_emb_CAA34454_ (X16431) elongation factor
1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_
(X16431) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
>gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
>gi_1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]

Seq. No. 143689

Seq. ID LIB3168-031-P1-K1-A11

Method BLASTX
NCBI GI g1628583
BLAST score 543
E value 1.0e-56
Match length 117
% identity 92

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143690

Seq. ID LIB3168-031-P1-K1-A12

Method BLASTN NCBI GI g3985958



```
BLAST score
                  5.0e-68
E value
Match length
                  405
                  100
% identity
```

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MZN1, complete sequence [Arabidopsis thaliana]

Seq. No. 143691

Seq. ID LIB3168-031-P1-K1-A3

Method BLASTN NCBI GI g4199934 BLAST score 70 3.0e-31 E value 106

Match length % identity 94

Genomic sequence for Arabidopsis thaliana BAC T3P18, NCBI Description

complete sequence [Arabidopsis thaliana]

Seq. No. 143692

Seq. ID LIB3168-031-P1-K1-A4

Method BLASTX NCBI GI g1628583 BLAST score 200 2.0e-15 E value Match length 74 % identity 96

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143693

Seq. ID LIB3168-031-P1-K1-A5

Method BLASTN NCBI GI g2351071 BLAST score 381 0.0e + 00E value Match length 416 % identity 97

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MVA3, complete sequence [Arabidopsis thaliana]

Seq. No. 143694

Seq. ID LIB3168-031-P1-K1-A6

Method BLASTX NCBI GI g1628583 BLAST score 436 E value 3.0e-43 Match length 108 % identity 81

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143695

Seq. ID LIB3168-031-P1-K1-A7

Method BLASTX NCBI GI g112741



BLAST score E value 9.0e-60 Match length 116 92 % identity

2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi_68855 pir NWMU3 2S albumin 3 precursor -

Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143696

Seq. ID LIB3168-031-P1-K1-A8

Method BLASTX NCBI GI g112682 BLAST score 559 1.0e-59 E value Match length 130 % identity 92

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143697

Seq. ID LIB3168-031-P1-K1-A9

Method BLASTX NCBI GI g112739 BLAST score 450 E value 8.0e-45 Match length 127 72 % identity

NCBI Description

2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 143698

Seq. ID LIB3168-031-P1-K1-B10

Method BLASTX NCBI GI q112681 BLAST score 598 E value 3.0e-62 139 Match length % identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir \$08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143699



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LIB3168-031-P1-K1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2842474
BLAST score
                  128
                  1.0e-65
E value
                  273
Match length
                  57
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
NCBI Description
                  (ESSAII project)
Séq. No.
                  143700
Seq. ID
                  LIB3168-031-P1-K1-B12
                  BLASTX
Method
NCBI GI
                  q3335169
BLAST score
                  646
                  8.0e-68
E value
Match length
                  125
% identity
                  98
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
                  >gi 4455197 emb CAB36520.1 (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
                  143701
Seq. No.
Seq. ID
                  LIB3168-031-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  695
E value
                  1.0e-73
Match length
                  135
% identity
                  98
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  143702
Seq. No.
Seq. ID
                  LIB3168-031-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  541
                  2.0e-55
E value
Match length
                  133
                  80
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  143703
                  LIB3168-031-P1-K1-B5
```

Seq. ID

Method BLASTX NCBI GI g112681 BLAST score 551 E value 1.0e-56 Match length 133



% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143704

Seq. ID LIB3168-031-P1-K1-B6

Method BLASTN
NCBI GI g4538895
BLAST score 291
E value 1.0e-163

Match length 319 % identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8

(ESSA project)

Seq. No. 143705

Seq. ID LIB3168-031-P1-K1-B7

Method BLASTX
NCBI GI g112681
BLAST score 506
E value 2.0e-51
Match length 131
% identity 77

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143706

Seq. ID LIB3168-031-P1-K1-B8

Method BLASTX
NCBI GI g112682
BLAST score 631
E value 4.0e-66
Match length 133
% identity 89

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143707

Seq. ID LIB3168-031-P1-K1-B9

Method BLASTX
NCBI GI g1628583
BLAST score 652
E value 1.0e-68
Match length 131
% identity 95

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]



Seq. No. 143708

Seq. ID LIB3168-031-P1-K1-C1

Method BLASTN
NCBI GI g2623294
BLAST score 353
E value 0.0e+00
Match length 415
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T20B5 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 143709

Seq. ID LIB3168-031-P1-K1-C11

Method BLASTX
NCBI GI g112681
BLAST score 618
E value 1.0e-64
Match length 126
% identity 96

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143710

Seq. ID LIB3168-031-P1-K1-C12

Method BLASTX
NCBI GI g112681
BLAST score 703
E value 2.0e-74
Match length 140
% identity 95

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143711

Seq. ID LIB3168-031-P1-K1-C2

Method BLASTX
NCBI GI g112741
BLAST score 710
E value 2.0e-75
Match length 133
% identity 99

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__ NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143712



LIB3168-031-P1-K1-C3 Seq. ID Method BLASTX NCBI GI g112681 BLAST score 580 4.0e-60 E value Match length 135 % identity NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 143713 Seq. ID LIB3168-031-P1-K1-C4 Method BLASTX NCBI GI g1628583 BLAST score 529 4.0e-54 E value Match length 139 % identity 76 NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143714 Seq. ID LIB3168-031-P1-K1-C5 Method BLASTX NCBI GI q4138179 BLAST score 228 E value 2.0e-19 Match length 63 % identity 75 NCBI Description (AJ223969) elongation factor 1 alpha subunit [Malus domestica] Seq. No. 143715 Seq. ID LIB3168-031-P1-K1-C6 Method BLASTX NCBI GI g1628583 BLAST score 384 E value 4.0e-46 Match length 104 92 % identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143716 Seq. ID LIB3168-031-P1-K1-C7 Method BLASTX

NCBI GI g1628583 BLAST score 530 E value 3.0e-54 Match length 139 % identity 77

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis



thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143717

Seq. ID LIB3168-031-P1-K1-C8

Method BLASTX
NCBI GI g112681
BLAST score 523
E value 2.0e-53
Match length 133
% identity 78

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143718

Seq. ID LIB3168-031-P1-K1-D1

Method BLASTX
NCBI GI g1628583
BLAST score 496
E value 4.0e-57
Match length 119
% identity 91

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143719

Seq. ID LIB3168-031-P1-K1-D11

Method BLASTX
NCBI GI g1628583
BLAST score 505
E value 2.0e-51
Match length 111
% identity 88

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143720

Seq. ID LIB3168-031-P1-K1-D12

Method BLASTX
NCBI GI g4204298
BLAST score 533
E value 1.0e-54
Match length 120
% identity 86

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 143721

Seq. ID LIB3168-031-P1-K1-D2

Method BLASTX NCBI GI g112737 BLAST score 588



E value 5.0e-61 Match length 140 % identity 81 NCBI Description 2S SEED

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__ NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710 emb_CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143722

Seq. ID LIB3168-031-P1-K1-D3

Method BLASTX
NCBI GI g1628583
BLAST score 363
E value 1.0e-34
Match length 70
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143723

Seq. ID LIB3168-031-P1-K1-D7

Method BLASTX
NCBI GI g112739
BLAST score 421
E value 2.0e-41
Match length 127
% identity 70

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68854_pir_NWMU2 2S albumin 2 precursor Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit

2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi_4490711_emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 143724

Seq. ID LIB3168-031-P1-K1-D8

Method BLASTX
NCBI GI g1628583
BLAST score 475
E value 4.0e-48
Match length 98
% identity 95

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143725

Seq. ID LIB3168-031-P1-K1-E1

Method BLASTX
NCBI GI g1742951
BLAST score 634
E value 2.0e-66



Match length 139 % identity 93

NCBI Description (Y09817) Ca2+-ATPase [Arabidopsis thaliana]

Seq. No. 143726

Seq. ID LIB3168-031-P1-K1-E12

Method BLASTX
NCBI GI g1628583
BLAST score 586
E value 8.0e-61
Match length 125
% identity 91

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143727

Seq. ID LIB3168-031-P1-K1-E2

Method BLASTX
NCBI GI g231587
BLAST score 490
E value 1.0e-49
Match length 134
% identity 73

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR

>gi_283001_pir__S25304 H+-transporting ATP synthase (EC
3.6.1.34) beta chain precursor, mitochondrial - rice
>gi_218147_dbj_BAA01372_ (D10491) mitochondrial F1-ATPase

[Oryza satīva]

Seq. No. 143728

Seq. ID LIB3168-031-P1-K1-E4

Method BLASTX
NCBI GI g1628583
BLAST score 45
E value 3.0e-34
Match length 86
% identity 93

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143729

Seq. ID LIB3168-031-P1-K1-E5

Method BLASTX
NCBI GI g1628583
BLAST score 290
E value 3.0e-26
Match length 64
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143730

Seq. ID LIB3168-031-P1-K1-E6

Method BLASTX



NCBI GI g112682 BLAST score 438 E value 2.0e-43 Match length 112 % identity 76

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143731

Seq. ID LIB3168-031-P1-K1-E7

Method BLASTX
NCBI GI g112681
BLAST score 557
E value 2.0e-57
Match length 119
% identity 91

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143732

Seq. ID LIB3168-031-P1-K1-E8

Method BLASTX
NCBI GI g112682
BLAST score 323
E value 5.0e-30
Match length 115
% identity 59

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143733

Seq. ID LIB3168-031-P1-K1-E9

Method BLASTX
NCBI GI g585165
BLAST score 261
E value 1.0e-22
Match length 76
% identity 71

NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM

(G6PD) >gi 2129985 pir S60287 glucose-6-phosphate

1-dehydrogenase (EC 1.1.1.49) - potato

>gi_471345_emb_CAA52442_ (X74421) glucose-6-phosphate

1-dehydrogenase [Solanum tuberosum]

Seq. No. 143734

Seq. ID LIB3168-031-P1-K1-F1

Method BLASTN NCBI GI g2842474



BLAST score 188 E value 1.0e-101 Match length 312 % identity 90

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009

(ESSAII project)

Seq. No. 143735

Seq. ID LIB3168-031-P1-K1-F10

Method BLASTX NCBI GI g1628583 BLAST score 658 E value 3.0e-69 Match length 131 % identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143736

Seq. ID LIB3168-031-P1-K1-F11

Method BLASTX NCBI GI q112741 BLAST score 699 E value 5.0e-74 Match length 132 % identity 98

2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143737

Seq. ID LIB3168-031-P1-K1-F12

Method BLASTX NCBI GI g1628583 BLAST score 625 E value 2.0e-65 Match length 120 100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143738

Seq. ID LIB3168-031-P1-K1-F2

Method BLASTX NCBI GI g1628583 BLAST score 554 E value 4.0e-57 Match length 117 % identity 92

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S



cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143739 Seq. ID LIB3168-031-P1-K1-F3 Method BLASTX NCBI GI g1628583 BLAST score 512 E value 3.0e-52 102 Match length % identity 96 (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143740 Seq. ID LIB3168-031-P1-K1-F4 Method BLASTX NCBI GI g112681 BLAST score 564 E value 3.0e-58 Match length 132 % identity 83 NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__\$08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 143741 Seq. ID LIB3168-031-P1-K1-F5 Method BLASTN NCBI GI g4757405 BLAST score 65 E value 3.0e-28 Match length 177 84 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MOJ10, complete sequence Seq. No. 143742 Seq. ID LIB3168-031-P1-K1-F6 Method BLASTX NCBI GI g1628583 558 BLAST score E value 2.0e-57 Match length 143 % identity 78 (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143743 Seq. ID LIB3168-031-P1-K1-F7

Method BLASTX
NCBI GI g585165
BLAST score 283
E value 3.0e-25



Match length 79 71 % identity

GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM NCBI Description

(G6PD) >gi_2129985 pir_S60287 glucose-6-phosphate

1-dehydrogenase (EC 1.1.1.49) - potato

>gi_471345_emb_CAA52442_ (X74421) glucose-6-phosphate
1-dehydrogenase [Solanum tuberosum]

143744 Seq. No.

Seq. ID LIB3168-031-P1-K1-F8

BLASTN Method NCBI GI q16472 BLAST score 257 1.0e-142 E value Match length 360 % identity 93

NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No. 143745

Seq. ID LIB3168-031-P1-K1-F9

Method BLASTX NCBI GI g3915866 BLAST score 314 E value 4.0e-29 Match length 85 % identity 69

GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS) NCBI Description

>gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine

synthetase [Lupinus luteus]

143746 Seq. No.

Seq. ID LIB3168-031-P1-K1-G1

Method BLASTN NCBI GI g2924655 BLAST score 133 1.0e-68 E value 435 Match length 96 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MKD10, complete sequence [Arabidopsis thaliana]

Seq. No. 143747

Seq. ID LIB3168-031-P1-K1-G10

Method BLASTX NCBI GI g112681 BLAST score 473 1.0e-47 E value Match length 117 % identity 79

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seg. No. 143748

Seq. ID LIB3168-031-P1-K1-G11



BLASTN Method NCBI GI g3962376 BLAST score 142 2.0e-74 E value Match length 146 99 % identity NCBI Description Arabidopsis thaliana mRNA for heat shock protein Seq. No. 143749 Seq. ID

LIB3168-031-P1-K1-G12

Method BLASTX NCBI GI g82220 BLAST score 610 1.0e-63 E value Match length 137 86 % identity

NCBI Description hypothetical protein 581 - common tobacco chloroplast >gi 225240 prf 1211235BY ORF 581 [Nicotiana tabacum]

143750 Seq. No.

Seq. ID LIB3168-031-P1-K1-G3

Method BLASTX NCBI GI g2129657 BLAST score 387 2.0e-37 E value Match length 112 74 % identity

oleosin isoform - Arabidopsis thaliana NCBI Description

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 143751

Seq. ID LIB3168-031-P1-K1-G5

Method BLASTX NCBI GI q112737 BLAST score 550 1.0e-56 E value Match length 137 79 % identity

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

143752 Seq. No.

Seq. ID LIB3168-031-P1-K1-G6

Method BLASTX NCBI GI q112681 BLAST score 223 1.0e-23 E value Match length 76 % identity 80

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509



cruciferin precursor (CRA1) - Arabidopsis thaliana
>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 143753

Seq. ID LIB3168-031-P1-K1-G7

Method BLASTN
NCBI GI g515373
BLAST score 264
E value 1.0e-147
Match length 276
% identity 99

NCBI Description Arabidopsis thaliana chloroplast DNA

Seq. No. 143754

Seq. ID LIB3168-031-P1-K1-G9

Method BLASTX
NCBI GI g112681
BLAST score 217
E value 4.0e-18
Match length 63
% identity 68

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143755

Seq. ID LIB3168-031-P1-K1-H1

Method BLASTX
NCBI GI g112743
BLAST score 671
E value 9.0e-71
Match length 129
% identity 95

NCBI Description 2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_

(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4

precursor [Arabidopsis thaliana]

Seq. No. 143756

Seq. ID LIB3168-031-P1-K1-H10

Method BLASTN
NCBI GI g1785619
BLAST score 407
E value 0.0e+00
Match length 415
% identity 100

NCBI Description A.thaliana ORFb, ORFc and AtPK2324 gene

Seq. No. 143757

Seq. ID LIB3168-031-P1-K1-H11



```
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  697
E value
                  8.0e-74
Match length
                  134
                  96
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  143758
Seq. No.
Seq. ID
                  LIB3168-031-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  g2842474
BLAST score
                  65
                  9.0e-29
E value
Match length
                  73
% identity
                  97
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
                   (ESSAII project)
                  143759
Seq. No.
Seq. ID
                  LIB3168-031-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g4204298
BLAST score
                  264
E value
                  4.0e-41
Match length
                  105
% identity
                  81
                   (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  143760
Seq. ID
                  LIB3168-031-P1-K1-H3
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  92
E value
                  8.0e-27
Match length
                  88
% identity
                  72
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143761
                  LIB3168-031-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  398
                  7.0e-39
E value
Match length
                  111
% identity
                  72
```

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE



PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870 (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No. 143762 Seq. ID LIB3168-031-P1-K1-H6 Method BLASTX NCBI GI g112682 BLAST score 337 E value 7.0e-32 83 Match length 77

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143763

% identity

Seq. ID LIB3168-031-P1-K1-H7

Method BLASTX NCBI GI g1628583 BLAST score 359 E value 2.0e-34 Match length 96 78 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

143764 Seq. No.

Seq. ID LIB3168-031-P1-K1-H9

Method BLASTX NCBI GI g112682 BLAST score 444 2.0e-44 E value Match length 101 82 % identity

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir \$08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

143765 Seq. No.

Seq. ID LIB3168-032-P1-K1-A1

Method BLASTX NCBI GI q4558669 BLAST score 625 E value 2.0e-65 Match length 125 % identity

NCBI Description (AC007063) putative vanadate resistance protein

[Arabidopsis thaliana]

E value

Match length

% identity

5.0e-45

132

73



Seq. No. 143766 Seq. ID LIB3168-032-P1-K1-A11 Method BLASTX NCBI GI q1628583 BLAST score 82 E value 1.1e-01 Match length 77 100 % identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 143767 Seq. No. Seq. ID LIB3168-032-P1-K1-A3 Method BLASTX NCBI GI g1628583 BLAST score 633 E value 2.0e-66 Match length 125 % identity 98 NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143768 Seq. ID LIB3168-032-P1-K1-A5 Method BLASTX g4033349 NCBI GI BLAST score 596 E value 5.0e-62 Match length 130 % identity 89 (AJ223496) phosphoenolpyrovate carboxylase [Brassica NCBI Description juncea] Seq. No. 143769 Seq. ID LIB3168-032-P1-K1-A7 Method BLASTX NCBI GI g82051 BLAST score 290 4.0e-26 E value Match length 110 55 % identity lipid body-associated membrane protein - carrot NCBI Description >gi 259453 bbs 117620 (S47635) lipid body membrane protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide, 180 aa] [Daucus carota] Seq. No. 143770 Seq. ID LIB3168-032-P1-K1-A8 Method BLASTX NCBI GI g112681 BLAST score 451



NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143771

Seq. ID LIB3168-032-P1-K1-B1

Method BLASTX
NCBI GI g1769895
BLAST score 401
E value 4.0e-39
Match length 77
% identity 99

NCBI Description (X96598) CaLB protein [Arabidopsis thaliana]

Seq. No. 143772

Seq. ID LIB3168-032-P1-K1-B10

Method BLASTX
NCBI GI g119143
BLAST score 592
E value 2.0e-66
Match length 131
% identity 96

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_81606_pir__S06724 translation elongation factor eEF-1
alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
(X16430) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1369927_emb_CAA34454_ (X16431) elongation factor
1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_
(X16431) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana]
>gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana]
>gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

143773

Seq. ID LIB3168-032-P1-K1-B12

Method BLASTX
NCBI GI g112682
BLAST score 564
E value 3.0e-58
Match length 132
% identity 81

Seq. No.

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143774

Seq. ID LIB3168-032-P1-K1-B2

Method BLASTX
NCBI GI g1628583
BLAST score 49
E value 2.0e-69
Match length 138
% identity 97



NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143775

Seq. ID LIB3168-032-P1-K1-B3

Method BLASTX
NCBI GI g112682
BLAST score 757
E value 8.0e-81
Match length 143
% identity 100

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143776

Seq. ID LIB3168-032-P1-K1-B5

Method BLASTX
NCBI GI g2462756
BLAST score 411
E value 3.0e-40
Match length 94
% identity 86

NCBI Description (AC002292) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 143777

Seq. ID LIB3168-032-P1-K1-B6

Method BLASTX
NCBI GI g112681
BLAST score 584
E value 1.0e-60
Match length 135
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir \$08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143778

Seq. ID LIB3168-032-P1-K1-B7

Method BLASTN
NCBI GI g2342673
BLAST score 301
E value 1.0e-169
Match length 316
% identity 99

NCBI Description Sequence of BAC F7G19 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 143779

Seq. ID LIB3168-032-P1-K1-C1

Method BLASTX NCBI GI g1345840



```
BLAST score 280
E value 3.0e-45
Match length 134
% identity 64
```

NCBI Description CRUCIFERIN BNC1 PRECURSOR (11S GLOBULIN) (12S STORAGE PROTEIN) >gi_762919_emb_CAA41984_ (X59294) cruciferin

storage protein [Brassica napus]

Seq. No. 143780

Seq. ID LIB3168-032-P1-K1-C10

Method BLASTX
NCBI GI g416652
BLAST score 251
E value 2.0e-21
Match length 97
% identity 65

NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN

PCNT107) >gi 19793 emb CAA39707 (X56266) auxin-induced

protein [Nicotiana tabacum]

Seq. No. 143781

Seq. ID LIB3168-032-P1-K1-C11

Method BLASTN
NCBI GI g3789706
BLAST score 227
E value 1.0e-124
Match length 408
% identity 100

NCBI Description Arabidopsis thaliana chromosome 1 BAC F15K9 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 143782

Seq. ID LIB3168-032-P1-K1-C3

Method BLASTX
NCBI GI g4006881
BLAST score 522
E value 3.0e-53
Match length 132
% identity 59

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 143783

Seq. ID LIB3168-032-P1-K1-C6

Method BLASTX
NCBI GI g3287679
BLAST score 688
E value 9.0e-73
Match length 139
% identity 100

NCBI Description (AC003979) T22J18.6 [Arabidopsis thaliana]

Seq. No. 143784

Seq. ID LIB3168-032-P1-K1-C7

Method BLASTX
NCBI GI g4006834
BLAST score 232
E value 9.0e-51



Match length 107 % identity 99

NCBI Description (AC005970) enoyl-ACP reductase (enr-A) [Arabidopsis

thaliana]

Seq. No. 143785

Seq. ID LIB3168-032-P1-K1-C9

Method BLASTX
NCBI GI g112682
BLAST score 476
E value 7.0e-48
Match length 105
% identity 86

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143786

Seq. ID LIB3168-032-P1-K1-D1

Method BLASTX
NCBI GI g135858
BLAST score 497
E value 3.0e-50
Match length 138
% identity 72

NCBI Description TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)

>gi_99760_pir__S22201 tonoplast intrinsic protein alpha Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551)
tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
[Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast

intrinsic protein alpha [Arabidopsis thaliana]

Seq. No. 143787

Seq. ID LIB3168-032-P1-K1-D10

Method BLASTX
NCBI GI g266693
BLAST score 245
E value 8.0e-21
Match length 121
% identity 50

NCBI Description OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis

thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_ (AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No. 143788

Seq. ID LIB3168-032-P1-K1-D2

Method BLASTX
NCBI GI g82051
BLAST score 369
E value 2.0e-35
Match length 141
% identity 52

NCBI Description lipid body-associated membrane protein - carrot





>qi 259453 bbs 117620 (S47635) lipid body membrane protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide, 180 aa] [Daucus carota]

143789 Seq. No.

Seq. ID LIB3168-032-P1-K1-D3

BLASTX Method NCBI GI q4678383 BLAST score 426 E value 5.0e-42 86 Match length

% identity 100

(AL049656) histone H2A.F/Z-like protein [Arabidopsis NCBI Description

thalianal

143790 Seq. No.

Seq. ID LIB3168-032-P1-K1-D5

Method BLASTN NCBI GI g4567300 BLAST score 273 E value 1.0e-152 Match length 297 % identity 97

Arabidopsis thaliana chromosome II P1 MHK10 genomic NCBI Description

sequence, complete sequence

Seq. No. 143791

Seq. ID LIB3168-032-P1-K1-D6

Method BLASTX g1628583 NCBI GI BLAST score 625 2.0e-65 E value Match length 120 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

143792 Seq. No.

Seq. ID LIB3168-032-P1-K1-D7

BLASTN Method NCBI GI g4757407 BLAST score 361 0.0e+00E value Match length 417 97 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MQD19, complete sequence

143793 Seq. No.

Seq. ID LIB3168-032-P1-K1-E1

BLASTX Method NCBI GI g1871174 BLAST score 373 E value 4.0e-39 Match length 107 % identity 71



```
NCBI Description (U90439) actin isolog [Arabidopsis thaliana]
```

 Seq. No.
 143794

 Seq. ID
 LIB3168-032-P1-K1-E12

 Method
 BLASTX

 NCBI GI
 g112737

NCBI GI g112737 BLAST score 561 E value 7.0e-58 Match length 135 % identity 81

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143795

Seq. ID LIB3168-032-P1-K1-E2

Method BLASTX
NCBI GI g112737
BLAST score 464
E value 2.0e-46
Match length 101
% identity 86

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143796

Seq. ID LIB3168-032-P1-K1-E3

Method BLASTN
NCBI GI 94757395
BLAST score 194
E value 1.0e-105
Match length 391
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21L13, complete sequence

Seq. No. 143797

Seq. ID LIB3168-032-P1-K1-E5

Method BLASTX
NCBI GI 94056502
BLAST score 603
E value 9.0e-63
Match length 126
% identity 92

NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No. 143798

Seq. ID LIB3168-032-P1-K1-E6



Method BLASTX
NCBI GI g633890
BLAST score 319
E yalue 2.0e-29
Match length 107
% identity 61

NCBI Description (S72926) glucose and ribitol dehydrogenase homolog [Hordeum

vulgare]

Seq. No. 143799

Seq. ID LIB3168-032-P1-K1-E9

Method BLASTN
NCBI GI g3063438
BLAST score 351
E value 0.0e+00
Match length 416
% identity 95

NCBI Description Complete sequence of Arabidopsis F22013, complete sequence

[Arabidopsis thaliana]

Seq. No. 143800

Seq. ID LIB3168-032-P1-K1-F10

Method BLASTN
NCBI GI g4006885
BLAST score 313
E value 1.0e-176
Match length 424
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 143801

Seq. ID LIB3168-032-P1-K1-F11

Method BLASTX
NCBI GI g1628583
BLAST score 49
E value 3.0e-63
Match length 132
% identity 95

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143802

Seq. ID LIB3168-032-P1-K1-F2

Method BLASTX
NCBI GI g112681
BLAST score 616
E value 3.0e-64
Match length 131
% identity 92

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.



```
Seq. No.
                   143803
Seq. ID
                  LIB3168-032-P1-K1-F5
                  BLASTX
Method
NCBI GI
                   g1628583
BLAST score
                   355
                   1.0e-34
E value
                   77
Match length
                   99
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   143804
Seq. ID
                  LIB3168-032-P1-K1-F6
Method
                  BLASTX
NCBI GI
                   g21913
BLAST score
                   187
                   5.0e-14
E value
                   77
Match length
% identity
                   44
                  (X62626) vicilin [Theobroma cacao]
NCBI Description
Seq. No.
                  143805
Seq. ID
                  LIB3168-032-P1-K1-F8
Method
                  BLASTX
NCBI GI
                   q4325344
BLAST score
                   669
                   2.0e-70
E value
Match length
                   127
                   99
% identity
                   (AF128393) similar to beta-transducins (Pfam: PF00400,
NCBI Description
                  Score=71.7, E=1.5e-17, N=6) [Arabidopsis thaliana]
Seq. No.
                   143806
Seq. ID
                  LIB3168-032-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                   287
E value
                   1.0e-45
Match length
                   108
                   88
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143807
                  LIB3168-032-P1-K1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3128143
BLAST score
                  118
E value
                  1.0e-59
Match length
                   327
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTI20, complete sequence [Arabidopsis thaliana]
```

1.

143808



```
LIB3168-032-P1-K1-G12
Seq. ID
                  BLASTX
Method
                  g4741940
NCBI GI
                  554
BLAST score
                  5.0e-57
E value
Match length
                  101
% identity
                  66
                  (AF134120) Lhca2 protein [Arabidopsis thaliana]
NCBI Description
                  143809
Seq. No.
Seq. ID
                  LIB3168-032-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q2499535
                  201
BLAST score
                  1.0e-15
E value
Match length
                  44
% identity
                  82
                  2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi 595681
NCBI Description
                  (U13238) 2-oxoglutarate/malate translocator [Spinacia
                  oleracea]
Seq. No.
                  143810
Seq. ID
                  LIB3168-032-P1-K1-G3
Method
                  BLASTX
                  g2245130
NCBI GI
                  254
BLAST score
                  7.0e-22
E value
Match length
                  140
% identity
                  44
                  (Z97344) GLABRA2 homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  143811
                  LIB3168-032-P1-K1-G5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g16472
                  398
BLAST score
                  0.0e + 00
E value
Match length
                  418
                  99
% identity
NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type
Seq. No.
                  143812
Seq. ID
                  LIB3168-032-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  661
                  1.0e-69
E value
Match length
                  128
                  99
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  143813
Seq. No.
Seq. ID
                  LIB3168-032-P1-K1-G9
```

Method BLASTX NCBI GI g1628583



```
BLAST score
                  2.0e-65
E value
                  120
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143814
Seq. ID
                  LIB3168-032-P1-K1-H10
                  BLASTX
Method
                  q4204298
NCBI GI
BLAST score
                  525
                  1.0e-53
E value
                  120
Match length
                  85
% identity
```

(AC003027) lcl_prt seq No definition line found NCBI Description [Arabidopsis thaliana]

Seq. ID LIB3168-032-P1-K1-H12 Method BLASTX q633890 NCBI GI BLAST score 287 8.0e-26 E value 88 Match length

Seq. No.

65 % identity (S72926) glucose and ribitol dehydrogenase homolog [Hordeum NCBI Description vulgare]

143816 Seq. No. Seq. ID LIB3168-032-P1-K1-H2 Method BLASTX

143815

NCBI GI g112682 BLAST score 337 2.0e-65 E value Match length 141 87 % identity

12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis tha \overline{l} iana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

143817 Seq. No.

Seq. ID LIB3168-032-P1-K1-H3

Method BLASTX NCBI GI g1362003 BLAST score 729 1.0e-77 E value Match length 141 % identity 100

protein phosphatase 2A B regulatory chain 55K - Arabidopsis NCBI Description thaliana >qi 710330 (U18129) 55 kDa B regulatory subunit of

phosphatase 2A [Arabidopsis thaliana]

Seq. No. 143818



LIB3168-032-P1-K1-H5 Seq. ID BLASTX Method NCBI GI g3157937 BLAST score 644 E value 1.0e-67 Match length 128 97 % identity (AC002131) Identical to aspartic proteinase cDNA gb U51036 NCBI Description from A. thaliana. ESTs gb N96313, gb T21893, gb $R3\overline{0}158$, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb T44552, gb T22542, gb T76533, gb T44350, gb Z34591, gb AA728734, gb Seq. No. 143819 Seq. ID LIB3168-032-P1-K1-H6 Method BLASTN NCBI GI q3849811 BLAST score 355 0.0e+00E value Match length 391 % identity 98 NCBI Description Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana] 143820 Seq. No. Seq. ID LIB3168-032-P1-K1-H8 Method BLASTN NCBI GI g16473 BLAST score 411 0.0e+00E value 419 Match length % identity 100 NCBI Description Arabidopsis thaliana 25S-18S ribosomal DNA spacer 143821 Seq. No. Seq. ID LIB3168-032-P1-K1-H9 BLASTX Method NCBI GI q3128168 BLAST score 593 1.0e-61 E value 140 Match length 73-% identity (AC004521) putative carboxyl-terminal peptidase NCBI Description [Arabidopsis thaliana]

Seq. No. 143822

Seq. ID LIB3168-033-P1-K1-A1

Method BLASTX g112681 NCBI GI BLAST score 564 E value 3.0e-58 Match length 132 % identity 83

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

BLAST score

Match length

E value

414

87

9.0e-41



storage protein [Arabidopsis thaliana]

143823 Seq. No. Seq. ID LIB3168-033-P1-K1-A10 BLASTX Method NCBI GI g2129657 BLAST score 293 2.0e-26 E value Match length 88 % identity 72 NCBI Description oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin [Arabidopsis thaliana] Seq. No. 143824 Seq. ID LIB3168-033-P1-K1-A2 Method BLASTX NCBI GI g3421123 BLAST score 598 3.0e-62 E value Match length 116 % identity 99 (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis NCBI Description thaliana] 143825 Seq. No. Seq. ID LIB3168-033-P1-K1-A3 Method BLASTX g1628583 NCBI GI BLAST score 622 E value 5.0e-65 Match length 120 99 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143826 Seq. ID LIB3168-033-P1-K1-A5 BLASTX Method NCBI GI g1628583 BLAST score 625 E value 2.0e-65 Match length 120 % identity 100 NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143827 Seq. ID LIB3168-033-P1-K1-A7 BLASTX Method NCBI GI q112682



% identity 90 NCBI Description 12S

12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143828

Seq. ID LIB3168-033-P1-K1-A8

Method BLASTX
NCBI GI g1169544
BLAST score 668
E value 2.0e-70
Match length 135

% identity 99

NCBI Description ERD1 PROTEIN PRECURSOR >gi_541859_pir__JN0901 ERD1 protein

- Arabidopsis thaliana >gi_497629_dbj_BAA04506_ (D17582)

ERD1 protein [Arabidopsis thaliana]

Seq. No. 143829

Seq. ID LIB3168-033-P1-K1-A9

Method BLASTX
NCBI GI g1345973
BLAST score 488
E value 3.0e-49
Match length 106
% identity 83

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 143830

Seq. ID LIB3168-033-P1-K1-B10

Method BLASTN
NCBI GI g2264313
BLAST score 405
E value 0.0e+00
Match length 405
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOP10, complete sequence [Arabidopsis thaliana]

Seq. No. 143831

Seq. ID LIB3168-033-P1-K1-B11

Method BLASTX
NCBI GI g82220
BLAST score 556
E value 3.0e-57
Match length 137
% identity 83

NCBI Description hypothetical protein 581 - common tobacco chloroplast

E value

Match length

1.0e-62

132



>gi 225240_prf__1211235BY ORF 581 [Nicotiana tabacum]

143832 Seq. No. LIB3168-033-P1-K1-B2 Seq. ID Method BLASTX NCBI GI g2213615 BLAST score 461 4.0e-46 E value Match length 136 % identity 59 (AC000103) F21J9.9 [Arabidopsis thaliana] NCBI Description Seq. No. 143833 LIB3168-033-P1-K1-B3 Seq. ID Method BLASTX NCBI GI q112682 BLAST score 535 E value 8.0e-55 Match length 129 80 % identity 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description cruciferin precursor (CRB) - Arabidopsis thaliana >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 143834 Seq. ID LIB3168-033-P1-K1-B4 Method BLASTX g1628583 NCBI GI BLAST score 625 2.0e-65 E value Match length 120 100 % identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 143835 Seq. No. LIB3168-033-P1-K1-B5 Seq. ID BLASTX Method NCBI GI g1628583 BLAST score 625 2.0e-65 E value Match length 120 100 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 143836 Seq. No. Seq. ID LIB3168-033-P1-K1-B6 Method BLASTX NCBI GI g4454051 BLAST score 601



% identity 86

NCBI Description (AL035394) putative polygalacturonase [Arabidopsis

thaliana]

Seq. No. 143837

Seq. ID LIB3168-033-P1-K1-B7

Method BLASTX
NCBI GI g1628583
BLAST score 652
E value 1.0e-68
Match length 127
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143838

Seq. ID LIB3168-033-P1-K1-B8

Method BLASTX
NCBI GI g112681
BLAST score 513
E value 3.0e-52
Match length 102
% identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143839

Seq. ID LIB3168-033-P1-K1-B9

Method BLASTX
NCBI GI g112741
BLAST score 604
E value 6.0e-63
Match length 128
% identity 89

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit

Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712 emb_CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143840

Seq. ID LIB3168-033-P1-K1-C1

Method BLASTN
NCBI GI g4263694
BLAST score 391
E value 0.0e+00
Match length 411
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F22D22 genomic

sequence, complete sequence [Arabidopsis thaliana]



143841 Seq. No. Seq. ID LIB3168-033-P1-K1-C10 BLASTX Method g1628583 NCBI GI BLAST score 653 1.0e-68 E value 127 Match length % identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143842

Seq. ID LIB3168-033-P1-K1-C11

Method BLASTN
NCBI GI g3047074
BLAST score 323
E value 0.0e+00
Match length 379
% identity 99

NCBI Description Arabidopsis thaliana BAC F21E10

Seq. No. 143843

Seq. ID LIB3168-033-P1-K1-C12

Method BLASTX
NCBI GI g3894178
BLAST score 270
E value 9.0e-24
Match length 57
% identity 88

NCBI Description (AC005312) putative nucleic acid binding protein

[Arabidopsis thaliana]

Seq. No. 143844

Seq. ID LIB3168-033-P1-K1-C2

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143845

Seq. ID LIB3168-033-P1-K1-C3

Method BLASTX
NCBI GI g4467123
BLAST score 162
E value 4.0e-11
Match length 108
% identity 34

NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No. 143846

Seq. ID LIB3168-033-P1-K1-C4



Method BLASTX
NCBI GI g1628583
BLAST score 46
E value 2.0e-60

E value 2.0e-6 Match length 134 % identity 90

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143847

Seq. ID LIB3168-033-P1-K1-C5

Method BLASTN
NCBI GI g2980787
BLAST score 341
E value 0.0e+00
Match length 407
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2

(ESSAII project)

Seq. No. 143848

Seq. ID LIB3168-033-P1-K1-C6

Method BLASTX
NCBI GI g112682
BLAST score 444
E value 4.0e-44
Match length 99
% identity 86

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143849

Seq. ID LIB3168-033-P1-K1-C7

Method BLASTX
NCBI GI g4490732
BLAST score 354
E value 1.0e-33
Match length 97
% identity 74

NCBI Description (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like

protein [Arabidopsis thaliana]

Seq. No. 143850

Seq. ID LIB3168-033-P1-K1-C9

Method BLASTX
NCBI GI g112743
BLAST score 600
E value 2.0e-62
Match length 111
% identity 98

NCBI Description 2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor -

Arabidopsis thaliana >gi 166617 (M22033) albumin 2S subunit



4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

143851 Seq. No. Seq. ID LIB3168-033-P1-K1-D10 Method BLASTX NCBI GI g1628583 BLAST score 668 E value 2.0e-70 Match length 128 100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143852

Seq. ID LIB3168-033-P1-K1-D11

Method BLASTX
NCBI GI g3355468
BLAST score 411
E value 3.0e-40
Match length 123
% identity 74

NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis

thaliana]

Seq. No. 143853

Seq. ID LIB3168-033-P1-K1-D2

Method BLASTN
NCBI GI g3075383
BLAST score 205
E value 1.0e-111
Match length 410
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T1D16 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 143854

Seq. ID LIB3168-033-P1-K1-D3

Method BLASTN
NCBI GI g4589450
BLAST score 219
E value 1.0e-120
Match length 363
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

T31K7, complete sequence

Seq. No. 143855

Seq. ID LIB3168-033-P1-K1-D4

Method BLASTX
NCBI GI g112681
BLAST score 581
E value 3.0e-60
Match length 134

17779



% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143856

Seq. ID LIB3168-033-P1-K1-D6

Method BLASTX
NCBI GI g1628583
BLAST score 614
E value 4.0e-64
Match length 120
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143857

Seq. ID LIB3168-033-P1-K1-D7

Method BLASTX
NCBI GI g112681
BLAST score 684
E value 3.0e-72
Match length 132
% identity 98

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143858

Seq. ID LIB3168-033-P1-K1-D8

Method BLASTX
NCBI GI g4165488
BLAST score 548
E value 2.0e-56
Match length 101
% identity 100

NCBI Description (AJ132399) alpha-tubulin 3 [Hordeum vulgare]

Seq. No. 143859

Seq. ID LIB3168-033-P1-K1-D9

Method BLASTN
NCBI GI g1313927
BLAST score 45
E value 4.0e-16
Match length 190
% identity 83

NCBI Description B.oleracea mRNA for IFA binding protein (sp10)

Seq. No. 143860

Seq. ID LIB3168-033-P1-K1-E1

Method BLASTX NCBI GI g4263771



BLAST score 303 E value 1.0e-27 Match length 76 % identity 71 NCBI Description (AC0062

(AC006218) putative nonspecific lipid-transfer protein

precursor [Arabidopsis thaliana]

>gi_4726121_gb_AAD28321.1_AC006436_12 (AC006436) putative nonspecific lipid-transfer protein precursor [Arabidopsis

thaliana]

Seq. No. 143861

Seq. ID LIB3168-033-P1-K1-E10

Method BLASTX
NCBI GI g2129657
BLAST score 305
E value 7.0e-28
Match length 91
% identity 73

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
thaliana] >gi 987016 emb CAA90878_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 143862

Seq. ID LIB3168-033-P1-K1-E11

Method BLASTX
NCBI GI g112682
BLAST score 411
E value 2.0e-40
Match length 123
% identity 70

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143863

Seq. ID LIB3168-033-P1-K1-E12

Method BLASTX
NCBI GI g4539316
BLAST score 96
E value 5.0e-39
Match length 114
% identity 80

NCBI Description (AL035679) putative fructose-bisphosphate aldolase

[Arabidopsis thaliana]

Seq. No. 143864

Seq. ID LIB3168-033-P1-K1-E3

Method BLASTX
NCBI GI g1707364
BLAST score 266
E value 3.0e-23
Match length 110
% identity 41

NCBI Description (X94626) AATP2 [Arabidopsis thaliana]



Seq. No. 143865

Seq. ID LIB3168-033-P1-K1-E4

Method BLASTX
NCBI GI g112682
BLAST score 651
E value 2.0e-68
Match length 136
% identity 90

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143866

Seq. ID LIB3168-033-P1-K1-E5

Method BLASTX
NCBI GI g112741
BLAST score 700
E value 4.0e-74
Match length 130
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143867

Seq. ID LIB3168-033-P1-K1-E6

Method BLASTN
NCBI GI g2980757
BLAST score 314
E value 1.0e-176
Match length 314
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18

(ESSAII project)

Seq. No. 143868

Seq. ID LIB3168-033-P1-K1-E8

Method BLASTX
NCBI GI g112741
BLAST score 686
E value 2.0e-72
Match length 127
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]



Seq. No. 143869 Seq. ID LIB3168-033-P1-K1-E9 BLASTX Method g112682 NCBI GI

BLAST score 476 5.0e-48 E value 107 Match length % identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>qi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >qi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143870

Seq. ID LIB3168-033-P1-K1-F1

Method BLASTN g3450888 NCBI GI BLAST score 389 E value 0.0e + 00Match length 397 % identity 99

NCBI Description Arabidopsis thaliana 19S proteosome subunit 9 mRNA,

complete cds

Seq. No. 143871

Seq. ID LIB3168-033-P1-K1-F10

Method BLASTX NCBI GI g112737 BLAST score 533 1.0e-54 E value Match length 113 89 % identity

NCBI Description

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143872

Seq. ID LIB3168-033-P1-K1-F11

Method BLASTX NCBI GI g1628583 BLAST score 516 E value 1.0e-52 Match length 129 % identity 80

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

143873 Seq. No.

Seq. ID LIB3168-033-P1-K1-F12

Method BLASTN

17783



```
NCBI GI
                  q3292807
BLAST score
                  244
E value
                  1.0e-135
Match length
                  279
                  100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19
                  (ESSAII project)
                  143874
Seq. No.
Seq. ID
                  LIB3168-033-P1-K1-F3
```

Method BLASTX
NCBI GI g1550740
BLAST score 692
E value 3.0e-73
Match length 135
% identity 98

NCBI Description (Y07961) GDP-associated inhibitor [Arabidopsis thaliana]

Seq. No. 143875

Seq. ID LIB3168-033-P1-K1-F4

Method BLASTX
NCBI GI g2541876
BLAST score 239
E value 4.0e-20
Match length 138
% identity 35

NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein

[Nicotiana tabacum]

Seq. No. 143876

Seq. ID LIB3168-033-P1-K1-F5

Method BLASTX
NCBI GI g1628583
BLAST score 655
E value 7.0e-69
Match length 131
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143877

Seq. ID LIB3168-033-P1-K1-F6

Method BLASTN
NCBI GI g2564044
BLAST score 253
E value 1.0e-140
Match length 417
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19P17, complete sequence [Arabidopsis thaliana]

Seq. No. 143878

Seq. ID LIB3168-033-P1-K1-F7

Method BLASTX NCBI GI g1350680 BLAST score 688



E value 9.0e-73 Match length 134 % identity 99

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 143879

Seq. ID LIB3168-033-P1-K1-F8

Method BLASTX
NCBI GI g1172872
BLAST score 542
E value 1.0e-55
Match length 106
% identity 98

NCBI Description CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718

drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_

(D13042) thiol protease [Arabidopsis thaliana]

>gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible
cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No. 143880

Seq. ID LIB3168-033-P1-K1-F9

Method BLASTX
NCBI GI g112682
BLAST score 563
E value 4.0e-58
Match length 134
% identity 80

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143881

Seq. ID LIB3168-033-P1-K1-G1

Method BLASTX
NCBI GI g1628583
BLAST score 609
E value 2.0e-63
Match length 120
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143882

Seq. ID LIB3168-033-P1-K1-G11

Method BLASTX
NCBI GI g112681
BLAST score 46
E value 5.0e-26
Match length 60
% identity 86

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis



thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 143883

Seq. ID LIB3168-033-P1-K1-G12

Method BLASTX
NCBI GI g112681
BLAST score 591
E value 2.0e-61
Match length 137
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir _S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143884

Seq. ID LIB3168-033-P1-K1-G2

Method BLASTX
NCBI GI g112743
BLAST score 697
E value 8.0e-74
Match length 128
% identity 98

NCBI Description 2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68856_pir_ NWMU4 2S albumin 4 precursor Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit
4 precursor [Arabidopsis thaliana] >gi 395202 emb CAA80869_

(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4

precursor [Arabidopsis thaliana]

Seq. No. 143885

Seq. ID LIB3168-033-P1-K1-G3

Method BLASTX
NCBI GI g112737
BLAST score 669
E value 2.0e-70
Match length 138
% identity 91

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__ NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143886

Seq. ID LIB3168-033-P1-K1-G4

Method BLASTX
NCBI GI g112681
BLAST score 519
E value 6.0e-53
Match length 137
% identity 77



12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

143887 Seq. No.

Seq. ID LIB3168-033-P1-K1-G5

Method BLASTX NCBI GI q112739 BLAST score 415 E value 9.0e-41 Match length 108 % identity 76

2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -

Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi 395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 · [Arabidopsis thaliana]

>gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 143888

LIB3168-033-P1-K1-G6 Seq. ID

Method BLASTX NCBI GI g1107501 BLAST score 397 E value 1.0e-38 Match length 99 % identity 81

(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) NCBI Description

Match to gb X91954 orf gene product from A. thaliana. ESTs gb Z17604, gb H76594, gb_AA597972 and gb_AA394824 come from

this gene. [Arabidopsis thaliana]

143889 Seq. No.

Seq. ID LIB3168-033-P1-K1-G7

Method BLASTX g1817544 NCBI GI BLAST score 506 2.0e-51 E value 99 Match length % identity 100

NCBI Description (D83025) proline oxidase precursor [Arabidopsis thaliana]

143890 Seq. No.

Seq. ID LIB3168-033-P1-K1-G8

Method BLASTX g112737 NCBI GI BLAST score 540 2.0e-55 E value 131 Match length % identity 80

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870_



(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No. 143891 Seq. ID LIB3168-033-P1-K1-G9 Method BLASTN NCBI GI g4455321 BLAST score 210 E value 1.0e-114 Match length 387 % identity 100 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project) Seq. No. 143892 Seq. ID LIB3168-033-P1-K1-H12 Method BLASTN NCBI GI g16131 BLAST score 272 E value 1.0e-151 Match length 291 % identity 99 NCBI Description Arabidopsis thaliana genes for 5.8S rRNA and 25S rRNA with 18S rRNA fragment Seq. No. 143893 Seq. ID LIB3168-033-P1-K1-H2 Method BLASTX NCBI GI g1628583 BLAST score 426 4.0e-42 E value Match length 119 72 % identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 143894 Seq. ID LIB3168-033-P1-K1-H4 Method BLASTX NCBI GI g112737 BLAST score 280 6.0e-25 E value

Match length 124 52 % identity

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870 (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No. 143895

Seq. ID LIB3168-033-P1-K1-H7

Method BLASTX



NCBI GI g1628583 BLAST score 553 E value 6.0e-57 Match length 131 % identity 82

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143896

Seq. ID LIB3168-033-P1-K1-H8

Method BLASTX
NCBI GI g1628583
BLAST score 563
E value 4.0e-58
Match length 119
% identity 92

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143897

Seq. ID LIB3168-034-P1-K1-A1

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143898

Seq. ID LIB3168-034-P1-K1-A10

Method BLASTN
NCBI GI g2696018
BLAST score 283
E value 1.0e-158
Match length 396
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXC9, complete sequence [Arabidopsis thaliana]

Seq. No. 143899

Seq. ID LIB3168-034-P1-K1-A11

Method BLASTX
NCBI GI g2832674
BLAST score 686
E value 2.0e-72
Match length 137
% identity 100

NCBI Description (AL021712) fibrillin precursor-like protein [Arabidopsis

thaliana]

Seq. No. 143900

Seq. ID LIB3168-034-P1-K1-A12

17789



Method BLASTX
NCBI GI g112737
BLAST score 554
E value 5.0e-57
Match length 134
% identity 81

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143901

Seq. ID LIB3168-034-P1-K1-A2

Method BLASTX
NCBI GI g112737
BLAST score 613
E value 6.0e-64
Match length 134
% identity 88

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204 emb CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143902

Seq. ID LIB3168-034-P1-K1-A4

Method BLASTX
NCBI GI 94204298
BLAST score 521
E value 4.0e-53
Match length 100
% identity 99

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 143903

Seq. ID LIB3168-034-P1-K1-A5

Method BLASTX
NCBI GI g4006915
BLAST score 177
E value 8.0e-13
Match length 107
% identity 39

NCBI Description (299708) hypothetical protein [Arabidopsis thaliana]

Seq. No. 143904

Seq. ID LIB3168-034-P1-K1-A6

Method BLASTX
NCBI GI g3687228
BLAST score 45
E value 3.0e-68



Match length 138 % identity 94

NCBI Description (AC005169) putative malate dehydrogenase [Arabidopsis

thaliana]

Seq. No. 143905

Seq. ID LIB3168-034-P1-K1-A7

Method BLASTX
NCBI GI g112741
BLAST score 578
E value 7.0e-60
Match length 124
% identity 88

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143906

Seq. ID LIB3168-034-P1-K1-A8

Method BLASTN
NCBI GI 94376087
BLAST score 348
E value 0.0e+00
Match length 413
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 143907

Seq. ID LIB3168-034-P1-K1-A9

Method BLASTX
NCBI GI g1628583
BLAST score 423
E value 1.0e-41
Match length 122
% identity 75

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143908

Seq. ID LIB3168-034-P1-K1-B1

Method BLASTX
NCBI GI g112682
BLAST score 748
E value 8.0e-80
Match length 140
% identity 100

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >qi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]



92

% identity

NCBI Description

```
143909
Seq. No.
Seq. ID
                  LIB3168-034-P1-K1-B11
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  607
E value
                  3.0e-63
Match length
                  120
                  97
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143910
                  LIB3168-034-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  482
E value
                  1.0e-48
Match length
                  101
% identity
                  91
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143911
Seq. ID
                  LIB3168-034-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q1531762
BLAST score
                  195
                  6.0e-15
E value
Match length
                  51
% identity
                  75
                   (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
                  143912
Seq. No.
Seq. ID
                  LIB3168-034-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q3540180
BLAST score
                  699
                  5.0e-74
E value
Match length
                  135
% identity
                  99
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  143913
Seq. ID
                  LIB3168-034-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  91
                  6.0e-61
E value
Match length
                  131
```

12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

cruciferin precursor (CRA1) - Arabidopsis thaliana





thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

 Seq. No.
 143914

 Seq. ID
 LIB3168-034-P1-K1-B7

 Method
 BLASTX

 NCBI GI
 g2129657

 BLAST score
 433

 E value
 7.0e-43

 Match length
 116

Match length 116 % identity 78

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 143915

Seq. ID LIB3168-034-P1-K1-B8

Method BLASTX
NCBI GI g131150
BLAST score 714
E value 8.0e-76
Match length 136
% identity 94

NCBI Description PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2

>gi_81515_pir__S00445 photosystem I protein A2 - spinach chloroplast >gi_12271_emb_CAA27745_ (X04131) psaB gene product (aa 1-734) P700 chlorophyll a apoprotein [Spinacia oleracea] >gi_225422_prf__1303218B gene psaB [Spinacia

oleracea]

Seq. No. 143916

Seq. ID LIB3168-034-P1-K1-B9

Method BLASTN
NCBI GI g2645198
BLAST score 45
E value 4.0e-16
Match length 162
% identity 83

NCBI Description Arabidopsis thaliana chromosome I BAC T26J12 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 143917

Seq. ID LIB3168-034-P1-K1-C1

Method BLASTX
NCBI GI g112741
BLAST score 424
E value 4.0e-42
Match length 81
% identity 99

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]



```
Seq. No.
                  143918
Seq. ID
                  LIB3168-034-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g82051
BLAST score
                  333
E value
                  4.0e-31
Match length
                  125
% identity
NCBI Description
                  lipid body-associated membrane protein - carrot
                  >gi_259453_bbs_117620 (S47635) lipid body membrane
                  protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide,
                  180 aa] [Daucus carota]
                  143919
Seq. No.
Seq. ID
                  LIB3168-034-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  619
E value
                  1.0e-64
Match length
                  120
                  99
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  143920
                  LIB3168-034-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                   621
E value
                   5.0e-65
Match length
                   119
% identity
                   100
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   143921
                  LIB3168-034-P1-K1-C3
Seq. ID
Method
                  BLASTX
                   q1628583
NCBI GI
BLAST score
                   616
E value
                   3.0e-64
                   120
Match length
                   98
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
```

cruciferin seed storage protein [Arabidopsis thaliana]

143922 Seq. No.

LIB3168-034-P1-K1-C4 Seq. ID

BLASTX Method NCBI GI g2129773 BLAST score 580 4.0e-60 E value 108 Match length



% identity 100

NCBI Description xyloglucan endotransglycosylase-related protein XTR3 -

Arabidopsis thaliana (fragment) >gi_1244752 (U43485) xyloglucan endotransglycosylase-related protein

[Arabidopsis thaliana]

Seq. No. 143923

Seq. ID LIB3168-034-P1-K1-C6

Method BLASTX
NCBI GI g1628583
BLAST score 332
E value 5.0e-31
Match length 74
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143924

Seq. ID LIB3168-034-P1-K1-C8

Method BLASTX
NCBI GI g3540180
BLAST score 706
E value 7.0e-75
Match length 135
% identity 100

NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 143925

Seq. ID LIB3168-034-P1-K1-C9

Method BLASTX
NCBI GI g112741
BLAST score 277
E value 1.0e-24
Match length 123
% identity 53

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir_ NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201 emb CAA80868

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 143926

Seq. ID LIB3168-034-P1-K1-D1

Method BLASTX
NCBI GI 94115388
BLAST score 670
E value 1.0e-70
Match length 129
% identity 95

NCBI Description (AC005967) putative prolylcarboxypeptidase [Arabidopsis

thaliana]

Seq. No. 143927

Seq. ID LIB3168-034-P1-K1-D10



Method BLASTX
NCBI GI g119350
BLAST score 696
E value 1.0e-73
Match length 136
% identity 99

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase

[Arabidopsis thaliana]

>gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase
(2-phospho-D-glycerate hydroylase);identical to P25696

[Arabidopsis thaliana]

Seq. No. 143928

Seq. ID LIB3168-034-P1-K1-D12

Method BLASTX
NCBI GI g112681
BLAST score 571
E value 5.0e-59
Match length 132
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 143929

Seq. ID LIB3168-034-P1-K1-D2

Method BLASTX
NCBI GI g112737
BLAST score 528
E value 5.0e-54
Match length 112
% identity 89

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit

Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 143930

Seq. ID LIB3168-034-P1-K1-D3

Method BLASTX
NCBI GI g2352492
BLAST score 706
E value 7.0e-75
Match length 136
% identity 100

NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis

thaliana] >gi_2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]



143931 Seq. No. Seq. ID

LIB3168-034-P1-K1-D4

BLASTX Method NCBI GI g112739 BLAST score 450 7.0e-45 E value Match length 127 72 % identity

2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 143932

Seq. ID LIB3168-034-P1-K1-D5

Method BLASTX NCBI GI g1628583 BLAST score 556 E value 3.0e-57 Match length 139 79 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 143933

LIB3168-034-P1-K1-D7 Seq. ID

Method BLASTX NCBI GI g112681 555 BLAST score 4.0e-57 E value Match length 130 83 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

143934 Seq. No.

LIB3168-034-P1-K1-D9 Seq. ID

Method BLASTX NCBI GI q2244750 BLAST score 591 2.0e-61 E value Match length 126 89 % identity

(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] NCBI Description

>gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase

[Arabidopsis thaliana]

Seq. No. 143935

LIB3168-034-P1-K1-E1 Seq. ID

Method BLASTX